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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

## NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

### 1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such  
5 polynucleotides, along with uses for these polynucleotides and proteins, for example in  
therapeutic, diagnostic and research methods.

### 2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as  
10 lymphokines, interferons, circulating soluble factors, chemokines, and interleukins) has matured  
rapidly over the past decade. The now routine hybridization cloning and expression cloning  
techniques clone novel polynucleotides "directly" in the sense that they rely on information  
directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in  
the case of hybridization cloning; activity of the protein in the case of expression cloning). More  
15 recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA  
sequences based on the presence of a now well-recognized secretory leader sequence motif, as  
well as various PCR-based or low stringency hybridization-based cloning techniques, have  
advanced the state of the art by making available large numbers of DNA/amino acid sequences  
for proteins that are known to have biological activity, for example, by virtue of their secreted  
20 nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of  
PCR-based techniques, or by virtue of structural similarity to other genes of known biological  
activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for  
example, diagnostics, forensics, gene mapping; identification of mutations responsible for  
25 genetic disorders or other traits, to assess biodiversity, and to produce many other types of data  
and products dependent on DNA and amino acid sequences.

### 3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel  
30 isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules,  
cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic  
variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more  
epitopes present on such polypeptides, as well as hybridomas producing such antibodies.



The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

5 The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-5497. The polypeptides sequences are designated SEQ  
10 ID NO: 5498-10994. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, \* corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that  
15 hybridize to the complement of SEQ ID NO: 1-5497 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-5497. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ  
20 ID NO: 1-5497 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-5497. The sequence information can be a segment of any one of SEQ ID NO: 1-5497 that uniquely identifies or represents the sequence  
25 information of SEQ ID NO: 1-5497.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed  
30 to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their  
35 reverse or direct complements) according to the invention have numerous applications in a variety

of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

5 In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-5497 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-5497 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath  
10 et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-5497; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-5497;  
15 and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-5497. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-5497; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing  
20 (e.g., SEQ ID NO: 5498-10994); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

25 The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-5497; or (b) polynucleotides that hybridize to the complement of the  
30 polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably

produced by recombinant means using the genetically engineered cells (*e.g.* host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the  
5 polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of  
10 interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex  
15 and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and  
20 monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds  
25 that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a  
30 polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound that binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the  
35 administration of the polynucleotides or polypeptides of the invention to individuals exhibiting

symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in the sequence listing). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

#### 4. DETAILED DESCRIPTION OF THE INVENTION

##### 4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100

nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-5497.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-5497. The sequence information can be a segment of any one of SEQ ID NO: 1-5497 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-5497. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because  $4^{20}$  possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ( $1/4^{25}$ ) times the increased probability for mismatch at each nucleotide position ( $3 \times 25$ ). The probability that an

eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

5 The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic  
10 elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

15 The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino  
20 acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that  
25 have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

30 The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue  
35 may be removed from the protein during processing in the cell. The peptide may be produced



synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

5 The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

10 The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

15 Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of  
20 any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of  
25 similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and  
30 glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using  
35 recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

10 The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural

or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (*e.g.* Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*,

washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for  
5 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse  
10 functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less).  
15 Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this  
20 embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably  
25 at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence  
30 identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation  
35 of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be

disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

5 The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction  
10 of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the  
15 suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the  
20 context dictates otherwise.

## 4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the  
25 nucleotide sequences of SEQ ID NO: 1-5497; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 5498-10994; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 5498-10994. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of  
30 the nucleotides sequences of SEQ ID NO: 1-5497; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 5498-10994.  
35 Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in

receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-5497 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-5497 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-5497 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-5497, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most

preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-5497, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-5497 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-5497 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the

polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression



of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more  
5 domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization  
10 conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-5497, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also  
15 included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, *e.g.*,  
20 plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression  
25 vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-5497 or a fragment thereof or any  
30 other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-5497 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example,  
35 a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example.

Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia).

- 5 Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many  
10 suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed  
15 (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine  
20 kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct  
25 transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the  
30 periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination  
35 signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

#### 4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-5497, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO: 5498-10994 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-5497 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-5497), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

5       The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of  
10   an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified  
15   such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the  
20   control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an *an*omeric nucleic acid molecule. An *an*omeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual *an*omeric units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The  
25   antisense nucleic acid molecule can also comprise a 2'-*o*-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

#### 4.4 RIBOZYMES AND PNA MOIETIES

30       In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit  
35   translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-5497). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-5497 (see, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and  
5 Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical  
10 structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or  
15 solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral  
20 backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For  
25 example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or  
30 primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug  
35 delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

#### 4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3



cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultschi et al., each of which is incorporated by reference herein in its entirety.

#### 4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 5498-10994 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-5497 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-5497 or

- (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 5498-10994 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 5498-10994 or the corresponding full length or mature protein; and
- 5 "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity.
- 10 Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 5498-10994.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

15

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

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Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

30 The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

35

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

5 The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either  
10 cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 5498-10994.

15 The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or  
20 deliberately engineered. For example, modifications in the peptide or DNA sequence can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the  
25 molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved  
30 systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

35 Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing  
5 an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present  
10 invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification  
15 of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form that will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His-tag. Kits for expression and purification of such fusion proteins are commercially available  
20 from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other  
30 aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

#### 4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

#### 4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active  
5 portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to  
10 the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which  
15 the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*.  
20 The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays  
25 to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for  
30 appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can  
35 subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for



example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked  
5 in-frame to the protein of the invention.

#### 4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal  
10 activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example,  
15 Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or  
20 artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease  
25 states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be  
30 inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*,  
5 by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and  
10 PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard  
15 selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to  
20 replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or  
25 protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene  
30 under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally  
35 occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the

5 property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial

10 xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436

15 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or

20 inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be

25 prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and

30 PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even

35 replacing the homologous promoter to provide for increased protein expression. The

homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, *e.g.*, homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

#### 4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or

5 polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or

10 indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation

15 or in one of the other physiological pathways described herein.

#### 4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

20 protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic

25 disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as

30 an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of

35 the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its  
5 receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

10 Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch  
15 and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

#### 4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional  
20 sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the  
25 polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

#### 4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

30 A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one  
35 or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK,

- 5 HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in  
10 Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation,  
15 Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- $\gamma$ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells  
20 include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse  
25 and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1  
30 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in  
35 Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

- Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### 4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder



layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

5 Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and  
10 identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be  
15 used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In  
20 addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated  
25 cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al.,  
30 Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

*In vitro* cultures of stem cells can be used to determine if the polypeptide of the invention  
35 exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

#### 4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

- Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

#### 4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

- A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

- A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions that may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

5       A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

10       A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No.  
15   WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

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#### 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A  
25   protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More  
30   specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be  
5 sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

10 The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et  
15 al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune  
20 diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self-tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production  
25 of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine  
30 experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (*e.g.*, a B lymphocyte antigen function), as a means  
35 of up regulating immune responses, may also be useful in therapy. Upregulation of immune

responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

5           Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected  
10       cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

          A polypeptide of the present invention may provide the necessary stimulation signal to T  
15       cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and  $\beta_2$  microglobulin protein or an MHC class II alpha chain  
20       protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as  
25       the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

          The activity of a protein of the invention may, among other means, be measured by the  
30       following methods:

          Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;  
35       Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA



78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bowman et al., *J. Virology* 61:1992-1998; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

- 5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. *Immunol.* 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1  
10 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

- Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3,  
15 In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

- Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in:  
20 Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation*  
25 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research*  
30 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* 84:111-117, 1994; Fine et

al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

#### 4.10.8 ACTIVIN/INHIBIN ACTIVITY

5 A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention,  
10 alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as  
15 a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

20 The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci.  
25 USA 83:3091-3095, 1986.

#### 4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils,  
30 T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other  
35 trauma to tissues, as well as in treatment of localized infections. For example, attraction of

lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

- 5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

- 10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines  
15 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

#### 20 4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

- A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events  
25 in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

- 30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### 35 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention  
5 may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation,  
10 inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma,  
15 acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including  
20 bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma,  
25 tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically  
30 effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a  
35 portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or

modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D,

5 Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate  
10 (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

15 In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (*e.g.* exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

20 *In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30  
25 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available,  
30 *e.g.* from American Type Tissue Culture Collection catalogs.

#### 4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the  
35 invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors

and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen  
5 recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

10 The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28,  
15 Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a  
20 ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the  
25 present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent  
30 molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

#### 4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the  
35 novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques.

The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the

art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

#### 4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The responses of the two cell populations to the addition of ligand(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then



be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

#### 4.10.15 ANTI-INFLAMMATORY ACTIVITY

5 Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production  
10 of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or  
15 chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid  
20 arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

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#### 4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia,  
30 acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

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#### 4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- 10 (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord  
15 infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- 20 (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the  
25 nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to  
30 diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or  
35 injured by a demyelinating disease including but not limited to multiple sclerosis, human

immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

#### 4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye

color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or  
5 elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other  
10 than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or  
15 entity which is cross-reactive with such protein.

#### 4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis  
20 and treatment. Such polymorphisms may be associated with, *e.g.*, differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes  
25 possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the  
30 polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately  
35 adjacent to the position of the polymorphism is extended with one or more labeled nucleotides).

In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified  
5 nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*,  
10 by an antibody specific to the variant sequence.

#### 4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis are determined in an experimental animal model system. The experimental model  
15 system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, *Science*, 219:56, or by B. Waksman et al., 1963, *Int. Arch. Allergy Appl. Immunol.*, 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed *Mycobacterium tuberculosis* in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant  
20 mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed *Mycobacterium tuberculosis* in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and  
25 24 days after injection of *Mycobacterium* CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

#### 30 4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

#### 4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01  $\mu\text{g/kg}$  to 100 mg/kg of body weight, with the preferred dose being about 0.1  $\mu\text{g/kg}$  to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

#### 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents

include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance  
5 the activity of the protein or other active ingredient or complement its activity or use in  
treatment. Such additional factors and/or agents may be included in the pharmaceutical  
composition to produce a synergistic effect with protein or other active ingredient of the  
invention, or to minimize side effects. Conversely, protein or other active ingredient of the  
present invention may be included in formulations of the particular clotting factor, cytokine,  
10 lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-  
inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other  
hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as  
IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein  
of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or  
15 complexes with itself or other proteins. As a result, pharmaceutical compositions of the  
invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention  
including a first protein, a second protein or a therapeutic agent may be concurrently  
administered with the first protein (*e.g.*, at the same time, or at differing times provided that  
20 therapeutic concentrations of the combination of agents is achieved at the treatment site).  
Techniques for formulation and administration of the compounds of the instant application may  
be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest  
edition. A therapeutically effective dose further refers to that amount of the compound sufficient  
to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the  
25 relevant medical condition, or an increase in rate of treatment, healing, prevention or  
amelioration of such conditions. When applied to an individual active ingredient, administered  
alone, a therapeutically effective dose refers to that ingredient alone. When applied to a  
combination, a therapeutically effective dose refers to combined amounts of the active  
ingredients that result in the therapeutic effect, whether administered in combination, serially or  
30 simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically  
effective amount of protein or other active ingredient of the present invention is administered to  
a mammal having a condition to be treated. Protein or other active ingredient of the present  
invention may be administered in accordance with the method of the invention either alone or in  
35 combination with other therapies such as treatments employing cytokines, lymphokines or other

hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

#### 4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

#### 4.12.2 COMPOSITIONS/FORMULATIONS



Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate

to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use

in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may

be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B-lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01  $\mu\text{g}$  to about 100 mg (preferably about 0.1  $\mu\text{g}$  to about 10 mg, more preferably about 0.1  $\mu\text{g}$  to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systemically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally

capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above-mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue  
5 regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution  
10 and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

15 Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of  
20 proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

#### 4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include  
25 compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in  
30 the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the  $IC_{50}$  as determined in cell culture (*i.e.*, the concentration of

the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD<sub>50</sub> (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD<sub>50</sub> and ED<sub>50</sub>. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED<sub>50</sub> with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen that maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.



#### 4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

#### 4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen-binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$ ,  $F_{ab}'$  and  $F_{(ab)2}$  fragments, and an  $F_{ab}$  expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG<sub>1</sub>, IgG<sub>2</sub>, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of any of the full length proteins of the invention, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region on the surface of the protein of the invention, *e.g.*, a hydrophilic

region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

#### 5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of

adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (*The Scientist*, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

### 5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen-binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the

culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or

myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

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### 5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

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### 5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell  
5 hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by  
10 transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by  
15 introducing human immunoglobulin loci into transgenic animals, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126;  
20 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals  
25 which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast  
30 artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse<sup>TM</sup> as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B  
35 cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from

the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

#### 5.13.4 F<sub>ab</sub> Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F<sub>ab</sub> expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F<sub>ab</sub> fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F<sub>(ab')<sub>2</sub></sub> fragment produced by pepsin digestion of an antibody molecule; (ii) an F<sub>ab</sub> fragment generated

by reducing the disulfide bridges of an  $F_{(ab)2}$  fragment; (iii) an  $F_{ab}$  fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv)  $F_v$  fragments.

### 5.13.5 Bispecific Antibodies

5 Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the  
10 recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct  
15 bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion  
20 preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable  
25 host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the  
30 CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for  
35 increasing the yield of the heterodimer over other unwanted end-products such as homodimers.



Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.*  $F(ab')_2$  bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate  $F(ab')_2$  fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody  $F(ab')_2$  molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain ( $V_H$ ) connected to a light-chain variable domain ( $V_L$ ) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the  $V_H$  and  $V_L$  domains of one fragment are forced to pair with the complementary  $V_L$  and  $V_H$  domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

#### 5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptoputyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

#### 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can

be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*, 3: 219-230 (1989).

### 5.13.8 Immunoconjugates

5 The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been  
10 described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin,  
15 mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include  $^{212}\text{Bi}$ ,  $^{131}\text{I}$ ,  $^{131}\text{In}$ ,  $^{90}\text{Y}$ , and  $^{186}\text{Re}$ .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP),  
20 iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a  
25 ricin immunotoxin can be prepared as described in Vitetta et al., *Science*, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such  
30 streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn conjugated to a cytotoxic agent.

## 35 4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-5497 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-5497 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited

to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

#### 4.15 TRIPLE HELIX FORMATION

5 In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see 10 Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA 15 molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

#### 4.16 DIAGNOSTIC ASSAYS AND KITS

20 The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise 25 contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed 30 polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a 35 polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

5 Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard,  
10 T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the  
15 present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a  
20 sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present  
25 invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to  
30 another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which  
35 contain the reagents used to detect the bound antibody or probe. Types of detection reagents

include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the  
5 established kit formats which are well known in the art.

#### 4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (*e.g.*, where the polypeptide of the  
10 invention is involved in the immune response, for imaging sites of inflammation or infection). See, *e.g.*, Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

15

#### 4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:  
20 1-5497, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

(a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and

(b) determining whether the agent binds to said protein or said nucleic acid.

25

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

30

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.



Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene  
5 sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such  
10 methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

15 The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by  
20 the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed  
25 antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs  
30 of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation  
35 by binding to DNA or RNA. Such agents can be based on the classic phosphodiester,

ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see  
5 Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into  
10 polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents that bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the  
15 present invention can be formulated using known techniques to generate a pharmaceutical composition.

#### 4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid  
20 hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-5497. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-5497 can be used as an indicator of the presence of RNA of cell type of such a tissue  
25 in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The  
30 probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes  
35 *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA

polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

#### 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups ( $>NH$ ) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) *Anal. Biochem.* 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) *Nucleic Acids Res.* 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm<sub>7</sub>), is then added to a final concentration of 10 mM 1-MeIm<sub>7</sub>. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm<sub>7</sub>, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, *e.g.*, Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be

employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

#### 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of

these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI\*\*), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI\*\* digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI\*\* restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

#### 4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm<sup>2</sup>, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the

subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

- 5 Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm<sup>2</sup> and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers *e.g.* a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic  
10 strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader  
15 aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon  
20 consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

## 5.0 EXAMPLES

### 25 5.1 EXAMPLE 1

#### Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The  
30 inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Rapid  
5 Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

## 5.2 EXAMPLE 2

### Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from  
10 a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-5497 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases  
15 (*i.e.*, Hyseq's database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 103, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score  
20 greater than 300 and percent identity greater than 95%.

The novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-5497) of the present invention are incorporated in the attached Sequence Listing. A subset of the predicted polypeptide sequences contain an unknown amino acid; a stop codon; a possible nucleotide deletion; or a possible nucleotide insertion. These sequences have also been  
25 shown in their entirety in Table 2. Table 2 also shows the corresponding start and stop nucleotide locations to each of SEQ ID NO: 1-5497. Table 2 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson,  
30 Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers



to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

5 The nearest neighbor results for SEQ ID NO: 1-5497 were obtained by a BLASTX version 2.0a1 19MP-WashU search against Genpept release 122 and Geneseq release 200105 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-5497. The nearest neighbor results for SEQ ID NO: 1-5497 are incorporated in the attached Sequence Listing.

10 Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. The attached Sequence Listing provides the results obtained by eMatrix analysis for each polypeptide as follows: the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

15 Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. The attached Sequence Listing provides the results obtained by pFam analysis for each polypeptide, namely: the name of the domain found, the description, the p-value and the pFam score for the identified domain  
20 within the sequence.

Tables 1 and 2 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-5497. Table 2 shows the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 2 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID  
25 NO: in USSN 09/770,160.

Table 1

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	81-82 126 136 154-156 175-177 213-215 278-283 346-349 445-446 459 491-492 543 561-562 652-653 709-711 755-757 794-795 822-823 899 924 971-988 995 997-998 1017- 1021 1026-1027 1036-1037 1048 1085 1128 1143 1154 1173 1202-1204 1269-1270 1290- 1291 1300-1301 1320-1321 1353-1355 1357- 1359 1363-1371 1388 1394-1396 1410 1415- 1417 1422-1424 1426 1455-1456 1465-1470 1508-1510 1533-1535 1541-1546 1550 1580- 1581 1585 1588-1589 1592 1603-1608 1648 1655 1663 1674-1682 1685 1709 1719-1721 1723 1727-1734 1746 1753 1755-1756 1773- 1774 1805-1806 1827-1829 1839-1847 1876- 1877 1915-1918 1951 2005 2021-2024 2027- 2034 2042-2043 2054 2057 2072-2074 2092 2096-2097 2118 2144-2145 2177 2188-2190 2193-2195 2208-2210 2214-2215 2251-2252 2281-2283 2288-2291 2294-2299 2331 2344 2382 2417-2420 2422 2430 2437 2439-2441 2446 2456 2483 2496 2499 2510-2513 2552 2656 2686 2741-2743 2746-2747 2774-2778 2783 2786 2842-2843 2857-2860 2865 2873- 2874 2879-2881 2883-2884 2960-2962 2976- 2977 3009 3136-3137 3139-3148 3167-3168 3170-3171 3174 3198 3207 3213-3214 3220- 3222 3230 3240 3257-3259 3276-3277 3280- 3282 3289-3290 3304-3307 3323-3324 3345- 3346 3394-3395 3456 3477-3478 3536-3543 3558-3562 3587 3689 3694-3696 3729-3730 3737-3738 3772 3822-3825 3831-3833 3864- 3865 3891 3963-3965 4001 4055-4056 4060- 4061 4093 4098 4112-4113 4123 4125 4136- 4141 4230-4231 4273-4274 4291-4295 4520 4546-4548 4569-4571 4575-4576 4691-4692 4740-4741 4796-4797 4804-4805 4864-4865 4900 4907-4909 5148-5149 5276-5277 5295- 5296 5298-5302 5464-5466
adult brain	GIBCO	ABD003	1-11 52 64 81-82 123 154-156 175-177 233 248 258-260 278-283 313-315 335 339 354 357-361 365 379-380 388-390 394 459 491- 492 557 561-562 574-577 582 597-598 607 652-653 670-671 677-678 682-684 719-722 743-744 794-795 799-800 814-816 818 822- 823 840-844 863-869 873-875 878 882-886 889-897 909-914 916-920 924 927 930-936 944-960 964-966 969 971-988 993-995 997- 999 1008-1009 1017-1021 1023-1027 1036-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			1037 1042-1048 1050-1051 1053-1054 1063- 1068 1070-1071 1075 1089-1091 1110-1113 1117-1121 1128-1136 1143 1154 1156 1159- 1164 1172 1175 1180-1184 1198-1204 1217- 1218 1235-1236 1244-1246 1249-1255 1269- 1273 1281-1282 1297 1300-1301 1307 1315- 1316 1319-1322 1349-1350 1352-1355 1357- 1358 1374 1388-1393 1398-1399 1410 1413 1422-1424 1426 1438-1441 1446-1449 1451- 1456 1463-1466 1473 1478-1479 1485 1498- 1499 1507-1510 1516-1517 1532 1536-1539 1541-1546 1551-1552 1559-1560 1580-1581 1588-1589 1605-1608 1612 1620-1623 1639 1648 1654 1661-1663 1665 1671-1673 1685 1688-1690 1694-1699 1703-1704 1708-1709 1715-1716 1719-1721 1723 1727 1737-1739 1743-1746 1753-1756 1765-1769 1780-1783 1805-1817 1831-1838 1845-1851 1860 1870- 1875 1878 1900-1911 1915-1922 1926-1927 1951-1962 1964-1965 1978-1979 1981-1983 1990-1991 2000-2002 2005 2010-2013 2027- 2030 2038 2042-2043 2048 2050-2051 2057- 2061 2066-2067 2072-2074 2083-2084 2086- 2087 2092-2093 2096-2102 2107 2115-2116 2118 2125-2130 2144 2146-2147 2177 2186- 2188 2214-2215 2223 2230-2232 2251-2252 2254 2258-2260 2267-2270 2273 2281-2282 2284 2288-2291 2296-2299 2310 2318-2320 2324 2331 2333-2334 2377-2382 2389-2390 2403-2404 2416-2417 2419-2424 2430 2439- 2441 2444 2446-2447 2467 2469 2475 2483 2488 2499 2510-2513 2536-2538 2573-2575 2592 2594-2595 2597 2603-2604 2628-2632 2644-2648 2656 2666 2668 2672-2674 2677- 2680 2686 2696-2697 2726 2734 2745-2748 2751 2760 2763-2764 2768-2771 2777-2778 2780-2783 2786 2805-2806 2814 2820 2824- 2826 2828 2836-2839 2843 2854 2857-2860 2865 2894-2897 2906 2914-2917 2925-2929 2954 2960 2964 2969-2973 2996-2998 3009 3035-3036 3054 3084-3085 3088-3089 3094- 3095 3100 3110 3133-3135 3139-3148 3151- 3152 3158 3167-3168 3170-3173 3189-3191 3195 3199 3203-3204 3213-3214 3219 3223 3226-3228 3230-3233 3253-3255 3257-3259 3276-3277 3280-3282 3288-3290 3310-3311 3313 3323-3324 3331-3332 3339-3340 3345- 3346 3372-3373 3409-3417 3442 3477-3478 3491-3495 3505-3506 3536-3543 3554-3556 3558-3560 3576 3587-3589 3599-3601 3628-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			3630 3638-3640 3693 3729-3730 3810 3815-3821 3830-3833 3867-3869 3882-3883 3911-3919 3941-3942 3955-3957 3959-3960 3962 4014-4015 4040-4045 4055-4056 4062-4064 4076 4087-4093 4101-4102 4112-4116 4123 4125 4127-4130 4136-4137 4140-4141 4241-4242 4252-4253 4285-4286 4291-4295 4335-4337 4439 4546-4549 4552 4570-4571 4598-4601 4616-4621 4652-4653 4679 4691-4692 4740-4741 4764-4766 4796-4797 4807-4808 4862-4863 4907-4909 4971 4976-4979 5021-5023 5137-5140 5177-5179 5181-5183 5276-5277 5284-5289 5291 5295-5296 5308-5309 5389-5391 5399-5401 5421-5422 5427-5429 5443-5444 5464-5466 5485 5490-5491
adult brain	Clontech	ABR001	3-11 70 137 175-177 478 491-492 597-598 755-757 796 852-854 910-914 964-966 1026-1027 1049 1158-1159 1173 1198-1201 1271 1274 1281-1282 1297 1351 1363-1371 1389 1479 1671-1673 1685 1719-1721 1784-1790 1870-1875 1900-1902 1919-1922 1926-1927 2035 2072-2074 2224-2228 2298-2299 2305-2306 2404 2419-2420 2436 2528-2531 2644 2713-2714 2751 2762 2774-2776 2786 2978 3113 3151-3152 3181-3183 3213-3214 3424-3427 3554-3556 3577-3582 3587 3595-3596 3638-3640 3663 3742-3744 3853 3911-3919 3931 3941-3942 3962 4036-4039 4077-4079 4125 4220-4223 4320 4545 4549 4570-4571 4672-4674 4738-4739 4764-4766 4781 4815 4910 5001-5003 5435-5437 5464-5466
adult brain	Clontech	ABR006	47 126 130 154-156 278-283 395 561-562 583-590 661-662 709-711 855-856 889-897 903-905 909 945 961-962 1063-1067 1069 1088 1095 1154-1155 1235-1236 1281-1282 1349-1350 1360-1362 1394 1418-1420 1580-1584 1626 1634-1637 1671-1673 1688-1689 1694-1698 1715-1716 1728-1734 1763-1764 1770-1771 1773-1774 1839-1844 1903-1911 1913-1914 2027-2030 2035 2054-2056 2076-2077 2121-2124 2145 2163-2168 2188 2197-2199 2214-2215 2445 2591-2592 2598 2650 2686 2737-2738 2745 2774-2778 2857-2860 3323-3324 3328-3330 3342-3344 3354 3396-3398 3498-3501 3536-3543 3658-3660 3856-3857 4300-4308 4379-4380 4410-4412 4451-4452 4481-4489 4549 4624-4626 4660 4824-4826 4832-4834 4967-4970 5050-5052 5278-5279
adult	Clontech	ABR008	30-31 39-40 45-46 62 74-77 81-82 116-119

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
brain			129-130 136-137 143-148 154-156 175-177 187-190 195-196 216-218 227-230 254 258- 260 294-295 301-303 313-315 340 388-390 395-398 400-404 407-410 413-414 435 449 465 493-495 499 509 520-521 531-532 545 557-560 579-581 592-594 602-603 607 611 629-630 647-649 652-653 659-660 675-676 685 697-698 709-711 747-750 758-759 796 804-808 817-818 829-831 836-837 840-844 885-886 903-905 909-914 916-918 924 944 946-949 957-960 971-974 993-994 997-1002 1017-1021 1028 1038-1040 1042-1049 1053- 1054 1070-1072 1076 1095 1117-1119 1128- 1136 1139-1143 1151-1154 1160-1164 1175 1182-1184 1192 1202-1204 1222-1223 1228 1230-1232 1235-1236 1271 1278-1282 1285 1294-1296 1320-1321 1323-1327 1349-1350 1353-1354 1357-1359 1380 1383-1384 1386- 1387 1389 1398-1401 1403-1404 1407 1411 1421-1423 1426-1432 1446-1449 1451-1456 1463-1464 1479-1480 1485 1488 1491-1494 1508-1510 1527-1538 1547-1548 1557 1580- 1584 1605-1608 1629-1632 1634-1638 1640- 1645 1648 1667-1670 1685 1691-1692 1694- 1698 1701-1704 1706-1709 1715-1716 1724 1727 1737-1739 1742-1746 1754 1765-1769 1773-1774 1780-1783 1796-1817 1827-1829 1839-1844 1848-1851 1870-1875 1879-1885 1896-1897 1900-1911 1915-1922 1926-1927 1950 1952-1962 1966-1974 1978-1979 1981- 1983 1990-1991 2005-2007 2010-2013 2017- 2020 2025-2030 2040-2041 2044 2048 2052- 2053 2055-2056 2058-2059 2062-2064 2068- 2074 2076-2079 2095 2118 2134-2136 2138- 2142 2144-2147 2161-2162 2174-2177 2186- 2188 2191-2199 2204-2215 2223-2233 2254- 2257 2281-2282 2286-2291 2347-2356 2362 2380-2381 2419-2420 2437 2456 2464 2496 2511-2513 2534-2536 2548 2554-2556 2592 2596 2603-2604 2626 2629-2631 2633-2637 2645-2647 2650-2655 2657-2658 2665 2669- 2671 2675-2680 2696-2697 2702-2705 2709- 2711 2728-2729 2749-2750 2762 2777-2778 2784 2828-2829 2843 2846-2850 2857-2862 2865 2869-2870 2885-2888 2904 2925-2929 2931-2939 2945-2946 2955 2969-2973 3084- 3085 3118 3136-3137 3172-3173 3196 3208- 3209 3213-3216 3219 3229-3230 3234 3240 3243 3304-3307 3312 3331-3332 3342-3346 3371 3403-3404 3406-3407 3424-3427 3444-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult brain	Clontech	ABR011	154-156 388-390 1076 1128 1182-1184 1193 1202-1204 1422-1424 2072-2074 2144 2251- 2252 2549-2550 4062-4064 5298-5302
adult brain	BioChain	ABR012	440-441 602-603 889-897 997-998 1582- 1584 1719-1721 1780-1783 2072-2074 2186- 2187 2223 2377-2379 3394-3395 4291-4295 4581-4582 5123-5124
adult brain	Invitrogen	ABR013	341-344 491-492 1205-1207 1580-1581 1599-1602 1857-1859 1925 2072-2074 2186- 2187 2208-2210 2377-2379 2469 3250-3252 3304-3307 4267-4270 4796-4797
adult brain	Invitrogen	ABT004	12-13 38 52 70 92-95 126 175-177 255-257 291 341-344 346-349 354 478 557 583-590 612-620 675 789-793 796 840-844 871-872 879-884 909 919-920 964-966 997-998 1017- 1021 1026-1027 1042-1043 1051 1070-1071 1076 1088 1108 1151-1153 1160-1164 1193 1217-1218 1228-1229 1269-1270 1281-1282 1320-1321 1349-1350 1385 1427-1431 1467- 1469 1485 1532 1575-1576 1626 1629-1632 1640-1645 1708 1715-1716 1727 1742-1746 1773-1774 1799-1804 1807-1813 1852 1860 1865-1875 1900-1911 1948-1949 1954-1962 1964-1965 1981-1983 1990-1991 2010-2013 2036-2037 2054 2072-2074 2078-2082 2086- 2087 2143-2147 2174-2176 2186-2187 2224- 2228 2231-2232 2255-2257 2264 2284 2310- 2312 2369-2375 2397-2399 2419-2420 2436 2526-2527 2592 2604 2624 2626 2629-2631 2696-2697 2734 2751 2785 2813 2857-2860

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			2886-2887 2925-2929 2981-2984 3124-3128 3195 3212-3214 3219-3222 3253-3255 3258- 3259 3313 3339-3340 3403-3404 3411-3417 3466-3468 3508-3513 3554-3556 3599-3601 3661-3662 3693 3835 3959-3960 3997-3998 4036-4039 4060-4061 4068-4069 4077-4079 4093 4124 4131 4291-4295 4297-4299 4330- 4331 4379-4380 4391-4393 4542-4544 4549 4569 4672-4674 4861 4870 4900 4923-4925 5000 5021-5023 5222-5224 5282 5387-5388
cultured preadipocytes	Stratagene	ADP001	74-77 134 154-156 175-177 201-205 213-215 278-283 313-315 489-492 520-521 652-653 670-671 680-684 736-740 743-744 784-786 796 814-816 822-823 857-859 885-886 944 950 964-966 994 1028 1042-1043 1052 1069- 1071 1089-1091 1129-1130 1143 1154 1156 1172 1198-1204 1249-1255 1278-1280 1317- 1318 1320-1321 1351 1359 1380 1410 1455- 1456 1473 1507 1532-1535 1547-1548 1553- 1556 1559-1560 1588-1589 1611 1617-1619 1640-1645 1648 1663 1666 1723-1724 1727 1746 1755-1756 1765-1769 1773-1774 1780- 1783 1839-1844 1870-1877 1925 1990-1991 2060-2061 2118 2193-2195 2197-2199 2223 2234-2242 2298-2299 2310 2331 2380-2381 2443 2452-2454 2524-2525 2572-2573 2591- 2592 2594-2595 2604 2672-2674 2709-2711 2734 2739 2819 2843-2847 2861-2862 2899- 2900 2913 2925-2929 2979 2985 3013-3014 3159-3162 3181-3183 3189-3191 3220-3222 3253-3255 3285 3310-3311 3462 3486-3487 3587 3638-3640 3673-3677 3754 3804-3806 3815-3816 3871-3872 3969-3971 4014-4015 4036-4039 4068-4069 4140-4141 4241-4242 4254 4341 4534 4554-4555 4570-4571 4581- 4582 4622-4623 4740-4741 4864-4865 4910 5001-5003 5038-5039 5095-5097 5137-5140
adrenal gland	Clontech	ADR002	1-2 12-13 35 52 62 100-106 121-122 140-142 153-156 191-192 213-215 221 232 301-303 306 313-315 341-344 366-367 394 459 491- 492 513 551-553 583-590 592-595 652-653 670-671 719-722 728-733 743-744 747-750 755-757 772 784-786 814-816 847 849-851 889-897 909-914 916-920 944 946-949 961- 962 993-995 997-999 1049 1070-1071 1078 1089-1091 1117-1119 1128 1151-1153 1160- 1164 1175 1182-1184 1193 1220-1221 1269- 1270 1272-1273 1287 1307 1352 1355 1357- 1359 1407 1415-1417 1422-1423 1480 1485 1498-1499 1505 1507-1510 1526 1541-1546

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			1553-1556 1580-1581 1585 1597 1613-1619 1638-1639 1649-1652 1656 1683-1684 1701- 1704 1708 1715-1717 1727-1736 1747-1751 1753 1770-1771 1799-1806 1835-1838 1870- 1877 1896 1903-1911 1915-1922 1950-1951 1992 2000-2002 2010-2013 2025-2026 2038 2050-2051 2057-2059 2062-2064 2072-2074 2086-2087 2115 2144 2153-2155 2179-2181 2186-2187 2196-2199 2208-2210 2214-2215 2224-2228 2234-2242 2258-2260 2262 2264 2267-2270 2296-2299 2324 2327-2330 2347- 2348 2360 2368 2389-2390 2419-2420 2425- 2426 2465 2499 2511-2513 2523 2560 2573 2650 2665 2668 2672-2674 2726 2735 2741- 2743 2800-2801 2813 2824-2826 2840-2841 2844-2845 2852-2854 2861-2862 2871-2872 2894-2895 2898 2909-2911 2925-2929 2931- 2939 2945-2946 2961-2962 2992 3013-3014 3017-3022 3026-3027 3035-3036 3054 3076- 3078 3172-3173 3189-3191 3195 3218 3229 3242 3250-3252 3285 3309 3316-3318 3323- 3324 3342-3344 3396-3398 3428-3429 3444- 3445 3472-3473 3477-3478 3519 3561-3562 3588 3602-3604 3621-3625 3637 3667 3673- 3677 3689 3691 3693 3699 3724-3725 3784- 3786 3807 3851 3860-3861 3877 3936 3955- 3957 3969-3971 4024-4025 4027 4055-4056 4060-4061 4076 4082-4084 4100 4112-4116 4123 4138-4139 4219 4228 4230-4231 4243- 4244 4287-4288 4330-4331 4342 4382 4391- 4393 4410-4412 4473 4529 4537-4541 4546- 4548 4581-4582 4629-4632 4796-4798 4835 4864-4865 4905-4910 5001-5003 5034-5036 5190-5192 5210 5234 5278-5279
adult heart	GIBCO	AHR001	45-46 52 56 100-106 133-134 140-142 154- 156 173 175-177 192 195-196 201-205 212- 218 227-230 235 278-283 286-287 301-303 313-315 323 332-333 341-344 346-352 366- 367 379-380 395 400-404 413-414 436 469 478 491-492 511 520-521 531-532 551-553 557 574-577 583-590 599-601 604 607 612- 620 652-653 675 677-678 680-685 697 707 743-744 784-786 789-796 799-800 814-816 822-823 847 885-886 889-897 915-920 924- 929 931-936 944-945 950 957-960 964-966 969 971-979 992 994-1002 1017-1027 1044- 1050 1052-1054 1056-1057 1063-1067 1070- 1071 1075 1110-1113 1117-1119 1127-1136 1139-1143 1154 1156 1159 1172-1173 1182- 1185 1192-1193 1202-1207 1220-1221 1228



Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			1230-1232 1235-1236 1244-1246 1249-1255 1264 1271 1281-1282 1287 1297 1300-1301 1315-1319 1322-1327 1330-1331 1349-1350 1353-1355 1357-1362 1374 1386-1387 1389 1397 1403-1407 1414 1422-1423 1438 1440- 1443 1450-1462 1465-1466 1478-1479 1481- 1485 1489 1498-1499 1507 1515 1524 1532 1539 1541-1546 1550-1556 1569-1576 1579 1585 1588-1589 1591 1605-1608 1611 1629- 1632 1639-1652 1663-1664 1666-1673 1685 1691-1692 1694-1698 1701-1704 1707 1709 1715-1716 1719-1721 1723-1724 1728-1739 1746 1753-1756 1765-1769 1780-1783 1792- 1798 1805-1817 1831-1834 1839-1851 1853 1860 1865-1869 1876-1877 1879-1885 1897 1919-1922 1925-1927 1948-1962 1978-1979 1981-1983 2004-2005 2035-2038 2042-2043 2045-2047 2050-2057 2060-2064 2072-2074 2086-2091 2096-2097 2111-2114 2116 2118 2144 2146-2147 2151-2160 2173 2179-2183 2188-2195 2208-2213 2216-2221 2223 2229- 2232 2234-2242 2251-2252 2254-2257 2262 2267-2270 2281-2282 2284 2288-2291 2296- 2297 2303-2304 2310 2318-2320 2327-2331 2369-2375 2382 2388 2405-2413 2418 2443 2452-2454 2467 2470-2472 2488 2499 2510- 2513 2534-2538 2558-2559 2574-2575 2579- 2584 2592 2598 2604 2629-2631 2633-2636 2645-2647 2649 2656-2658 2665 2667 2700 2747-2748 2752-2753 2760-2761 2774-2776 2781 2785 2800-2801 2808-2809 2818-2819 2824-2826 2843-2847 2865 2888 2898 2901- 2903 2914-2917 2931-2939 2944 2954 2960- 2962 2965-2973 2990 2992 2996-2998 3013- 3014 3017-3020 3025-3027 3031-3032 3035- 3036 3054 3075 3084-3085 3096-3097 3100 3139-3147 3156-3157 3159-3162 3167-3168 3170-3173 3181-3184 3189-3191 3195 3204 3210-3211 3224-3228 3240 3276-3277 3289- 3290 3302 3310-3311 3323-3324 3336-3338 3341 3420 3428-3429 3444-3445 3451-3455 3470-3471 3505-3506 3558-3560 3595-3596 3606-3607 3619-3625 3632-3634 3663 3670- 3671 3689 3691 3699 3707 3724-3725 3729- 3730 3735 3742-3744 3747 3795-3800 3804- 3806 3854 3858-3859 3864-3865 3882-3883 3959-3960 3962 3969-3971 4014-4015 4030- 4031 4033-4034 4040-4042 4055-4056 4060- 4064 4068-4069 4087-4089 4101-4102 4114- 4116 4123 4126 4137 4140-4141 4157-4158

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult kidney	GIBCO	AKD001	32-34 36-37 39-40 42 45-47 74-78 87 100- 106 116-119 136 165 175-177 213-218 220 223-231 235 244 252-253 258-260 278-283 298-300 313-320 324-325 332-333 341-344 346-349 364 366-367 379-380 394 396-398 419 436 440-441 445-446 452 474 491-492 498 519 548-553 557 574-577 583-590 602- 603 607 629-630 652-653 677-678 682-684 707 709-711 719-722 728-733 736-740 778- 786 789-793 799-800 806-808 814-816 822- 823 836-838 840-844 852-854 857-859 871- 875 879-886 889-897 899-905 909-915 919- 920 924-926 931-936 944-962 964-966 969- 974 980-988 994-995 997-998 1000-1009 1017-1021 1026-1027 1036-1040 1042-1043 1049-1050 1052 1063-1071 1075-1076 1078- 1079 1081-1082 1085 1088-1091 1110-1113 1116-1121 1127-1130 1137-1142 1151-1155 1159 1172-1173 1182-1184 1189-1193 1198- 1207 1217-1218 1220-1221 1230-1232 1235- 1236 1249-1260 1269-1271 1278-1280 1287 1294-1297 1300-1301 1307 1315-1321 1328 1334-1335 1349-1350 1352-1354 1357-1362 1374 1385-1389 1397-1399 1403-1407 1410 1414-1420 1422-1423 1425-1426 1435-1436 1438 1440-1441 1444 1451-1462 1465-1466 1470-1472 1475-1477 1479 1481-1485 1488- 1489 1498-1499 1504-1505 1507-1510 1515- 1517 1524 1527-1532 1536-1538 1540-1548 1551-1557 1561-1563 1569-1576 1579-1589 1591 1597 1603-1608 1611-1619 1625-1626 1634-1648 1653-1654 1656 1663-1665 1667- 1682 1685 1688-1692 1694-1698 1701-1704 1707-1708 1710-1716 1719-1721 1723-1724 1727-1739 1743-1746 1753 1755-1758 1763- 1771 1773-1783 1796-1798 1805-1806 1814- 1817 1830-1847 1857-1860 1865-1877 1882- 1885 1903-1911 1913-1922 1925-1927 1948- 1953 1964-1974 1978-1979 1981-1983 1993-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			1998 2004-2005 2010-2013 2021-2038 2042- 2043 2045-2047 2055-2061 2068-2083 2086- 2087 2092 2094 2096-2100 2111-2114 2116 2118 2125-2133 2137-2142 2144 2146-2147 2151-2152 2156-2160 2173-2181 2186-2188 2191-2195 2197-2199 2202-2203 2208-2213 2216-2221 2223-2230 2234-2242 2244-2248 2251-2252 2254-2257 2261 2267-2270 2272- 2273 2280-2282 2284 2288-2291 2296-2297 2302 2310 2318-2320 2331 2333-2334 2338- 2340 2368 2377-2382 2386 2388-2392 2403 2405-2415 2422-2424 2427 2430 2440-2441 2446-2447 2451 2467-2472 2475 2483-2485 2488 2490-2491 2496 2499 2510-2513 2521- 2525 2528-2531 2536 2546 2554-2556 2564- 2572 2574-2575 2579-2584 2591-2592 2596 2604 2629-2637 2645-2649 2672-2676 2693 2696-2697 2702-2706 2709-2711 2716-2718 2721 2726 2730 2734 2747-2748 2754-2758 2760-2761 2763 2768-2772 2774-2778 2781 2785 2800-2801 2805-2806 2809 2814 2818 2828 2836-2839 2842-2843 2854-2863 2865 2873-2874 2888 2894-2898 2901-2903 2913 2925-2929 2931-2939 2945-2946 2960-2962 2969-2976 2979 3009 3013-3014 3017-3022 3026-3027 3054 3076-3078 3082 3098-3100 3102-3105 3109 3136-3137 3139-3147 3151- 3162 3167-3168 3170-3174 3189-3191 3195 3204 3215-3216 3218 3224-3230 3234 3240 3242 3256-3267 3276-3277 3280-3282 3285 3288-3290 3292-3293 3296-3299 3313 3323- 3324 3331-3335 3339-3340 3342-3344 3367- 3368 3374-3382 3394-3398 3403-3404 3406- 3407 3409-3410 3428-3429 3438-3441 3443- 3445 3456 3462 3466-3468 3470-3471 3519 3535-3543 3554-3556 3561-3562 3576-3580 3589 3605 3610-3613 3619-3625 3628 3632- 3634 3638-3640 3664-3665 3667 3670-3671 3673-3677 3684 3686-3691 3716 3724-3725 3742-3744 3747 3760-3761 3780-3781 3815- 3816 3822-3824 3826 3830 3837-3838 3870 3880 3882-3883 3895 3897-3905 3911-3919 3939-3951 3955-3957 3959-3960 3966-3971 3997-3998 4014-4015 4036-4039 4055-4056 4060-4064 4071-4075 4077-4079 4082-4084 4093 4098 4101-4102 4114-4116 4119-4123 4136 4138-4143 4220-4223 4230-4235 4243- 4244 4252-4253 4255-4257 4260 4267-4270 4285-4288 4322 4335-4337 4342 4363 4383- 4384 4391-4393 4400 4430-4432 4439 4451-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult kidney	Invitrogen	AKT002	1-2 70 278-283 313-315 379-380 457 491- 492 574-577 582 604 652-653 699-701 707 709-711 719-722 764-771 794-795 814-816 822-823 840-844 906-909 924 944 950 963 975-988 993 995 1017-1021 1042-1043 1063- 1067 1070-1071 1076 1079 1110-1113 1117- 1119 1128 1137-1143 1172 1182-1184 1193 1208-1212 1220-1221 1235-1242 1278-1280 1287 1297 1315-1318 1323-1328 1355 1357- 1358 1360-1371 1374 1397 1405-1406 1414 1418-1420 1425 1457-1462 1488 1507 1515 1536-1538 1547-1548 1551-1552 1559-1560 1579 1626 1656 1664 1674-1682 1685-1689 1691-1693 1706 1708 1710-1716 1719-1721 1728-1734 1737-1739 1753 1773-1774 1845- 1851 1870-1875 1897 1903-1911 1913-1914 1925 1948-1949 1951-1953 1978-1979 1981- 1983 1990-1991 2004-2005 2017-2020 2027- 2030 2038 2048 2054 2062-2064 2072-2074 2076-2077 2116 2118 2125-2133 2156-2160 2174-2176 2179-2181 2186-2188 2208-2210 2214-2215 2224-2228 2275 2277 2296-2297 2321 2377-2379 2391 2397-2399 2421 2428 2452-2454 2473-2474 2492-2494 2499 2528- 2531 2536 2560 2579-2584 2592 2594-2595 2608-2616 2706 2734 2781 2785 2818 2843- 2845 2854 2861-2862 2886-2887 2974-2975 2979 2984 2996-2998 3008 3100 3139-3147 3149 3151-3152 3156-3157 3184 3195 3218 3250-3252 3260-3267 3269 3313 3325-3327 3336-3338 3341-3344 3424-3427 3550-3552 3554-3556 3590 3624-3625 3628 3658-3660 3663 3693 3791 3822-3824 3943-3948 4004 4040-4042 4055-4056 4076 4093 4109-4111 4232-4235 4241-4242 4275-4277 4534 4549 4622-4623 4633-4634 4740-4741 4764-4766

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult lung	GIBCO	ALG001	78 136 138-139 175-177 313-315 324-325 341-344 413-414 440-441 456 491-492 511 557 652-653 677-678 728-733 784-786 794- 795 822-823 849-851 855-856 885-886 919- 920 954-960 975-988 992-993 997-999 1003- 1006 1017-1021 1026-1027 1042-1043 1053- 1054 1075 1088 1129-1130 1143 1182-1184 1189-1191 1198-1201 1208-1212 1271 1297 1300-1301 1317-1318 1352-1355 1374 1407 1422-1423 1455-1462 1481-1484 1488-1489 1497 1507-1512 1516-1517 1532-1535 1541- 1548 1551-1556 1582-1584 1588-1589 1591 1603-1604 1611 1617-1619 1663 1723 1727- 1734 1742-1746 1753 1780-1783 1814-1817 1831-1834 1852 1870-1875 1919-1922 1925 1951 2005-2007 2038 2058-2061 2072-2074 2086-2087 2116 2118 2121-2136 2144 2153- 2155 2163-2168 2179-2181 2186-2187 2214- 2215 2223-2228 2230 2234-2242 2277 2283 2296-2299 2331 2380-2382 2389-2390 2467- 2469 2473-2474 2499 2536 2553 2564-2571 2574-2575 2604 2672-2674 2677-2680 2749- 2750 2759 2761 2774-2776 2843 2855-2856 2913 2957 2960 2969-2973 3081 3084-3085 3098-3099 3156-3157 3167-3168 3213-3214 3220-3222 3226-3228 3238 3256 3280-3282 3289-3290 3319-3322 3333-3335 3409-3410 3442 3466-3468 3558-3560 3588 3621-3625 3628 3689 3776-3777 3815-3816 3893 3908 4040-4042 4068-4069 4114-4116 4136 4232- 4235 4291-4295 4335-4337 4404-4407 4439 4545 4672-4674 4756-4757 4796-4797 4804- 4805 4886 4907-4909 5001-5003 5046-5047 5095-5097 5142-5143 5387-5388 5464-5466
lymph node	Clontech	ALN001	39-40 143-148 154-156 269 278-283 313-315 445-446 728-733 736-742 764-771 814-816 822-823 931-936 950 961-962 994 1000-1002 1017-1021 1129-1130 1139-1142 1151-1153 1182-1184 1198-1204 1244-1246 1256 1319 1359 1398-1399 1425 1438 1455-1462 1478 1504 1507 1511-1512 1532 1539 1547-1549 1553-1556 1575-1576 1617-1619 1648 1659- 1660 1663 1719-1721 1735-1736 1753 1755- 1756 1839-1844 1857-1859 1919-1922 1925 1951 1993-1998 2004 2038 2042-2043 2048

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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young liver	GIBCO	ALV001	48-50 78 100-110 210-211 255-257 261-266 278-283 286-287 313-320 332-333 381-383 395 419 435-436 491-492 548-553 574-577 652-653 677-678 709-711 755-757 784-786 789-793 799-803 806-808 822-823 840-844 852-854 910-914 916-918 924 944 969 995 997-998 1056-1057 1063-1068 1085 1089- 1091 1116 1120-1121 1128-1130 1139-1142 1151-1155 1172 1177-1179 1182-1184 1189- 1191 1198-1201 1205-1207 1217-1218 1220- 1221 1230-1232 1249-1256 1269-1273 1290- 1291 1300-1301 1310-1314 1323-1328 1357- 1358 1360-1362 1374 1410 1418-1420 1479- 1484 1497 1507 1516-1517 1527-1531 1541- 1546 1551-1552 1557 1579-1581 1585 1590 1592 1613-1619 1626 1656 1664 1685 1691- 1692 1694-1698 1701-1702 1708-1709 1723 1725-1726 1735-1739 1753 1759-1762 1765- 1771 1773-1774 1780-1790 1796-1798 1827- 1829 1835-1838 1848-1852 1865-1875 1882- 1885 1903-1911 1913-1914 1919-1922 1925 1951 1964-1965 1978-1979 2005 2031-2034 2060-2061 2075 2086-2091 2096-2097 2118 2144 2153-2160 2174-2176 2188 2200-2201 2223-2228 2234-2242 2244-2245 2281-2282 2288-2291 2321 2358 2380-2382 2414-2415 2423-2424 2427 2447 2451 2469 2477-2479 2484-2485 2503-2504 2510 2533 2543-2544 2560 2564-2571 2579-2584 2587 2648 2761 2836-2839 2843 2865 2873-2874 2879-2881 2945-2946 2951-2952 2957 2974-2975 3013- 3014 3076-3078 3139-3147 3151-3152 3156- 3157 3181-3183 3195 3226-3228 3242 3250- 3252 3280-3282 3299 3310-3311 3328-3330 3345-3346 3403-3404 3456 3462 3561-3562 3599-3601 3619-3625 3628 3654-3657 3815-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult liver	Invitrogen	ALV002	35-37 62 70 107-110 131-132 175-177 192 233 255-257 261-266 278-283 313-315 337 354 365 374-375 445-446 450-451 478 491-492 652-653 801-803 840-844 848 852-854 903-905 944 954-956 995 997-998 1003-1006 1026-1027 1032-1034 1042-1047 1049 1056-1060 1063-1071 1078 1089-1091 1117-1119 1139-1143 1151-1154 1158-1159 1177-1181 1188-1191 1193 1205-1207 1217-1218 1230-1232 1278-1282 1307 1310-1314 1323-1327 1337-1345 1351 1360-1371 1380 1451-1454 1485 1533-1535 1547-1548 1569-1574 1592 1626 1640-1647 1656 1663 1691-1692 1708-1709 1723 1725-1726 1735-1739 1759-1762 1770-1771 1773-1774 1827-1829 1835-1844 1913-1914 1919-1922 1925 1948-1949 1954-1962 1981-1983 2010-2013 2025-2026 2054 2060-2061 2118 2171 2174-2176 2186-2190 2193-2195 2208-2210 2223 2254 2267-2270 2276-2277 2296-2297 2308 2322 2338-2340 2380-2381 2499 2533 2536 2543-2544 2560 2579-2584 2629-2631 2648 2659-2662 2665 2741-2743 2800-2801 2828 2843 2865 2879-2882 2905 2914-2917 2925-2929 2957 2960-2962 2974-2975 3013-3014 3054 3089 3156-3157 3181-3183 3199 3220-3222 3229 3310-3311 3328-3330 3371-3373 3462 3466-3469 3472-3473 3536-3543 3577-3580 3667 3749-3752 3793 3997-3998 4014-4015 4036-4039 4082-4084 4096-4097 4282 4330-4331 4376-4377 4381 4451-4452 4616-4621 4633-4634 4636-4637 4649 4687-4689 4738-4739 4754-4755 4768-4771 4796-4797 5050-5052 5057-5065 5082-5083 5130-5131 5145 5148-5149 5164-5167 5229-5231 5335-5343 5367-5368 5387-5391 5414-5415 5451-5453
adult liver	Clontech	ALV003	341-344 370-371 849-851 946-949 1177-1179 1202-1204 1626 1759-1762 1770-1771 1913-1914 2484-2485 3328-3330 4403 4998-4999 5130-5131
adult ovary	Invitrogen	AOV001	12-13 32-34 39-40 42 44 47-50 52 63-64 70 74-78 87 100-110 116-119 133 135-139 153

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			173 175-177 185 201-205 212-215 220 222 227-230 233 245 267-268 277-283 286-287 291 301-303 313-315 321 341-344 357-361 364 372 376-377 379-380 394 396-398 436 445-446 459 462 474 478 491-495 509 511 520-524 538 543 545 551-553 561-562 574- 577 583-594 604-607 611-620 629-630 641 652-653 677-678 682-684 697 699-703 707- 711 719-722 728-733 743-744 747-750 755- 757 764-771 784-786 789-795 801-803 806- 808 814-816 822-825 836-837 840-844 855- 856 863-869 871-875 879-886 889-897 899- 908 910-914 916-920 924 927 930-936 944 950-962 964-966 969 971-988 990-995 997- 1006 1008-1009 1017-1027 1032-1040 1042- 1047 1049 1052-1054 1068 1070-1071 1075- 1076 1078-1079 1081-1082 1089-1091 1095 1108 1117-1121 1128-1142 1151-1156 1158- 1164 1171-1173 1175 1180-1185 1189-1193 1198-1207 1217-1218 1220-1221 1228-1232 1235-1242 1244-1246 1249-1256 1269-1271 1278-1280 1287 1290-1293 1297-1301 1307 1315-1328 1332-1335 1348-1359 1363-1371 1374 1380 1383-1384 1386-1389 1395-1396 1398-1399 1403-1410 1413-1417 1421-1423 1426 1432 1435-1436 1438-1444 1446-1449 1451-1464 1467-1473 1475-1480 1485 1488 1491-1494 1498-1499 1504-1505 1507-1512 1515-1517 1520 1527-1538 1541-1548 1550- 1557 1569-1576 1580-1589 1591 1603-1608 1611-1612 1617-1619 1621-1623 1625 1629- 1632 1638-1645 1648-1654 1656-1658 1663- 1664 1666-1670 1674-1682 1685-1686 1688- 1692 1694-1698 1701-1702 1707-1709 1717 1719-1721 1723 1727-1739 1743-1746 1753 1755-1756 1758 1763-1769 1780-1783 1792- 1817 1827-1830 1835-1838 1848-1853 1860 1865-1877 1879-1885 1900-1911 1915-1922 1925-1936 1948-1953 1964-1965 1978-1979 1981-1983 1990-1991 1993-1998 2000-2002 2004-2005 2017-2024 2027-2037 2042-2043 2045-2048 2052-2061 2066-2067 2076-2077 2080-2082 2086-2091 2093-2094 2096-2100 2111-2115 2118 2125-2133 2138-2147 2151- 2160 2174-2177 2179-2181 2186-2187 2189- 2195 2197-2201 2204-2215 2223 2229 2231- 2232 2234-2242 2251-2252 2254-2262 2264- 2265 2267-2271 2273 2275 2277 2281-2284 2286-2291 2296-2300 2321 2331 2380-2381 2386-2392 2395 2397-2399 2403 2414-2415



Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			2421-2424 2427 2433 2437 2440-2441 2443 2445 2451-2454 2456 2463 2465 2467-2469 2473-2474 2483 2488 2492-2494 2499 2502 2510-2513 2521 2523 2536-2538 2546 2548- 2550 2552 2558-2562 2574-2575 2587 2591- 2595 2598 2604 2626 2628-2636 2639-2642 2645-2648 2650 2656-2662 2664-2665 2668 2675-2680 2686 2693 2696-2697 2702-2706 2721 2726 2734-2735 2739 2741-2743 2746- 2747 2754-2758 2760-2761 2763-2764 2768- 2771 2774-2778 2781 2783 2785-2789 2800- 2801 2807 2809 2814 2818-2820 2824-2826 2828-2829 2831-2832 2842-2843 2854-2862 2865-2867 2871-2874 2883-2884 2886-2888 2894-2900 2905 2914-2917 2931-2939 2945- 2947 2951-2952 2954 2961-2962 2965-2975 2979 2985 2989-2990 2996-2998 3000 3008- 3009 3011-3012 3017-3020 3030-3032 3035- 3036 3054 3068 3070 3084-3085 3089 3098- 3100 3102-3105 3109-3110 3121 3130 3133- 3138 3151-3152 3158 3166 3170-3174 3181- 3183 3192 3195 3197 3199-3203 3210-3216 3218-3230 3234 3240 3242-3243 3245 3250- 3259 3269 3276-3277 3280-3282 3285 3289- 3290 3302 3310-3312 3323-3327 3331-3340 3342-3344 3394-3395 3403-3404 3409-3417 3422 3424-3429 3438-3442 3446-3449 3456 3462 3466-3468 3470-3473 3477-3478 3480 3491-3495 3516-3517 3519 3522 3535-3543 3546 3550-3553 3558-3562 3577-3580 3586 3588 3591-3593 3621-3623 3628-3630 3632- 3634 3658-3662 3666-3667 3673-3677 3680 3689 3691 3701 3714 3723-3725 3735 3737- 3738 3761 3763 3770-3772 3784-3788 3795- 3800 3803-3807 3810 3815-3816 3822-3824 3828 3835 3837-3838 3870-3872 3878-3880 3882-3883 3897-3905 3911-3919 3925-3926 3931 3941-3942 3955-3957 3959-3960 3963- 3971 4001 4014-4018 4021 4023 4036-4045 4055-4056 4060-4061 4068-4069 4071-4079 4082-4084 4087-4089 4093 4096-4098 4100- 4102 4104-4105 4109-4116 4121-4123 4126- 4131 4136-4143 4145-4153 4215-4217 4220- 4223 4228 4230-4235 4241-4244 4252-4253 4255-4257 4261-4266 4272-4277 4285-4286 4291-4295 4326 4335-4337 4341 4374-4375 4379-4381 4383-4384 4391-4393 4425 4430- 4432 4438-4439 4461-4464 4481-4489 4501 4533 4542-4544 4549-4550 4598-4601 4611 4613 4616-4623 4642 4652-4653 4663 4668-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			4674 4681-4683 4691-4692 4740-4741 4748-4749 4751-4753 4764-4766 4777-4780 4784-4786 4796-4797 4804-4805 4812 4820 4854 4861-4865 4874-4875 4886 4902 4907-4910 4912 4918-4920 4923-4925 4953 4956-4957 4976-4979 5001-5003 5025 5040 5050-5052 5057-5065 5085-5088 5095-5097 5109 5115 5123-5127 5148-5149 5154-5157 5173 5222-5224 5241-5242 5251 5259 5261-5267 5276-5277 5281 5284-5289 5308-5309 5329-5330 5335-5343 5367-5368 5387-5391 5399-5401 5408-5410 5421-5425 5427-5429 5431-5433 5439 5455 5464-5466 5485 5490-5491
adult placenta	Clontech	APL001	313-315 491-492 605-606 719-722 736-740 834-835 950 971-979 1017-1022 1151-1153 1182-1184 1215-1216 1410 1418-1420 1532 1539-1540 1564-1566 1639 1719-1721 1747-1751 1870-1875 1925 1966-1974 1984 2101-2102 2230 2424 2510 2524-2525 2574-2575 2645-2647 2668 2818 2873-2874 3323-3324 3462 3483 4040-4042 4101-4102 4581-4582 4793-4795 5188-5189 5376
placenta	Invitrogen	APL002	12-13 192 364 491-492 520-521 709-711 755-757 789-793 840-844 885-886 975-979 1026-1027 1042-1043 1050 1070-1071 1076 1117-1119 1160-1164 1202-1207 1215-1216 1272-1273 1320-1321 1351 1360-1362 1380 1400-1401 1442-1443 1473 1553-1556 1564-1566 1603-1608 1621-1623 1694-1698 1724 1737-1739 1743-1745 1747-1751 1780-1783 1860 1948-1949 2062-2064 2072-2074 2101-2102 2111-2114 2146-2147 2186-2187 2204-2207 2310 2434-2435 2470-2472 2488 2511-2513 2594-2595 2645-2647 2677-2680 2696-2697 2737-2738 2831-2832 2836-2839 2899-2900 2925-2929 2954 3065-3067 3195 3199 3220-3222 3288 3313 3336-3338 3391 3403-3404 3466-3468 3536-3543 3624-3625 3638-3640 3932-3933 4082-4084 4273-4274 4291-4295 4410-4412 4701-4709 4740-4741 5431-5433 5435-5437
adult spleen	GIBCO	ASP001	78 137 154-156 175-177 213-215 274 278-283 313-315 324-325 332-333 341-344 346-349 420 456 479-480 491-492 511 530 557 612-620 652-653 659-660 677-678 699-701 728-733 741-744 764-771 784-786 814-816 822-823 849-851 924 944 950 964-966 975-988 994-995 997-998 1000-1002 1008-1009 1049 1052 1070-1071 1078 1088-1091 1128-1136 1151-1153 1171-1172 1193 1195-1196

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			1202-1204 1217-1218 1220-1221 1256 1269- 1271 1287 1294-1297 1315-1318 1332-1333 1349-1350 1352-1354 1359 1363-1371 1374 1383-1384 1386-1387 1397 1408-1409 1414 1418-1420 1422-1423 1425 1440-1441 1446- 1449 1486 1497 1507-1512 1514 1516-1517 1527-1532 1540-1548 1551-1552 1575-1576 1586-1589 1597 1603-1604 1612 1617-1619 1621-1623 1629-1632 1634-1637 1640-1645 1654 1656 1663 1686 1691-1692 1708 1710- 1714 1719-1721 1723-1724 1727 1737-1739 1746 1753 1765-1769 1773-1774 1780-1783 1796-1798 1807-1817 1827-1834 1853 1857- 1859 1870-1885 1903-1911 1913-1914 1919- 1922 1948-1949 1951 1964-1965 1978-1979 2025-2026 2035 2038 2040-2043 2045-2047 2054 2060-2061 2072-2074 2076-2079 2086- 2087 2111-2114 2116 2118 2131-2133 2137 2144 2148-2150 2153-2155 2178 2182-2183 2214-2215 2223 2230 2234-2242 2281-2283 2298-2299 2303-2304 2310 2331 2380-2382 2405-2413 2421 2440-2441 2452-2454 2456 2461 2469-2472 2488 2510-2513 2551 2560 2573 2603-2604 2608-2616 2650 2696-2697 2719-2720 2726 2747 2754-2758 2803 2818 2831-2832 2843-2845 2854 2861-2862 2873- 2874 2914-2917 2945-2946 2974-2976 3153 3158 3167-3168 3170-3171 3195 3210-3211 3215-3216 3226-3228 3250-3252 3258-3259 3280-3282 3289-3290 3336-3338 3385 3403- 3404 3428-3429 3466-3468 3536-3543 3561- 3562 3591-3593 3621-3625 3629-3630 3632- 3634 3716 3784-3786 3792 3815-3816 3878- 3879 3886 3935 3966-3971 4014-4015 4023 4036-4039 4060-4061 4077-4079 4090-4092 4098 4100 4126 4142-4143 4228 4232-4235 4239-4240 4335-4337 4374-4375 4400 4404- 4407 4451-4452 4554-4555 4598-4601 4622- 4623 4662 4668-4671 4740-4741 4796-4797 4832-4834 4864-4865 4907-4909 4912 4956- 4957 5001-5003 5034-5036 5074 5095-5097 5123-5124 5148-5149 5154-5157 5241-5242 5261-5267 5272-5274 5298-5302 5310-5311 5329-5330 5335-5343 5427-5429 5440-5441 5485
testis	GIBCO	ATS001	47 81-82 123 136 154-156 175-177 179 227- 230 278-283 313-315 341-344 366-367 379- 380 456 491-492 574-577 604 652-653 677- 678 682-684 699-701 743-744 764-771 784- 786 811-816 822-823 826-828 879-881 885-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			886 906-908 931-936 944-945 950 957-960 969 971-974 993-995 997-1002 1008-1009 1026-1027 1032-1034 1036-1037 1042-1043 1075-1076 1080 1108 1137-1138 1173 1189- 1191 1198-1204 1230-1232 1235-1236 1271 1278-1282 1297 1310-1314 1317-1319 1334- 1335 1349-1350 1357-1358 1374 1397 1403- 1404 1413 1418-1420 1422-1423 1435-1436 1451-1462 1485 1507 1516-1517 1547-1548 1551-1552 1561-1563 1611 1629-1632 1640- 1645 1648 1663 1667-1670 1685 1694-1698 1703-1704 1708 1715-1716 1719-1721 1724 1746 1753 1755-1756 1758 1770-1771 1780- 1783 1814-1817 1827-1829 1848-1851 1853 1865-1869 1882-1885 1898 1925-1927 1948- 1949 1951 1966-1974 1981-1983 2021-2024 2027-2030 2038 2042-2043 2052-2056 2060- 2064 2072-2074 2080-2082 2086-2087 2096- 2100 2118 2144 2146-2147 2153-2155 2177 2186-2187 2216-2221 2231-2232 2234-2242 2254 2267-2270 2275 2283 2310 2331 2380- 2382 2387 2424 2447 2452-2454 2456 2468 2473-2474 2499 2510 2536 2548 2573 2592 2604 2644 2657-2658 2706 2715-2718 2747 2754-2758 2761 2763-2764 2768-2771 2774- 2776 2783 2824-2826 2843 2865-2867 2894- 2895 2898 2945-2946 2961-2962 2989-2990 3008 3013-3014 3017-3020 3029 3139-3147 3167-3168 3195 3204 3212-3214 3217-3218 3226-3228 3242-3243 3256 3285 3289-3290 3304-3307 3339-3340 3442 3558-3562 3576 3588 3595-3596 3628 3689 3691 3707 3723 3735 3795-3800 3810 3871-3872 4014-4015 4040-4042 4060-4061 4071-4075 4114-4116 4121-4123 4126 4136 4142-4143 4230-4231 4241-4242 4252-4253 4335-4337 4379-4380 4449 4465 4542-4544 4549 4581-4586 4598- 4601 4740-4741 4796-4797 4832-4834 4864- 4865 4907-4910 5021-5023 5038-5039 5046- 5047 5107-5108 5284-5289 5372-5373 5387- 5391 5399-5401
Genomic DNA from BAC 63I18	Research Genetics (CITB BAC Library)	BAC001	3895
Genomic DNA from BAC 393I6	Research Genetics (CITB BAC Library)	BAC002	2639-2642

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
adult bladder	Invitrogen	BLD001	154-156 175-177 301-303 341-344 652-653 659-660 950 980-988 997-998 1042-1043 1069 1075 1139-1142 1160-1164 1193 1244- 1246 1307 1508-1510 1575-1576 1717 1728- 1734 1746 1805-1806 1870-1875 1882-1885 1903-1911 1981-1983 2004 2006-2007 2038 2060-2061 2072-2074 2118 2191-2192 2273 2283 2294-2295 2344 2639-2642 2721 2747 2818-2819 2914-2917 3112 3212 3280-3282 3424-3427 3470-3471 3536-3543 3664-3665 3691 3760 3791 3795-3800 4014-4015 4082- 4084 4335-4337 4613 4796-4797 4864-4865 4960 5001-5003 5241-5242 5387-5388 5431- 5433
bone marrow	Clontech	BMD001	30-31 42 48-50 74-78 114-115 120-123 137 143-165 175-177 213-215 227-230 232 235 278-290 297-303 305-309 313-315 324-325 335 341-344 354 379-380 394-398 435-438 440-441 447-455 462-471 491-492 513 516 520-521 538 551-553 557 561-562 641 652- 653 661-671 674 677-678 680-684 699-701 709-760 763-772 794-795 822-823 849-851 857-859 863-869 882-886 889-897 909-914 916-918 921 924-926 931-936 944-945 950- 956 969 980-988 992-995 997-1021 1026- 1027 1032-1034 1038-1040 1049 1053-1055 1070-1071 1075 1079 1108 1110-1113 1128- 1136 1139-1143 1151-1154 1173 1182-1184 1186-1187 1193 1198-1204 1217-1218 1220- 1221 1228 1230-1232 1249-1256 1264 1269- 1271 1274 1281-1282 1290-1291 1294-1297 1317-1319 1322-1345 1348-1362 1374-1379 1386-1387 1397-1399 1405-1407 1414-1417 1422-1423 1425 1437-1438 1440-1441 1444 1451-1464 1470 1479 1485-1489 1497-1500 1504-1505 1507-1512 1514-1515 1518-1520 1522-1526 1532-1563 1567-1576 1582-1585 1588-1589 1603-1608 1612 1621-1623 1625 1629-1632 1634-1637 1646-1648 1655-1656 1659-1660 1663-1664 1666-1670 1685-1690 1694-1698 1701-1702 1707-1708 1710-1716 1719-1721 1723-1724 1728-1739 1746 1752- 1753 1755-1756 1765-1771 1773-1779 1805- 1813 1830-1838 1853 1857-1860 1870-1875 1879-1881 1894-1896 1913-1922 1925-1936 1948-1951 1963 1966-1974 1978-1979 1993- 1998 2000-2003 2005 2017-2020 2027-2030 2036-2056 2060-2064 2066-2067 2080-2082 2086-2087 2095 2098-2102 2107-2108 2111- 2118 2121-2150 2153-2168 2172 2174-2177

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			2191-2195 2202-2203 2214-2221 2223 2229 2231-2242 2246-2248 2254 2262 2264 2273 2283 2288-2291 2294-2299 2302 2311-2312 2327-2330 2358 2377-2379 2387-2403 2418 2422-2424 2427 2440-2441 2443 2448-2465 2467-2469 2473-2474 2480 2488 2495 2510- 2513 2519-2520 2528-2531 2560 2572 2592 2598 2604 2628 2644-2648 2650 2656 2677- 2680 2686 2698-2699 2715 2719-2720 2722- 2744 2749-2750 2754-2758 2760-2761 2768- 2771 2774-2776 2781 2783 2785 2793-2820 2824-2826 2829 2843 2846-2847 2863-2867 2873-2874 2888 2891 2894-2895 2904-2905 2931-2939 2945-2946 2965-2973 2976 3008 3011-3012 3017-3022 3029 3041-3049 3054 3100 3102-3105 3150 3166-3175 3181-3186 3188-3194 3204 3208-3209 3212 3220-3222 3226-3230 3235-3243 3245-3252 3256-3273 3276-3277 3280-3283 3285 3289-3290 3299 3304-3307 3319-3322 3341-3346 3372-3373 3402 3406-3407 3422 3424-3427 3438-3441 3446-3449 3456 3466-3468 3470-3471 3486- 3487 3491-3495 3505-3506 3508-3513 3536- 3543 3550-3552 3557-3562 3566-3573 3576 3598-3607 3609-3614 3616-3628 3663-3665 3673-3677 3682 3707 3724-3725 3729-3730 3742-3744 3754 3761 3792 3794-3809 3817- 3821 3826 3828 3836-3861 3867-3869 3878- 3879 3881-3884 3897-3905 3911-3919 3955- 3957 3969-3971 4023 4028-4029 4052 4055- 4056 4082-4084 4094-4095 4101-4107 4109- 4120 4136 4142-4153 4156-4159 4167-4178 4208-4211 4215-4223 4227-4247 4267-4270 4275-4277 4285-4286 4291-4296 4383-4384 4430-4432 4494-4496 4501-4503 4517-4529 4531-4536 4554-4555 4572-4591 4596-4601 4624-4626 4649 4651 4662 4664-4665 4691- 4692 4729 4738-4741 4761-4780 4793-4810 4832-4834 4862-4865 4884 4907-4910 4923- 4928 4930-4931 4933-4935 4937-4943 4945 4961-4985 5001-5003 5038-5039 5050-5052 5080 5114-5115 5137-5141 5148-5149 5153- 5157 5180 5190-5192 5241-5242 5250 5252 5254-5277 5303-5305 5307-5325 5327-5343 5345-5354 5367-5374 5376-5379 5381-5385 5387-5388 5397-5398 5444 5460-5461 5464- 5466 5485
bone marrow	Clontech	BMD002	175-177 249-250 254 258-260 301-303 313- 315 324-325 413-414 440-441 491-492 540 574-577 580-581 592-594 599-601 612-620

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			652-653 724-733 741-750 804-805 814-816 846 849-851 889-897 903-905 910-914 957- 960 970 992 994 997-998 1010-1014 1023- 1027 1038-1040 1089-1091 1095 1110-1113 1128 1202-1207 1217-1218 1235-1236 1256 1271 1297 1319 1330-1333 1348-1350 1352- 1354 1357-1358 1383-1384 1397 1457-1462 1479 1491-1494 1497 1504 1507-1512 1532 1547-1548 1551-1552 1575-1576 1621-1623 1646-1647 1686 1719-1721 1727 1743-1745 1753-1754 1763-1764 1773-1779 1796-1798 1805-1806 1814-1817 1827-1830 1839-1844 1848-1851 1913-1918 1925 1993-1998 2040- 2043 2048 2052-2054 2060-2061 2078-2079 2088-2091 2116-2118 2131-2142 2148-2150 2172 2174-2176 2191-2195 2223 2246-2248 2318-2320 2537-2538 2553 2604 2638 2702- 2705 2709-2711 2713-2714 2739 2781 2796- 2798 2803 2931-2939 2961-2962 3026-3027 3055 3130 3159-3162 3181-3183 3246 3250- 3252 3304-3307 3402 3536-3543 3793 3847- 3849 3925-3926 4024-4025 4060-4061 4209- 4210 4228 4252-4253 4267-4270 4574 4581- 4582 4729 4787 4796-4797 4858 4907-4909 4974 4991-4993 5021-5023 5050-5052 5056 5148-5149 5260-5267 5272-5275 5278-5279 5335-5343 5377-5378 5416 5423-5425 5485
bone marrow	Clontech	BMD004	728-733 849-851 1349-1350 1486 1860 2050- 2051 2134-2136 2148-2150 2234-2242 2803 4209-4210 4598-4601 4652-4653 4907-4909 5261-5267 5272-5274
bone marrow	Clontech	BMD007	396-398 440-441 453-455 491-492 712-718 764-771 814-816 846 849-851 1096-1104 1146-1147 1315-1316 1486 1497 1522-1523 2134-2136 2148-2150 2223 2803 3250-3252 4598-4601 5001-5003 5050-5052 5310-5311
adult colon	Invitrogen	CLN001	1-2 32-34 64 175-177 251 278-283 452 478 814-816 832 870 889-897 944 957-960 1044- 1047 1069 1117-1119 1128 1139-1142 1195- 1196 1217-1218 1317-1318 1386-1387 1511- 1512 1547-1548 1640-1645 1709 1770-1771 1860 1870-1875 1882-1885 1948-1949 1952- 1953 1981-1983 2088-2091 2146-2147 2156- 2160 2174-2176 2208-2210 2254 2347-2348 2511-2513 2604 2629-2631 2737-2738 2831- 2832 2852-2853 2865 3035-3036 3156-3157 3220-3222 3246 3339-3340 3554-3556 3632- 3634 3663 3673-3677 3693 3780-3781 3870 3949-3951 4272 4275-4277 4330-4331 4534 4636-4637 4651 4668-4674 4776 4796-4797

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
Mixture of 16 tissues – mRNAs*	Various Vendors*	CTL016	210-211 910-914 995 1128 1479 1617-1619 1626 1784-1790 1913-1914 2901-2903 2979 3831-3833 4796-4797 5001-5003 5075-5077 5154-5157 5414-5415
Mixture of 16 tissues – mRNAs*	Various Vendors*	CTL021	175-177 237-240 652-653 801-803 849-851 950 993 1042-1043 1063-1067 1156 1310- 1314 1332-1333 1485 1511-1512 1533-1535 1746 2148-2150 2182-2183 2186-2187 2223- 2228 2233 2253 2484-2485 2843 2979 3189- 3191 3250-3252 4796-4797 4907-4909 5001- 5003 5050-5052 5196 5226
adult cervix	BioChain	CVX001	1-2 32-34 52 56 70 107-110 123 125 133-134 137 140-142 153-156 175-177 195-196 212 227-230 233 278-283 288-290 301-303 313- 315 324-325 335 341-344 365 379-380 394 396-398 491-492 514 520-521 539 583-590 597-598 611 682-684 697 699-701 708 719- 722 810 814-816 822-823 840-844 857-859 863-870 873-875 879-881 885-886 889-897 899 903-905 909 915 919-920 925-926 931- 936 950-953 957-962 975-988 992-995 997- 998 1000-1002 1022 1032-1034 1044-1047 1049 1052 1069 1075 1110-1113 1129-1130 1144-1145 1154-1155 1165-1170 1172-1173 1182-1184 1198-1204 1215-1216 1220-1221 1256 1263 1271 1287 1297 1300-1301 1319- 1321 1323-1328 1352-1355 1360-1371 1374 1397 1400-1401 1410 1413 1421 1440-1444 1455-1464 1470 1475-1477 1479-1480 1487 1491-1494 1504 1507-1510 1515-1517 1524 1547-1548 1551-1552 1557 1569-1574 1599- 1608 1611 1620 1625 1639 1648 1653-1654 1657-1658 1663 1683-1685 1690 1715-1716 1723 1735-1736 1753-1756 1763-1764 1780- 1783 1792-1795 1805-1806 1827-1829 1835- 1844 1852 1870-1877 1879-1881 1896 1925- 1927 1951 1964-1965 1993-1998 2000-2002 2005 2021-2024 2031-2035 2038 2042-2043 2048 2050-2056 2058-2059 2062-2064 2066- 2067 2072-2074 2078-2079 2086-2087 2096- 2100 2111-2114 2116 2118 2137 2143-2144 2146-2147 2156-2160 2177-2181 2191-2192 2216-2221 2223-2228 2234-2242 2249 2251- 2252 2254-2257 2273 2275 2277 2280-2282 2296-2299 2302 2327-2331 2333-2334 2341 2344 2349-2356 2358 2368 2377-2381 2389- 2390 2423-2424 2456 2467 2483 2490-2494 2499 2510-2513 2546 2549-2550 2560 2563 2573-2575 2591 2594-2595 2597 2603-2604 2628-2631 2645-2647 2651-2655 2706 2713-



Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			2715 2726 2752-2758 2760 2763 2768-2771 2774-2776 2783 2807 2809 2820 2824-2826 2829 2831-2832 2836-2839 2843-2845 2854 2865-2867 2871-2872 2898 2905 2925-2929 2931-2939 2945-2947 2954 2961-2962 2969- 2976 2979 2981-2983 2985 2989 3009 3017- 3020 3030 3080 3089 3093 3096-3097 3100 3109 3112 3130 3149 3156-3158 3170-3173 3181-3183 3195 3199 3206 3213-3214 3220- 3222 3224-3225 3247-3248 3253-3256 3258- 3267 3280-3282 3285 3289-3290 3292-3293 3310-3311 3319-3324 3341 3345-3346 3349- 3352 3394-3398 3403-3405 3409-3410 3420 3424-3427 3437-3441 3446-3449 3456 3462 3491-3495 3535-3543 3558-3560 3628-3630 3654-3657 3673-3677 3680 3691 3707 3714 3735-3736 3760 3772 3778 3795-3800 3807 3822-3824 3830 3870-3872 3882-3883 3891 3925-3926 3959-3960 3969-3971 4076 4098 4100-4102 4112-4116 4127-4130 4219-4223 4230-4231 4241-4242 4245 4289-4295 4322 4382 4391-4393 4403 4435-4437 4550 4581- 4582 4616-4621 4629-4632 4663 4675 4679 4681-4683 4761-4766 4785 4796-4797 4884 4910 4913 4953 4956-4957 4976-4979 5151- 5152 5177-5179 5272-5274 5284-5289 5293 5303-5305 5335-5343 5421-5425 5431-5433 5464-5466
diaphragm	BioChain	DIA002	574-577 1230-1232 1524 1605-1608 2116 2143 2843 3795-3800 4060-4061 4598-4601
endothelial cells	Stratagene	EDT001	1-2 32-34 38 45-46 56 70 74-77 137 140-142 165 173 175-177 187-190 195-196 213-215 220 231 278-283 294-295 313-315 330 332- 333 341-344 346-349 364 366-367 379-380 395 445-446 474 491-495 511 520-521 531- 532 545 548-553 574-577 612-620 652-653 682-684 697 704-706 709-711 719-722 801- 803 811-816 822-823 836-837 863-872 879- 881 885-886 889-897 899 903-914 919-920 927 930-936 944 950 954-962 964-966 969 971-988 993-995 997-998 1000-1002 1007- 1014 1017-1021 1026-1027 1032-1034 1036- 1040 1042-1052 1068-1071 1075-1076 1079 1089-1091 1095 1110-1113 1117-1119 1128- 1136 1139-1143 1151-1153 1155-1156 1160- 1164 1172 1192-1193 1198-1204 1217-1218 1220-1221 1235-1242 1244-1246 1249-1255 1281-1282 1287 1294-1297 1300-1301 1315- 1319 1328 1337-1345 1349-1355 1357-1359 1374 1380 1386-1387 1390-1393 1397-1401

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM001	2639-2642
esophagus	BioChain	ESO002	885-886 1639 2223
fetal brain	Clontech	FBR001	153 278-283 863-869 1156 1400-1401 1626 1691-1692 1727 2118 2229 2604 2645-2647 2844-2845 3174 3763 3780-3781 4090-4092 4140-4141 4545 4835
fetal brain	Clontech	FBR004	855-856 1017-1021 1470 1580-1581 1839- 1844 1978-1979 2052-2053 2084 2171 2249 3197 3451-3455 3713 4960
fetal brain	Clontech	FBR006	30-31 39-40 74-77 116-119 130 137 143-148 175-177 187-190 195-196 216-218 223-226 366-367 388-390 400-404 465 491-492 520- 521 557 602-603 607 647-649 652-653 670- 671 676 680-681 685 698 724-727 743-744 760 763 789-793 814-817 824-825 829-831 836-837 849-851 855-856 885-886 889-897 944 994 997-998 1000-1002 1017-1021 1026- 1027 1042-1043 1068-1069 1076 1089-1091 1095 1139-1142 1151-1153 1156 1176 1182- 1185 1192 1220-1221 1228 1230-1232 1332- 1333 1349-1350 1357-1358 1389 1394 1400- 1401 1403-1404 1408-1409 1413 1455-1456 1507-1510 1520 1605-1608 1617-1619 1629-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal brain	Clontech	FBRs03	1870-1875 1878 3424-3427 3554-3556 4907-4909 5137-5140
fetal brain	Invitrogen	FBT002	32-34 59-60 92-96 124 128 137 180-182 192 195-196 278-283 341-344 436 491-492 520-521 583-590 607 647-649 652-653 677-678 778-783 789-793 822-825 849-854 882-884 950 957-960 964-966 971-974 980-988 1026-1028 1038-1040 1042-1043 1050 1070-1071 1076 1127 1156 1205-1207 1230-1232 1271 1281-1282 1322 1337-1345 1349-1350 1360-1371 1386-1387 1400-1401 1414-1417 1427-1431 1435-1436 1470 1507-1510 1532 1603-1604 1617-1620 1633 1649-1653 1674-1682 1691-1692 1694-1698 1708 1710-1714 1727 1737-1739 1765-1769 1773-1774 1780-1783 1805-1806 1839-1844 1852 1870-1875 1882-1885 1896 1925 1964-1965 1978-1979 1990-1991 1993-1998 2031-2034 2058-2059 2084 2109-2110 2118 2173 2186-2187 2193-2195 2202-2203 2208-2210 2233 2254 2278 2288-2291 2305-2306 2414-2415 2496 2511-2513 2537-2538 2558-2559 2573 2579-2584 2590 2597 2604 2629-2631 2639-2642 2659-2662 2672-2674 2696-2697 2719-2720 2741-2743

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal heart	Invitrogen	FHR001	909 1089-1091 1128 1256 1514 1621-1623 3354 4228
fetal kidney	Clontech	FKD001	30-31 137 154-156 212 278-283 313-315 326-327 370-371 379-380 491-492 551-553 595 602-604 665-667 680-681 736-740 743- 744 822-823 900-902 950-956 995 1023-1025 1035 1085 1089-1091 1182-1184 1230-1232 1300-1301 1332-1333 1353-1354 1357-1359 1386-1387 1446-1449 1457-1462 1479 1515 1532 1551-1552 1580-1581 1588-1589 1612 1617-1619 1629-1632 1663 1667-1670 1719- 1721 1724 1746 1752-1754 1796-1798 1831- 1834 1845-1847 1896-1897 1925-1927 1951 1981-1983 1993-1998 2035 2045-2047 2111- 2114 2118 2144 2224-2228 2253 2360 2422 2440-2441 2502 2510 2526-2527 2549-2550 2645-2647 2650 2693 2763 2774-2776 2781 2831-2832 2844-2845 2879-2881 2898 2913 2960 2974-2975 2979 3031-3032 3054 3198 3230 3276-3277 3304-3307 3372-3373 3442 3446-3449 3491-3495 3536-3543 3714 3780- 3781 3853 4030-4031 4055-4056 4093 4581- 4582 4679 4864-4865 4907-4910 5001-5003 5038-5039 5050-5052 5142-5143 5148-5149 5329-5330 5372-5374
fetal kidney	Clontech	FKD002	313-315 551-553 699-701 743-744 784-786 1017-1021 1173 1182-1184 1403-1404 1753 2055-2056 2116 2118 2223 2253 4598-4601 4907-4909 5001-5003
fetal kidney	Invitrogen	FKD007	45-46 491-492 849-851 950-953 1507 1575- 1576 1746 2060-2061 2086-2087 2134-2136 2204-2207 2223-2228 2380-2381 2579-2584 3242 4581-4582
fetal lung	Clontech	FLG001	64 350-352 453-455 551-553 736-740 822- 823 863-869 997-998 1000-1002 1035 1042- 1043 1193 1275-1277 1317-1318 1374 1648 1674-1682 1707 1727 1746 1753 1830 1835- 1844 1852 1870-1875 1951 2004 2066-2071

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal lung	Invitrogen	FLG003	195-196 278-283 341-344 388-390 395 450-451 491-492 849-851 879-881 885-886 950 971-979 995 1128 1193 1237-1242 1269-1270 1386-1387 1450 1507 1514 1605-1608 1709 1746 1780-1783 1830 1835-1838 1848-1852 1860 1865-1875 1990-1991 2010-2013 2060-2061 2072-2074 2094 2174-2176 2233 2253 2283 2526-2527 2579-2584 2594-2595 2836-2839 2844-2845 2888 2896-2897 2913 2951-2952 2979 2985 3008 3123 3149 3200-3202 3212 3258-3259 3280-3282 3466-3468 3508-3513 3536-3543 3605 3629-3630 3691 3749-3752 3793 3840-3841 4016-4018 4114-4116 4258 4330-4331 4598-4601 4897 5102-5104 5119 5276-5277
fetal lung	Clontech	FLG004	154-156 971-974 1070-1071 1182-1184 1527-1531 1701-1702 1753 1896 3462 3629-3630 5001-5003 5241-5242
fetal liver-spleen	Columbia University	FLS001	1-13 24-27 29-50 52-99 111-113 115 126 133-134 136 140-142 154-156 166-192 195-222 227-230 232-236 241-283 286-287 291 307-310 313-327 330-334 336-361 365-367 369-375 379-383 386-394 396-420 422-431 435-446 453-456 461 474-475 478-481 483-505 507-532 534-545 548-553 557 561-562 565-567 569-577 580-581 583-607 611-620 629-631 633-650 652-653 655-662 682-684 699-701 704-706 709-711 724-727 736-740 743-744 747-750 755-759 773-829 832-835 839-854 857-877 882-886 889-905 909-921 924 927-966 968-969 971-988 990-995 997-1014 1017-1050 1052-1055 1058-1059 1063-1074 1076 1078-1082 1085-1088 1092 1094 1096-1104 1107-1108 1110-1113 1115-1121 1124 1127-1145 1148 1150-1175 1177-1223 1225-1256 1263-1289 1292-1301 1307-1327 1332-1335 1337-1345 1349-1350 1352-1355 1357-1371 1374-1379 1386-1387 1389-1393 1395-1397 1400-1401 1403-1406 1408-1410 1414-1423 1425 1432 1434 1437-1438 1440-1444 1446-1462 1467-1473 1479-1480 1485-1486 1495-1500 1504 1507-1510 1513-1514 1518-1519 1522-1524 1527-1538 1540-1548 1551-1557 1559-1576 1579-1608 1611-1623

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal liver-spleen	Columbia University	FLS002	3-11 24-27 35 38 42 44 48-50 57 67 70 73-77 85 88 98 107-111 136-142 151-153 165 173 195-196 198 201-205 210-215 219 222 232- 234 236 245 252-254 258-266 277 291 316- 320 332-333 337 354 357-361 365 374-375 381-383 394 406 415-416 418 436-438 445- 446 461 478-480 486 489-490 520-521 527 538 540 543 548-553 574-577 599-601 607 612-620 647-649 677-678 682-685 699-706 709-711 736-740 747-750 755-759 777 788- 793 814-816 818 822-828 833 852-854 863- 869 873-877 885-886 889-897 899-902 906- 914 916-920 924 927-936 946-949 951-956 961-962 969 975-988 990-991 993-995 999- 1014 1023-1037 1041-1047 1052 1055 1063- 1067 1070-1071 1076 1080 1085 1088 1108 1110-1119 1124 1128-1142 1144-1145 1148 1151-1156 1158 1160-1170 1172-1175 1177- 1184 1186-1187 1192-1193 1195-1197 1202- 1204 1208-1212 1215-1218 1220-1221 1225- 1227 1235-1236 1244-1246 1249-1256 1263 1266-1273 1278-1280 1285-1291 1297-1301 1307 1315-1316 1320-1327 1332-1333 1349- 1350 1352-1355 1357-1371 1374-1379 1385- 1387 1389 1395-1397 1405-1406 1410 1414- 1417 1421-1423 1425 1427-1432 1437 1442- 1444 1451-1456 1463-1464 1470-1473 1475- 1477 1479-1480 1485 1498-1499 1515 1536- 1538 1540-1546 1550-1557 1559-1560 1580- 1585 1597 1603-1608 1612-1616 1620 1625- 1627 1629-1632 1638-1653 1656 1661-1662 1664 1667-1682 1685 1691-1692 1694-1699 1701-1704 1706-1707 1709-1714 1717 1719-



Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal liver-spleen	Columbia University	FLS003	210-211 341-344 849-851 1089-1091 1177-1179 1310-1314 1320-1321 1349-1350 1440-1441 1514 1557 1624 1648 2042-2043 2134-2136 2223 2253-2254 2511-2513 2533 2843 2979 4163-4166 4273-4274 4687-4689 4738-4739 4998-4999 5075-5077 5414-5415 5452-5453
fetal liver	Invitrogen	FLV001	3-11 52 246-247 255-260 278-283 291 341-344 491-492 596 652-653 709-711 724-727 778-783 814-816 840-844 849-851 882-886 903-905 946-949 964-966 971-988 997-998 1003-1006 1010-1014 1026-1027 1038-1040 1044-1047 1063-1068 1070-1071 1089-1091 1137-1138 1143 1171 1177-1179 1182-1184 1193 1198-1201 1205-1207 1310-1314 1317-1318 1320-1321 1337-1345 1349-1350 1360-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal liver	Clontech	FLV002	1411 1605-1608 1625 4581-4582 5323-5325
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fetal muscle	Invitrogen	FMS001	3-11 154-156 216-218 278-283 313-315 341- 344 388-390 395 478 491-495 511 591 652- 653 704-706 814-816 822-823 889-897 903- 908 925-926 928-929 931-936 946-950 957- 960 980-988 993 1017-1021 1048-1050 1063- 1068 1171 1297-1299 1307 1320-1321 1359 1444 1507-1510 1514 1533-1535 1540 1553- 1556 1585 1605-1608 1639 1694-1698 1710- 1714 1717 1746 1753 1773-1774 1780-1783 1805-1813 1860 1879-1885 1915-1918 2004 2042-2043 2107 2118 2134-2136 2148-2150 2161-2162 2197-2199 2254-2257 2281-2282 2503-2504 2665 2686 2824-2826 2843 2852- 2853 2896-2897 2979 2985 3054 3058-3059 3159-3162 3213-3214 3226-3228 3280-3282 3299 3323-3324 3365-3366 3372-3373 3658-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal muscle	Invitrogen	FMS002	341-344 652-653 1298-1299 1389 1400-1401 1507 1727 1746 1753 2042-2043 2191-2192 2224-2228 2761 2979 3123 3257 4285-4286 4410-4412
fetal skin	Invitrogen	FSK001	1-2 39-40 70 92-95 137 157-159 175-177 213-215 246-247 278-283 291 298-300 313- 315 341-344 365 370-371 388-390 419 445- 446 452 478-480 511 516 522-524 538-539 548-553 580-581 597-598 602-603 633-634 647-649 652-653 677-678 685 709-711 784- 786 789-793 814-816 824-829 849-851 863- 870 879-884 903-905 909 919-920 925-926 946-949 957-960 980-988 992-994 997-1002 1010-1014 1017-1021 1035 1042-1047 1050- 1051 1076 1078 1110-1113 1117-1119 1129- 1130 1151-1155 1160-1164 1182-1184 1198- 1204 1237-1243 1256 1271 1290-1291 1307 1310-1314 1320-1321 1323-1327 1351 1355 1357-1359 1380 1385 1390-1393 1400-1401 1414 1418-1420 1432 1435-1436 1450 1457- 1462 1479 1488-1489 1507-1510 1524 1533- 1535 1547-1548 1550-1552 1567-1568 1575- 1576 1579 1585 1588-1589 1611 1617-1619 1621-1623 1653-1655 1663 1686 1688-1689 1691-1692 1694-1698 1703-1704 1710-1714 1743-1746 1753 1765-1771 1773-1774 1780- 1783 1807-1813 1830-1834 1848-1852 1865- 1878 1882-1885 1903-1911 1915-1918 1925- 1927 1954-1962 1964-1965 1981-1983 1990- 1991 2006-2007 2017-2030 2038 2054 2068- 2071 2076-2079 2088-2091 2098-2100 2107 2118 2145 2153-2155 2173 2177 2179-2181 2188 2191-2192 2204-2210 2214-2215 2246- 2248 2251-2253 2267-2271 2277 2280 2286- 2291 2305-2306 2310 2338-2340 2376 2386 2432 2434-2435 2437 2469 2483 2490-2491 2510-2513 2526-2527 2560 2563 2572-2573 2588-2589 2594-2595 2603 2628 2659-2662 2696-2697 2734 2741-2743 2754-2758 2782 2787-2789 2813 2819 2824-2826 2828 2831- 2832 2843-2845 2855-2860 2865 2873-2874 2905 2914-2917 2925-2929 2945-2946 2951- 2952 2955 2961-2962 2965-2975 2979 2981- 2983 2985 2989 2996-2998 3000 3008 3023 3082 3109-3110 3151-3153 3156-3157 3167- 3168 3195 3213-3216 3220-3222 3234 3247-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal skin	Invitrogen	FSK002	313-315 341-344 366-367 551-553 971-974 1038-1040 1151-1153 1271 1353-1354 1507-1510 1588-1589 1755-1756 1870-1875 1903-1911 1926-1927 1952-1953 2017-2020 2027-2030 2078-2079 2197-2199 2377-2379 2669-2671 2677-2680 2931-2939 3167-3168 3189-3191 4082-4084 4613 4907-4909 5423-5425
fetal spleen	BioChain	FSP001	175-177 743-744 1171 1202-1204 1457-1462 1753 2060-2061 2116 2143 2223 2253 2728-2729 4167-4168 5001-5003 5335-5343 5444
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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fetal brain	GIBCO	HFB001	3-11 32-34 39-40 42 78 81-82 100-110 116-119 124-142 154-156 165 175-177 195-196 201-205 212-218 220 278-283 286-287 291-296 313-315 335 341-344 346-349 366-367 379-380 388-390 396-398 419 456-461 491-492 511 551-553 557 561-562 574-577 583-590 651-653 676-679 682-694 697-711 743-744 784-786 804-805 814-816 822-825 848-851 855-859 863-869 871-872 882-884 899-902 915-918 927 930-936 944-945 951-953

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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macrophage	Invitrogen	HMP001	244 278-283 440-441 445-446 794-795 855-856 995 999 1017-1021 1353-1354 1507 1582-1584 2223 4228 4864-4865 5490-5491
infant brain	Columbia University	IB2002	32-35 39-40 45-47 64 70 74-77 81-82 92-95 100-110 116-119 124 126 136 154-156 175-177 180-182 195-196 213-218 227-230 246-247 254 278-283 291 296 340 346-352 362 364-365 388-390 413-414 419 445-446 459 491-492 509 511 551-553 574-577 579-590 592-594 607 652-653 675-676 680-681 743-744 755-757 789-793 796 806-808 824-825 832 849-851 855-859 863-872 900-918 924 927 944 951-956 964-966 971-988 990-995 997-998 1008-1009 1022 1026-1027 1036-1040 1042-1043 1049-1054 1069-1071 1088-1091 1110-1113 1117-1121 1127 1129-1130 1139-1143 1154-1155 1159 1172-1173 1175 1180-1181 1192-1193 1198-1207 1217-1218 1220-1221 1230-1232 1235-1236 1256 1263 1274 1281-1282 1290-1291 1297 1300-1301 1307 1315-1316 1319-1321 1328 1334-1335 1349-1350 1357-1359 1363-1371 1394-1399 1402-1404 1410-1411 1413-1420 1422-1424 1427-1431 1437 1439-1441 1444 1451-1462 1465-1470 1479 1485 1498-1499 1507-1510 1540 1547-1548 1550-1552 1580-1584 1586-1587 1592 1603-1608 1617-1620 1638-1639 1646-1648 1653 1656 1664-1673 1693-1699 1719-1721 1727-1734 1737-1739 1743-1745 1752-1756 1763-1769 1773-1774 1780-1783 1805-1806 1814-1817 1830-1834 1848-1852 1865-1885 1896-1897 1899 1903-1911 1926-1927 1951-1962 1964-1974 1978-1979 1990-1991 2000-2003 2010-2013 2017-2020 2025-2030 2052-2056 2058-2061 2066-2067 2092 2098-2100 2131-2133 2138-2144 2151-2152 2161-2162 2171 2177 2186-2190 2200-2201



Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			2208-2210 2214-2215 2224-2228 2244-2245 2249 2251-2253 2273 2288-2291 2296-2299 2303-2304 2310-2312 2333-2334 2361 2386 2414-2415 2417-2423 2427 2430 2432 2437 2439 2465 2499 2511-2513 2526-2527 2536 2548-2550 2552 2558-2559 2574-2575 2579- 2584 2587 2590-2597 2603 2626 2628 2637 2644 2648 2656 2659-2662 2664 2677-2680 2686 2692 2702-2705 2734 2741-2743 2745 2747-2748 2751-2753 2779 2781 2784 2786 2813 2818-2819 2821-2823 2828 2843 2848- 2850 2863 2865 2869-2870 2896-2898 2913 2925-2929 2931-2939 2951-2952 2965-2976 2978 2981-2983 2996-2998 3009 3017-3020 3026-3027 3031-3032 3082 3084-3085 3090 3096-3097 3102-3105 3110 3136-3137 3174 3189-3191 3198-3199 3203 3208-3209 3212- 3216 3219-3222 3229 3243 3260-3267 3312 3315 3319-3322 3325 3328-3330 3354 3372- 3373 3394-3398 3424-3427 3442 3462 3472- 3473 3477-3478 3505-3506 3514 3524-3532 3535-3543 3554-3556 3558-3560 3574-3580 3586-3588 3590 3599-3601 3624-3625 3628 3638-3640 3658-3663 3668-3669 3690-3691 3693 3699 3701 3707 3723 3728 3747 3761 3780-3781 3828 3864-3865 3871-3872 3891 3911-3919 3955-3958 3966-3974 3997-3998 4027 4030-4031 4040-4045 4048-4051 4055- 4056 4068-4069 4071-4075 4077-4079 4081- 4084 4087-4089 4098-4099 4124-4126 4131 4137-4139 4157-4158 4220-4223 4230-4235 4275-4277 4291-4295 4322 4329 4335-4337 4383-4385 4400 4425 4461-4464 4481-4489 4545-4548 4550 4554-4555 4558 4570-4571 4581-4582 4628 4633-4634 4636-4637 4652- 4653 4676 4776 4817 4907-4909 4946 4960 5000-5003 5046-5047 5075-5077 5095-5097 5100-5101 5116 5137-5140 5142-5143 5150- 5152 5154-5157 5184-5187 5234 5241-5242 5276-5279 5291 5310-5311 5414-5415 5445- 5447 5452-5453 5485 5497
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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infant brain	Columbia University	IBM002	133 491-492 682-684 743-744 889-897 1038- 1040 1427-1431 1474 1580-1581 1633 1903- 1911 2025-2026 2146-2147 2188 2310 2376 2726 2787-2789 2904 2992 3212-3214 3224- 3225 3325 3477-3478 3638-3640 3827 3966- 3968 4055-4056 4118 4131 4275-4277 4643 5044
infant brain	Columbia University	IBS001	153 197 350-352 459 574-577 743-744 826- 828 871-872 903-905 969 995 997-998 1042- 1043 1068 1127 1151-1153 1287 1349-1350 1559-1560 1694-1698 1773-1774 1848-1851 1978-1979 2054-2056 2111-2114 2143 2200- 2201 2365 2521 2664 2707-2708 2843 2945- 2946 2978 3260-3267 3424-3427 3599-3601 3624-3625 3737-3738 3891 4114-4116 4125 4245 4291-4295 4635 4907-4909
lung, fibroblast	Stratagene	LFB001	137 313-315 435 491-492 579 822-823 885- 886 910-914 944 950 961-962 994-995 997- 998 1000-1002 1026-1027 1049-1050 1052 1068 1075 1079 1110-1113 1129-1130 1143 1172 1182-1185 1192 1202-1204 1266-1267 1274 1287 1294-1296 1298-1299 1307 1315- 1318 1351 1374 1395-1396 1400-1401 1407 1411 1418-1420 1444 1455-1456 1473 1485 1507 1516-1517 1532-1535 1547-1548 1553-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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lung tumor	Invitrogen	LGT002	32-34 42 45-46 67 96 100-106 116-120 136- 139 153 175-177 179 195-196 213-218 227- 230 278-283 298-300 313-315 324-325 332- 333 341-344 346-349 357-361 365 379-380 393-394 400-404 420 436 474 478 483-485 491-492 513-514 538 548-550 557 574-577 580-581 605-607 611 652-653 682-684 699- 701 709-711 723 728-733 743-744 764-771 778-783 799-803 840-844 852-854 857-859 873-875 885-886 889-897 909-920 924 946- 956 964-966 969 971-979 992-995 997-1006 1008-1009 1023-1027 1036-1040 1042-1043 1048-1050 1063-1067 1088-1091 1110-1113 1117-1119 1128-1130 1139-1143 1151-1153 1155-1156 1160-1164 1172-1173 1185 1193 1202-1212 1217-1218 1220-1221 1229-1232 1235-1236 1244-1246 1269-1271 1300-1301 1315-1318 1323-1328 1330-1333 1349-1355 1357-1359 1363-1371 1374 1397 1403-1404 1408-1409 1418-1423 1432 1434 1438 1440- 1441 1446-1449 1463-1464 1467-1470 1473 1480 1491-1494 1505 1507-1512 1533-1535 1541-1548 1550-1557 1569-1574 1585 1591 1611-1612 1617-1619 1621-1623 1625 1629- 1632 1639-1645 1648 1654-1655 1657-1660 1663-1664 1671-1673 1685 1687-1689 1691- 1692 1694-1698 1706-1707 1710-1716 1719- 1721 1727-1739 1743-1746 1763-1771 1780-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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leukocyte	Clontech	LUC003	1-2 48-50 154-156 195-196 286-287 313-315 324-325 395 520-521 557 602-603 772 784- 786 814-816 822-823 863-869 885-886 906- 908 944 954-956 963 980-988 995 1050 1080 1122 1129-1130 1182-1184 1192 1198-1201 1317-1319 1348-1350 1353-1355 1357-1358 1374 1432 1450 1507 1516-1517 1532-1535 1547-1548 1664 1686 1715-1716 1737-1739 1753 1814-1817 1857-1859 1888-1893 1903- 1911 1919-1922 1950 1984 2010-2013 2035 2038 2054 2058-2061 2116 2118 2125-2133 2178 2191-2192 2223 2278 2572 2574-2575

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	1-2 52 96 138-139 278-283 313-315 479-480 491-495 511 799-800 822-823 829 847 863-869 871-875 889-897 944 951-953 957-962 980-988 993 1017-1021 1038-1040 1042-1043 1129-1130 1172-1173 1182-1184 1202-1204 1220-1221 1237-1242 1269-1270 1290-1291 1337-1345 1359 1400-1401 1403-1404 1432 1435-1436 1438 1442-1443 1457-1464 1475-1477 1489 1505 1507 1524 1532 1536-1538 1547-1548 1551-1556 1575-1576 1585 1603-1604 1611 1617-1619 1648 1663 1688-1689 1691-1692 1701-1702 1715-1716 1719-1721 1724 1735-1736 1746 1755-1756 1780-1783 1845-1847 1876-1877 1882-1885 1925 1954-1962 1981-1983 2005 2045-2047 2058-2061 2088-2091 2115 2118 2138-2142 2144 2178 2189-2190 2197-2199 2223 2254 2266 2277 2281-2282 2284 2298-2299 2310 2347-2348 2389-2390 2418 2424 2427 2440-2441 2443 2510-2513 2548 2591 2597 2637 2659-2662 2781 2783 2814 2824-2826 2843-2845 2857-2860 2898 2905 2945-2946 2955 2969-2973 3008 3029 3094-3095 3130 3166 3170-3173 3195-3196 3226-3228 3240 3258-3259 3339-3340 3438-3441 3443 3459-3460 3574-3575 3577-3580 3589 3599-3601 3635 3658-3660 3691 3753 3815-3816 3828 3878-3879 3941-3942 3966-3968 4077-4079 4104-4105 4121-4122 4132-4133 4142-4144 4241-4242 4275-4277 4287-4288 4326 4391-4393 4546-4548 4672-4674 4679 4737 4796-4797 4835 4902 5055 5057-5065 5085-5088 5280 5308-5309 5389-5391 5421-5422
mammary gland	Invitrogen	MMG001	1-2 12-13 39-40 47 62 81-82 96 116-119 126 173 175-177 180-182 195-196 213-215 227-230 236 246-247 258-260 274 278-283 313-315 321 341-344 346-349 354 365-367 399 419-420 445-446 450-451 478 491-492 520-521 538 543 580-581 583-590 602-603 607 629-630 647-649 652-653 670-671 677-678 682-684 697 709-711 728-733 743-744 764-771 789-793 796 801-803 806-808 814-816 840-844 870 879-881 885-886 900-905 909-



Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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induced neuron cells	Stratagene	NTD001	313-315 548-553 682-684 814-816 903-905 909 944 950 969 993 1017-1021 1026-1027 1036-1037 1070-1071 1088 1285 1294-1296 1315-1316 1322 1357-1358 1363-1371 1403- 1404 1520 1536-1538 1620 1629-1632 1638 1663 1701-1702 1707-1708 1724 1753 1770- 1771 1915-1918 1925-1927 1950 1993-1998 2017-2020 2025-2026 2058-2061 2083 2121- 2124 2144 2151-2152 2197-2199 2331 2386 2469 2573 2596 2628 2752-2753 2843 2898 2925-2929 2961-2962 2969-2973 3172-3173 3189-3191 3224-3225 3253-3255 3310-3311 3428-3429 3470-3471 3673-3677 3760 3969- 3971 4014-4015 4082-4084 4090-4092 4100 4114-4116 4140-4141 4272 4285-4286 4470 4616-4621 4691-4692 4761-4763 4864-4865 4907-4909 5137-5140 5298-5302
retinoic acid induced neuronal cells	Stratagene	NTR001	195-196 278-283 388-390 743-744 855-856 995 1038-1040 1139-1142 1418-1420 1533- 1535 1780-1783 1903-1911 2060-2061 2223 2592 3289-3290 3969-3971 4598-4601
neuronal cells	Stratagene	NTU001	74-77 195-196 246-247 278-283 294-295 341-344 388-390 491-492 566 652-653 680- 681 743-744 755-757 784-786 801-803 855- 856 863-869 900-902 919-920 950 964-966 995 997-998 1000-1002 1076 1159 1235- 1236 1294-1297 1432 1451-1454 1507 1533- 1535 1605-1608 1648 1667-1670 1688-1689 1691-1692 1694-1698 1703-1704 1746 1753 1765-1769 1831-1834 1848-1851 1900-1902 1925 1966-1974 2060-2061 2088-2091 2095

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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pituitary gland	Clontech	PIT004	175-177 227-230 491-492 796 822-823 849-851 992 995 1017-1021 1042-1043 1160-1164 1182-1184 1202-1204 1215-1216 1220-1221 1300-1301 1317-1318 1320-1321 1398-1399 1410 1479 1507 1540 1553-1556 1582-1585 1591 1625 1648 1657-1658 1663 1708 1753 1870-1875 1925 2060-2061 2068-2071 2118 2447 2604 2696-2697 2715 2774-2776 2843 2871-2872 3021-3022 3100 3203 3331-3332 3339-3340 3424-3427 3577-3580 3684 3787-3788 3959-3960 4549 5431-5433
placenta	Clontech	PLA003	1052 1215-1216 1694-1698 1919-1922 2116 3969-3971 4672-4674 5001-5003 5241-5242
prostate	Clontech	PRT001	42 165 246-247 335 511 548-550 675 847 873-875 879-881 889-897 910-914 946-949 980-988 993 995 1008-1009 1038-1040 1049 1128 1154 1157 1173 1182-1184 1202-1204 1297 1317-1318 1352 1357-1359 1398-1399 1414 1457-1462 1485 1498-1499 1524 1553-1556 1629-1632 1648 1683-1684 1688-1689 1718-1721 1746 1753 1770-1771 1792-1795 1831-1834 1860 1870-1875 1879-1881 1925-1927 1990-1991 2005 2035 2038 2045-2047 2055-2056 2060-2064 2083 2088-2091 2118 2144 2179-2181 2202-2203 2229 2254 2277 2283 2296-2297 2303-2304 2315 2337-2340 2387 2418 2423 2427 2445 2456 2468 2475 2492-2495 2510 2536 2543-2544 2546 2549-2550 2574-2575 2591-2592 2604 2645-2647 2649 2659-2662 2712 2721 2749-2750 2760 2857-2860 2871-2872 2894-2895 2909-2911 2925-2929 2951-2952 3005 3013-3014 3017-3020 3029 3081 3100 3121 3148 3174 3199 3226-3228 3242 3250-3252 3276-3277 3280-3282 3558-3560 3606-3607 3694-3696 3765 3891 3962 4067 4101-4102 4232-4235 4383-4384 4461-4464 4533 4546-4548 4581-4582 4796-4797 4882 4886 4899 4907-4910 4967-4970 5073 5078 5295-5296 5431-5433
rectum	Invitrogen	REC001	39-40 61 64 278-283 298-300 491-492 561-562 652-653 789-793 870 879-881 957-960 997-998 1007 1042-1043 1070-1071 1131-1136 1159 1217-1218 1235-1242 1272-1273 1275-1277 1317-1319 1363-1371 1380 1386-

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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salivary gland	Clontech	SAL001	48-50 116-119 154-156 175-177 313-315 396-398 491-492 543 591 784-786 826-828 910-914 924 950 994-995 999 1023-1025 1036-1037 1049 1128 1202-1204 1230-1232 1237-1242 1297 1322 1332-1333 1352 1418- 1420 1446-1449 1473 1480-1484 1498-1499 1507 1511-1512 1533-1535 1541-1546 1667- 1670 1686 1746 1763-1769 1792-1795 1839- 1844 1857-1859 1865-1875 1882-1885 1919- 1922 1948-1949 1951 1978-1979 2017-2020 2055-2056 2118 2125-2130 2138-2142 2146- 2147 2179-2181 2251-2252 2255-2257 2273 2280 2286-2287 2395 2403 2405-2413 2423 2499 2536 2591 2629-2631 2700 2712 2781 2784 2843-2845 2855-2856 2898 2965-2968 3008 3021-3022 3075 3236 3280-3282 3319- 3322 3462 3491-3495 3632-3634 3778 3867- 3869 3966-3968 4291-4295 4333 4581-4582 4598-4601 4681-4683 4729 4953 5001-5003 5148-5149 5270 5272-5274 5406-5407 5464- 5466
salivary gland	Clontech	SALs03	341-344 1089-1091 1435-1436 1511-1512 1664 1708 4907-4909 5272-5274
skin fibroblast	ATCC	SFB001	491-492 1089-1091 1182-1184 1685 2005 2223 5423-5425
skin fibroblast	ATCC	SFB002	175-177 1089-1091 1182-1184 1688-1689 1763-1764 3289-3290 5423-5425
skin fibroblast	ATCC	SFB003	366-367 840-844 1089-1091 1557 1688-1689 2005 3313 5423-5425
small intestine	Clontech	SIN001	154-156 179 191 201-205 212 277 341-344 357-361 435 457 652-653 698 873-875 944 969 997-999 1032-1034 1048 1063-1067

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			1078 1128 1131-1136 1139-1142 1154 1182-1184 1323-1327 1359 1451-1454 1511-1512 1540 1550-1552 1626 1634-1637 1640-1645 1655 1663 1688-1689 1703-1704 1710-1714 1805-1806 1827-1829 1839-1844 1964-1965 1981-1983 2004-2005 2055-2056 2068-2071 2086-2087 2096-2097 2156-2160 2234-2242 2311-2313 2321 2338-2340 2385 2510 2536 2603-2604 2628 2665 2748 2840-2841 2843 2951-2952 2954 2964 2969-2973 3100 3151-3152 3181-3183 3193 3309-3311 3331-3332 3403-3404 3470-3471 3590 3689 3729-3730 3810 3878-3879 3893 3941-3942 3959-3960 3973-3983 4004 4062-4064 4239-4240 4382 4560 4668-4671 4796-4797 4864-4865 4890-4891 4910 5001-5003 5057-5065 5080 5148-5149 5272-5274 5335-5343 5399-5401 5435-5437 5444-5447
skeletal muscle	Clontech	SKM001	1-2 154-156 175-177 216-218 245 313-315 346-349 354 574-577 849-851 928-929 957-960 971-974 1003-1006 1032-1034 1076 1300-1301 1334-1335 1395-1396 1403-1404 1432 1550 1691-1692 1735-1739 1746 1830 2049 2118 2548 2560 2592 2629-2631 2746 2785 2819 2843 3121 3181-3183 3310-3311 3432 3663 3737-3738 3943-3948 4534 5095-5097
skeletal muscle	Clontech	SKM002	1688-1689 2234-2242 2288-2291 3795-3800 5423-5425
skeletal muscle	Clontech	SKMs03	1688-1689 3795-3800
skeletal muscle	Clontech	SKMs04	1585 3536-3543 3795-3800 5154-5157
spinal cord	Clontech	SPC001	30-31 74-77 123 134 154-156 175-177 213-215 301-303 313-315 421 491-492 520-521 751 796 822-823 849-851 855-856 863-869 871-872 889-897 909 924 927 950-953 964-966 980-988 997-998 1017-1021 1026-1027 1049 1053-1054 1089-1091 1127 1151-1154 1159 1173 1175 1182-1184 1189-1191 1215-1216 1220-1221 1230-1232 1319-1321 1349-1350 1355 1359 1363-1371 1388-1393 1398-1399 1422-1423 1432 1446-1449 1470 1532 1539 1541-1546 1551-1552 1569-1574 1582-1584 1649-1653 1663 1685 1688-1689 1707 1715-1716 1727 1735-1736 1792-1798 1831-1834 1839-1844 1915-1922 1951 1992 2005 2017-2020 2035 2042-2043 2057 2060-2061 2072-2074 2086-2087 2096-2097 2118 2143-2144 2173 2186-2187 2193-2195 2208-2210

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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adult spleen	Clontech	SPLc01	491-492 548-550 561-562 641 652-653 801- 803 863-869 944 969 971-974 995 1128 1171 1205-1207 1271 1290-1291 1330-1331 1353- 1354 1508-1510 1547-1548 1551-1552 1605- 1608 1621-1623 1625 1694-1698 1743-1745 1753 1796-1798 1827-1829 1848-1851 2054 2066-2067 2098-2100 2111-2114 2179-2181 2193-2195 2537-2538 2604 2925-2929 3017- 3020 3234 3240 3250-3252 3289-3290 3402 3536-3543 3667 3975-3983 4114-4116 4136 4549 4652-4653 4691-4692 4796-4797 4907- 4909 5001-5003 5050-5052 5144 5241-5242 5270 5335-5343 5346-5354 5389-5391
stomach	Clontech	STO001	47 134 154-156 286-287 394 440-441 468 707 754 950-953 961-962 995 1041 1050 1070-1071 1075 1160-1164 1182-1185 1195- 1196 1256 1414 1507 1511-1512 1524 1638 1648 1664 1674-1682 1687 1724 1746 1780- 1783 1819 1952-1953 2093 2118 2121-2124 2188 2216-2221 2234-2242 2251-2252 2258- 2260 2273 2424 2464 2511-2513 2522 2548 2626 2645-2647 2650 2664 2675-2676 2686 2726 2820 2842 2898 2957 3008 3114 3172- 3173 3197 3258-3259 3285 3310-3311 3374- 3382 3428-3429 3456 3508-3513 3584-3585 3693 3882-3883 3906 3969-3971 4241-4242 4400 4498-4500 4672-4674 4910 4967-4970 5431-5433 5497
thalamus	Clontech	THA002	14-22 52 70 96 131-132 154-156 235 296 313-315 354 400-404 436 551-553 709-711 822-823 829 964-966 969 997-998 1026-1027 1038-1040 1044-1047 1051 1129-1130 1154 1175 1182-1184 1193 1244-1246 1249-1255

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
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thymus	Clontech	THM001	28 39-40 42 52 125 137 157-159 165 175-177 198 235 274 277 284 366-367 394 450-451 491-492 499 516 583-590 605-606 659-660 707-711 764-771 822-823 840-844 847 852- 854 863-869 899 944 950-953 980-988 997- 999 1017-1021 1026-1027 1075-1076 1080 1131-1136 1139-1142 1173-1174 1182-1184 1202-1204 1230-1232 1290-1291 1308-1309 1359 1380 1389 1397 1410 1414 1418-1423 1434 1444 1450 1470 1479 1485 1507 1511- 1512 1516-1517 1524 1551-1557 1569-1574 1597 1611 1617-1619 1659-1660 1663 1686 1709-1714 1719-1721 1727 1746 1753 1763- 1764 1792-1795 1827-1829 1857-1859 1876- 1877 1879-1881 1915-1922 1926-1927 1954- 1962 2000-2002 2031-2034 2038 2049 2054 2060-2061 2098-2100 2118 2125-2133 2138- 2142 2145 2148-2150 2153-2160 2191-2192 2214-2215 2246-2248 2254-2257 2267-2270 2273 2280 2284 2298-2299 2301 2307 2338- 2340 2427 2456 2468 2490-2491 2536 2542 2561-2562 2604 2730 2739 2752-2758 2820 2843 2866-2867 2873-2874 2913-2917 2919- 2920 2954 2974-2975 3009 3025 3035-3036 3088 3094-3095 3117 3149 3170-3171 3210- 3211 3226-3229 3235 3238 3250-3255 3283 3289-3290 3314 3342-3344 3428-3429 3508- 3513 3591-3593 3605 3608 3624-3625 3632- 3634 3636 3689 3691 3723 3772 3778 3780- 3781 3784-3786 3815-3816 3864-3865 3882- 3883 3891 3897-3905 3925-3926 3958 3962 4093 4100 4112-4116 4126-4130 4228 4287- 4288 4581-4582 4598-4601 4652-4653 4662

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			4796-4797 4839 4910 5000-5003 5137-5140 5148-5149 5190-5192 5272-5274 5317-5320 5384 5483
thymus	Clontech	THMc02	39-40 52 74-77 92-96 136 154-159 168 175- 177 244 258-260 301-303 316-320 365-367 400-404 462 471 491-492 498 516 522-524 531-532 551-553 557 602-603 607 647-649 670-671 697 699-701 709-711 728-733 784- 786 822-823 829 833 840-844 863-869 885- 886 925-926 931-936 944 950 971-974 993 995 997-999 1003-1006 1017-1021 1042- 1047 1070-1071 1075 1110-1113 1128 1131- 1136 1171 1182-1184 1192 1202-1207 1271 1275-1277 1315-1319 1322 1332-1333 1357- 1359 1363-1371 1389 1398-1401 1405-1407 1432 1440-1441 1446-1449 1455-1462 1467- 1469 1479 1507-1510 1524 1526 1533-1535 1540 1551-1552 1569-1574 1588-1589 1617- 1619 1634-1637 1646-1647 1656 1694-1698 1701-1702 1707 1715-1716 1727 1743-1746 1754 1763-1764 1792-1795 1831-1834 1839- 1844 1848-1851 1857-1860 1870-1877 1879- 1881 1903-1911 1913-1918 1952-1962 1966- 1974 1981-1983 2010-2013 2017-2024 2048 2052-2053 2060-2061 2072-2074 2080-2082 2086-2087 2098-2100 2131-2133 2138-2142 2148-2150 2153-2160 2178 2191-2192 2196 2208-2210 2214-2221 2230 2234-2242 2249 2286-2287 2331 2338-2340 2360 2388 2391 2464 2511-2513 2519-2520 2537-2538 2604 2645-2647 2651-2655 2657-2658 2672-2674 2677-2680 2737-2738 2741-2743 2781 2829 2846-2847 2896-2897 2901-2903 2918 2976 3009 3068 3124-3128 3138 3196 3215-3216 3220-3222 3230 3240 3250-3252 3274 3289- 3290 3299 3310-3311 3331-3332 3394-3395 3403-3404 3406-3407 3459-3460 3466-3468 3535-3543 3554-3556 3591-3593 3654-3657 3729-3730 3737-3738 3768-3769 3795-3800 3817-3821 3846 3867-3872 3878-3879 3882- 3883 3925-3926 3969-3971 3975-3983 4100 4106 4285-4288 4291-4296 4326 4343-4347 4360 4376-4377 4439 4529 4534 4542-4544 4581-4582 4598-4601 4613-4615 4622-4623 4629-4632 4651 4657 4660 4672-4674 4729 4747-4749 4796-4797 4864-4865 4903 4907- 4909 5001-5003 5046-5047 5130-5131 5148- 5149 5210 5241-5242 5261-5267 5276-5277 5298-5302 5313-5315 5322 5329-5330 5332- 5333 5335-5343 5346-5354 5421-5425 5440-



Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			5442
thyroid gland	Clontech	THR001	1-2 47 62 70 74-78 100-106 134 136 138-139 154-156 175-177 185 191 197 222 231 237- 240 252-253 278-283 313-315 332-333 341- 344 357-361 365 379-380 394 400-404 415- 416 419 437-438 463 491-492 511 513 574- 577 583-590 631 652-653 670-671 685 699- 701 704-707 728-733 796 822-823 840-844 847 863-870 889-898 903-908 910-914 916- 918 927-929 931-936 944 951-953 969 971- 974 980-988 992-995 997-999 1003-1006 1008-1009 1017-1021 1032-1034 1036-1037 1049 1052-1054 1056-1057 1063-1067 1070- 1071 1075 1079 1110-1113 1117-1121 1128- 1136 1154 1172-1173 1175 1180-1187 1198- 1204 1217-1218 1220-1223 1228 1235-1236 1243-1246 1249-1255 1266-1267 1269-1271 1275-1277 1286 1297 1300-1301 1307 1310- 1319 1323-1327 1332-1333 1349-1350 1353- 1355 1359-1362 1374 1386-1387 1389-1393 1395-1399 1403-1404 1412 1414-1420 1427- 1431 1438 1440-1444 1446-1449 1455-1456 1463-1464 1470 1473 1479-1480 1488 1507- 1510 1520 1524 1536-1538 1547-1548 1551- 1552 1558 1569-1574 1582-1584 1586-1589 1611-1612 1617-1620 1639-1645 1648 1657- 1658 1663-1665 1667-1670 1683-1684 1686 1691-1692 1701-1702 1707 1715-1716 1723 1735-1739 1746 1753 1755-1756 1765-1771 1773-1774 1780-1783 1792-1798 1805-1813 1827-1834 1839-1844 1848-1852 1870-1877 1897 1903-1911 1915-1918 1925-1927 1951 1954-1962 1964-1974 1999-2003 2005 2010- 2013 2017-2020 2025-2026 2036-2038 2042- 2043 2045-2048 2050-2059 2062-2064 2066- 2071 2075 2083 2086-2091 2093 2101-2102 2111-2114 2116 2118 2125-2133 2143-2144 2156-2160 2163-2168 2173-2176 2179-2181 2186-2187 2200-2210 2223 2230 2253-2260 2262 2267-2270 2273 2288-2292 2296-2297 2303-2304 2327-2331 2358 2377-2379 2386 2418 2421 2423 2427 2434-2435 2444 2449 2452-2454 2467 2496 2502 2510-2513 2534- 2536 2549-2550 2554-2556 2564-2571 2573- 2575 2598 2604 2626 2629-2631 2645-2648 2650-2655 2657-2662 2672-2676 2686 2700 2702-2706 2709-2711 2726 2741-2743 2746- 2748 2760-2761 2763 2772 2777-2778 2805- 2806 2813-2814 2818 2828 2833 2843 2852- 2853 2861-2862 2866-2867 2898-2900 2905

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			2913 2925-2929 2945-2946 2965-2973 2992 3008 3010-3012 3021-3022 3024 3084-3085 3088 3094-3095 3123 3131 3133-3135 3138 3153-3158 3170-3171 3189-3191 3195 3210- 3212 3218 3220-3222 3226-3228 3240 3242- 3243 3256 3258-3259 3279-3282 3288 3297- 3299 3313 3319-3322 3325 3331-3335 3342- 3346 3372-3382 3399 3408 3418 3424-3429 3438-3441 3444-3445 3456 3466-3468 3474 3477-3478 3516-3517 3522 3524-3532 3535 3544-3545 3554-3556 3558-3562 3577-3580 3583 3586 3589 3591-3593 3602-3605 3610- 3613 3628 3638-3640 3658-3660 3673-3677 3680 3685 3691 3693 3708 3724-3725 3747 3762 3791-3792 3804-3807 3815-3816 3822- 3824 3867-3869 3871-3872 3886 3891 3895 3908 3930 3949-3951 3962 3966-3971 4004- 4007 4014-4015 4024-4025 4033-4034 4043- 4045 4093 4100 4104-4105 4109-4111 4123 4126 4140-4141 4169 4220-4223 4230-4235 4241-4244 4275-4277 4379-4380 4383-4385 4435-4437 4461-4464 4520 4522 4537-4544 4568 4581-4582 4598-4601 4633-4635 4640 4681-4683 4691-4692 4764-4766 4785 4796- 4797 4864-4865 4873 4890-4891 4907-4910 4980 5085-5088 5092 5107-5108 5147-5149 5154-5157 5241-5242 5280 5308-5309 5329- 5330 5335-5343 5369 5389-5391 5399-5401 5406-5407 5423-5425 5427-5429 5442 5448- 5450 5464-5466 5497
trachea	Clontech	TRC001	1-2 39-40 52 231 288-290 306 379-380 511 822-823 889-897 909 951-953 963 990-991 1026-1027 1052 1110-1113 1129-1130 1182- 1184 1272-1273 1292-1293 1297 1300-1301 1307 1349-1350 1352 1363-1371 1397 1440- 1441 1457-1462 1511-1512 1532 1547-1548 1586-1587 1612 1648 1664 1667-1670 1687 1690 1708 1735-1736 1746 1770-1771 1876- 1877 1900-1902 1948-1949 1951-1953 2000- 2002 2004 2021-2024 2036-2037 2054-2056 2060-2064 2118 2422 2452-2454 2470-2474 2511-2513 2604 2659-2662 2681-2685 2748 2879-2881 2898 2925-2929 2974-2975 3026- 3027 3170-3171 3223 3242 3260-3267 3394- 3395 3446-3449 3456 3663 3673-3677 3686- 3688 3761 3969-3971 4014-4015 4140-4141 4275-4277 4477 4554-4555 4570-4571 4664- 4665 4761-4763 4864-4865 4878-4879 4892 5241-5242 5272-5274 5438
uterus	Clontech	UTR001	116-119 137-139 278-283 313-315 379-380

Tissue origin	RNA Source	Library Name	SEQ ID NOS:
			491-492 548-550 583-590 592-594 789-793 814-816 822-823 930 995 999 1050 1068 1143 1202-1207 1230-1232 1297 1323-1327 1351 1363-1371 1383-1384 1388 1425 1438 1451-1454 1507 1551-1552 1582-1584 1627 1663 1688-1689 1691-1692 1719-1721 1746 1753 1755-1756 1765-1769 1792-1795 1839- 1844 1878 1919-1922 1951 1988 2017-2024 2045-2047 2055-2056 2118 2193-2195 2208- 2210 2254 2273 2296-2297 2444 2469 2552 2604 2665 2696-2697 2768-2771 2781 2802 2861-2862 2955 3156-3157 3419 3451-3455 3577-3580 3708 3729-3730 3749-3752 3880 3934 3966-3968 4043-4045 4062-4064 4239- 4240 4374-4375 4629-4632 4666 4796-4797 5024 5148-5149 5181-5183 5389-5391 5485

\*The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

Table 2

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
1	5498	C	1	239	322	MGGALLKEPILSPGGGKGIFFWGPQN*
2	5499	A	2	1441	2129	SVIA*SCRASVASKQS*PTLLPSACARPHA\STVDAPASGGAPRASSP\SSDCLWSTSSSSTPLSASASSS/SPPSFNP AADARGSQGPGARGRSCSPSSSERH VRRRVSAARQAGAASAGGGRQAGLAGRSLSA/SRSSARASSSATPALAQST\PSSESECAPLKSRSGLTSSL SKPAS*ATLGKKGSGSSWRFPPE SIHGRHPLSASCWNKSVAAAAAPT GATAP PKAGP
3	5500	C	3	36	236	MGPTIPDXSXFFWRKPITWMPTWEGTSNVGPQPLSSSKSLHSXRGHPAPIPTGQAGPRDSGPGASP*
4	5501	A	4	109	300	GGGKQIPFKGGKFKWGP GPVLKKG EREKPGGNPKKTPWKKASSRPAPRIHPCFT*HAPDRPLY
5	5502	A	5	2	73	
6	5503	A	6	27	375	EHSQVRQALCFGTASQRPSQQPAPSGPGPPGEPG*ERLCASHKAFISHKQSH*SPQ*PCQAGVTLSRLQTTNSPRPHSQKGLRGPRQTLSLT SQPTACSEN SQGSQPSPKRTLS
7	5504	B	7	50	204	XKEGSLCDEYWNPAANLINVCSLFLRQGPRLALMQGEPVDKGCLGVLE NK*
8	5505	A	8	379	623	ATTVSVPFPTAKLLERPGLHLLVFLPNLQFPLQPLVS*LALLRGSTLTKQVPSAPDKPLLVS PPAKHPPVPPSCGPG LQG
9	5506	B	9	185	366	XHPGDGFRPNQEGDERPARKKTWVRDGGPHQGLFRSFHPQFFSRPSRATAHVPAVYFSVEWX*
10	5507	A	10	29	308	WLPPNPGRRRREARQEEDLGPGWWAPSGPLQLPSAVLQPTQPGHGPRA SL**SVCFSFADKEGSLCDEYWNPA A/KPH*RLQPLPSTRPEISPL
11	5508	A	11	663	1269	TAGTWAVASLGRLKNCGWKLRLKEALMGPTIPDKSSPLAGLSSPFWFGRKPITLECPTWERDPRNVGPPAPSPARKSLPQPTGTTLQPYSPRDKAGPK KTLGPRG/APL*VRRTRPLN*WTPA DLGVRTRGAGPLPDAGTLRPRGAVEPSVSACGKWAPSPTSQGCCEGR CDAVPKHEGLAHTVLSINVPVLN QKKKKK
12	5509	A	12	190	715	
13	5510	A	13	270	713	KLTLDCQFTG*QR*KFNG*NLRNR/HSPSRWDGAKPLYKALKL*SSSSSVGAFIFIFTRSRLRAYLFSFAH/LRRPLLAGHLLCSPEQAVELSALLAQTKFG DYNQNTAKYNYEELCAKELSSATL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
14	5511	A	14	1575	1968	NSIVAKHKELEGTSQASAEYQVL REMGFRHVGQTGLELLTSGDLPTSA SQSAGITGVSHHTWPKTLFVLRQSL TLSPGLECSGTISAHCSPHLPCSSNS CAPASRVAESTEAAH/LCPDNLHISS REGASPCWPGCS*TPELKRPAPPCR DQLGH
15	5512	A	15	185	720	KVSHVYLFLHRHGNHPISQTFPHLS PLSIPQNCCHHGPFMSWCWRIKYL GIQLTRDVKDLFEN*KPLLSKIKED TNKWKNIPCSWIGRINIVKMAILP/K ELEKTTLKFIWNQKRACIAKTILSQ KNKAGDITLPDFKLYYKATVTKTA WEAQNRDIDQWNRIEPSEITPHIYNY LIF
16	5513	A	16	1114	2193	GSFTKRVRRAFKVLDRDNPVAKLS QVKKHWYFTWNHKLRLKIAKAILSK KNKPGGITLPDFKL*YRATVSKTVW YWHKNRHINQWNRIRNPEANAHTY I*LIFDKGAKNIHWVKTSLFNKWCW EN*ISIC\KEWEKISANYPSDKGLITR IYKEL/K/QL*EKKSNNLIKQAKDL NRHFSKEDK*MANRHMKKCSMLIT REMQIKTTMKYHFTPVKMVYIQA GNDKCWQGCGEKGTFFHC*WECK LV*PL*RTVWRFLEKL/E/LELP*DPA IPLLGIYPK*RKS/CVIKEITVAKIWK QPKCPSTDKWIKKMWYIYTMYYYS ALKKNEILSFPTTWMLKIVILSVIG QSQKDKHCMFSLICGS
17	5514	A	17	149	328	WQDPLQDPCCHQPFHLCLRR*TLH* LRQQ*WPLLRLRGKIMLILLNTHP EHPCVLLDL
18	5515	A	18	615	734	ENSCWTATLQMGKNWQSL*PVLTS YYR*DNSYWREILQV
19	5516	A	19	1	181	MRARRLPWALTVAELGWDQTGG DQTSPPGGNDRMSMEAECSTTVSP LSCSIPTGCGQTREEVSARATPPPSL GASLLQTLTPDTHCTGVSA*KLATF FTFVGFLSSMNCLMLSKG*GTAKSF ATFTTFVGLLSSVYPLMSS
20	5517	A	20	1	665	
21	5518	A	21	401	1739	DNSHWRETLQM*RMWQSF*PFFNP C*T*ENSYW/MRNPTNVKNVAKLL AIPQPLLIIR*LILKRNPNTNVKNVTKL LSDSQPLLNK*YMLERNSTNVKNV AKLLIDLQILLYISLFIERNLTSVKN VAKHLTGQALLNIKDFIERNPSN VKNVAKHLYGLQP*LDIRGYTLER NPTNVKNVAKLLAILQPLLNIREFIL ERNPTNVKNVAKLLAVLQPLLNIRE FIERNPTNVKNVAKLLAIPQPLLIIR
22	5519	A	22	618	1655	DIPERNASNVKNVSSHFAVYTKTQ HKCVYITEKSKCKEKECTFHWST LTNHKEIHTEDKPYKCEECGKAFKQ LSTLTTHKIICAKEKIYKCEECGAF LWSSTLTRHKRIHTGEKPYKCEECG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KAFSHSSTLAKHKRIHTGEKPYKCE ECGKAFSHSSALAKHKRIHTGEKPY KCKEKGKAFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTKHKIIH AGEKLYKCEECGKAFNRSSNLTIHK FIHTGEKPYKCEECGKAFNWSSSLT KHKRFHTREKPFKCKEKGKGIWSS TLTRHKRIHTGEKPYKCEECGKA QSSTLTKHKIIHTGEKPYKFEECGK AFRQSLTLNKHKIIHSREKPYKCKE CGKAFKQFSTLTTHKIIHAGKKLYK CEECGKAFNHSSSLSTHKIIHTGEKS YKCEECGKAFLWSSTLRRHKRIHTG EKPYKCEECGKAFSHSSALAKHKRI HTGEKPYKCKEKGKAFSNSSTLAN HKITHTEEKPYKCKECDKTFKRLST LTKHKIIHAGEKLYKCEECGKAFNR SSNLTIHKFIHTGEKPYKCEECGKAF NWSSSLTKHKRIHTREKPFKCKEKG KAFIWSSTLTRHKRIHTGEKPYKCE ECGKAFSRSSSTLTKHKTIHTGEKPY KCKEKGKAFKHSSALAKHKIIHAGE KLYKCEECGKAFNQSSNLTTHKIIH TKEKPSKSECDKAFIWSSTLTEHK RIHTREKPYKCEECGKAQSPSHLT THKRMHTGEKPYKCEECGK/RP*PI LNPYYT*DNSYWRETLQM*RMWQ SF*EIFNSY*T*DNSYWRETLQM*R MWQSI*PILNPN*TYEDAHWRETIQ M*RMWESF*SILKAYYT*DNSYWR ETLQI
23	5520	A	23	1	3476	MTLNEHAAFKHLFNKAHLAPPLIHL TLSGHSTCFREHRVGAKSNNPPASK GVWALQSARVKFAETTAGQKGMN TTWVFYYPNVASTWWGAMIPVHV VLPGGCHDASTLGDKEKRAGEAVL NVPGFQDSLESHGRIVNCLIPDVQE NNPSTGNESWLKSHQRLGEPTSRR WLITLPTVTSRSNSIGHLKGTGKSKE EIKATVCAPTLKNGFWIAERVMTVS GHEGAASSRALREELRLLFSSCAQG RLTPHIAGYPSKAKLREERSGSNICC SAIFAVLQPLLLIPRGTGSGVDLLQT PTDLQLRVLTVRRKTNKQEGHPHQ NPTCTSPSSKTKDRSTRNRVKKDTQ ELNSALRQVDLIDYRTLHPKSKREYT FFSAPHRTYSKIDHTVGSKALLSKR KRTEIITNCLSHHSAIKLELRIKKLTQ NRSTTWKLNLLNDYVWHNEMK AEIKIFFETNENKDTTYQNLWDTFK AVCRGKFIALNAHKRKQERSKIDTL TSQLEKEKQEQTHSKASRRQEITKI RAELKEIETQKNLQKINEFRS/W/PW QRHNKKKKFWTNTPDHQCCKNPQ *NTGKPNPAAHQKGYPP*SSGLHPW DARLVQHTKINKRNPYKQNRQK PHDYLNRCRKGL*QNSTALHAKNS Q*IRY*WDVSQNNKSYL*QTHSQYH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SECAETGSIPFENWHKTGMPSLTTP QHVSQSSGQGNHAGERNKGYSIRK RGSQIVPVC*HDCAFRKPYGLSPK SP*ADKQLQQLRIQNQCTKTTSILI HQ*QTNREPHE*TSIHNCFKENKIL RNPTYKGCEGPLQGELOTTAQ*NK RGYKQMEEHSMMLMGRISYHENG HIAQGNLQIQCHPHQATNDFLHRTG KNYFKVHMEPKKSPHHQGNPKPKA QSWRHHTT*LQTLQGYSNQNSMV LVPKQRYRSMQNRALRNATYLO LSDL*QT*EKQAMGKGFT**TVLG KLASHM*KAETGSLPYTYKN*FK MD*RLKR*T*NHKNPRRKPRHYHS GHRHGQGLHV*NTKSNNGKSNQNG QMGSN*TKELLHSKRNYHQSEQAT YKMGENFRNLLI*QRANIQNLRQTQ TNLQEKNKOPYQKVGKGHEQTLK RRHLCSQKTHEKMLIITGHQRNAN QNHNEIPSHTN*NGNH*KVRKQQG HG
24	5521	B	24	1	8442	MIPARFAGVLLALALILPGTLCAEG TRGRSSTARCSLFGSDFVNTFDGSM YSFAGYCSYLLAGGCQKRSFSIIGDF QNGKRVSLSVYLGEFFDIHLFVNGT VTQGDQRVSMFYASKGLYLETEAG YYKLSGEAYGFVARIDGSGNFQVL LSDRYFNKTCGLCGNFNFAEDDFM TQEGTLTSDPYDFANSWALSSGEQ WCERASPPSSSCNISSGEMQKGLWE QCQLLKSTSVFARCHPLVDPEPFVA LCEKTLCECAGGLECACPALLEYAR TCAQEGMVLYGWTDSACSPVCPA GMEYRQCVSPCARTCQSLHINEMC QERCVDGCSCPEGQLLDEGLCVST EPCVHSGKRYPPGTSLSRDCNTCI CRNSQWICSNEECPEGLVTGQSHF KSFDNRYFTFSGICQYLLARDCQDH SFSIVETVQCADDRDAVCTRSVTV RLPGLHNSLVKLKHGAGVAMDGQ DVQLPLLKGDRLRIQRTVTASVRLSY GEDLQMDWDGRGRLLVKLSPVYA GKTCGLCGNYNGNQGDDFLTPSGL AEPRVEDFGNAWKLHGDCQDLQK QHSDPCALNPRMTRFSEEACAVLTS PTFEACHRAVSPPLPYLRNCRYDVCS CSDGRECLCGALASYAAACAGRGV RVAWREPGRCENCPKGQVYLQCG TPCNLTCSRSLSPDEECNEACLEG FCPPGLYMDERGDCVPKACPCYY DGEIFQPEDIFSDHHTMCYCEDGFM HCTMSGVPGSLLPDAVLSSPLSHRS KRSLSRPPMVKLVCADNLRAEG LECTKTCQNYDLECMMSGCVSGCL CPPGMVRHENRCVALERCPCFHQ KEYAPGETVKIGCNTVCVCRDRKWN CTDHVCDATCSTIGMAHYLTFDGL KYLFPGECQYVLVQDYCGSNPGTF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RILVGNKGCSHPSVKCKKRVTLVE GGEIELFDGEVNVKRPMKDETHFE VVESGRYIILLGKALSVMWDRHLS ISVVLKQTYQEKVCGLCGNFDGIQN NDLTSSNLQVEEDPVDFGKSWEVSS QCADTRKVPLDSSPATCHNNIMKQ TMVDSSCRILTSDVFQDCNKLVDPE PYLDVCIYDTCSCESIGDCACFCDTI AAYAHVCAQHKGKVVVWRTATLCP QSCEERNLRENGYECEWRYNSCAP ACQVTCQHPEPLACPVQCVEGCHA HCPPGKILDELLQTCVDPEDCPVCE VAGRRFASGKKVTLNPSDPEHCQIC HCDVVNLTCEACQEPGGLVVPPTD APVSPTTLYVEDISEPPLHDFYCSRL LDLVFLLDGSSRLSEAEFEVLKAFV VDMMERLRISQKWVRVAVVEYHD GSHAYIGLKDRKRPSLRRIASQVK YAGSQVASTSEVLKYTLFQIFSKIDR PEASRIALLMASQEPQRMRSRNFVR YVQGLKKKKVIVIPVGIGPHANLKQ IRLIEKQAPENKAFVLSSVDELEQQR DEIVSYLCDLAPEAPPPTLPPDMAQ VTVGPGLLGVS TLGPKRNSMVL DV AFVLEGSDKIGEADFNRSKEFMEEV IQRMDVGQDSIHVTVLQYSYMTV EYPFSEAQSKGDILQVRVREIRYQGG NRTNTGLALRYLSDHSFLVSQGDRE QAPNLVYMTGNPASDEIKRLPGDI QVVPVIGVGNANVQELERIGWPNAP ILIQDFETLPREAPDLVLQRCCSGEG LQIPTLSPAPDCSQPLDVILLDGSSS FPASYFDEMKSFAKAFISKANIGPRL TQVSVLQYGSITTIDVPWNVPEKA HLLSLVDVMQREGGPSQIGDALGF AVRYLTSEM HGARPGASKAVVILV TDVSVDSVDAADAARSNRVTVP IGIGDRYDAAQLRILAGPAGDSNVV KLQRIEDLPTMVTLGNSFLHKLCSG FVRICMDEDGNEKRPDGVWTL PDQ CHTVTCQPDGQTLLKSHRVNCDRG LRPSCPNSQSPVKVEETCGCRWTC CVCTGSSTRHIVTFDQG NFKL TGSC SYVLFQNK EQDLEVILHNGACSPGA RQGCMKSIEVKHSALSVELHSDME VTVNGRLVSPYVGGNMEVNVYG AIMHEVRFNHLGHIFTFPQNNEFQ LQLSPKTFASKTYGLCGICDENGAN DFMLRDGTVT TDWKT LVQEWTVQ RPGQTCQPILEEQCLVPDSSHQCVL LLPLFAECKVLAPATFYAICQQDS SHQEQVCEVIASAHLCRTNGVCV DWRTPDFCAMSCPPSLVYNHCEHG CPRHCDGNVSSCGDHPSEGFCPPD KVMLEGSCVPEEACTQCIGEDGVQ HQFLEAWVPDHQPCQICTCLSGRK VNCTTQPCPTAKAPTCLCEVARLR QNADQCCPEYENGRLVSPYVGGN



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MEVNVYGAIMHEVRFNHLGHIFT TPQNEFQLQLSPKTFASKTYGLCG ICDENGANDFMLRDGTVTIDWKT VQEWTVQRPQTCCPILEEQCLVPD SSHQVLLLPLFAECHKVLAPATFY AICQQDSSHQEQVCEVIASIAHLR TNGVCVDWRTPDFCAMSCPPSLVY NHCEHGCPRHCDGNVSSCGDHPSE GCFPPDKVMLEGSCVPEEACTQCI GEDGVQHGFLEAWVPDHPQCQICT CLSGRKVNCTTQPCPTAKAPTCGLC EVARLRQNADQCCPEYENPCPLGY KEENNTGECCGRCLPTACTIQLRGG QIMTLKRDETLQDGCDFHCKVNE RGEYFWEKRVTCPPFDEHKCLAE GGKIMKIPGTCCDTCPEESNDITAR LQYVKVGSCKSEVEVDIHYCQGKC ASKAMYSIDINDVQDQSCCSPTRT EPMQVALHCTNGSVVYHQVLNAM ECKCSPRKSSK*
25	5522	A	25	364	477	VIEHLVSQDGLDFLT*SARLGLPKC WDYRREPPRPVH
26	5523	A	26	6838	7166	GSRRPGCHCNSHTGRRSSRHGHLP SPAASRGHSPSAGPPRS*GARRPSL YAGYEAYLSGGGAGRPGHPWQLLP HASVSQGCCAGQAAGR*RSRGCTQR RGQSSPGQSQ
27	5524	A	27	817	1299	RKSHIFFFFLRWSLALSPRLECSGA ILAHCKLLLP/GFKPFSCLSQPSSWD YRHPPRPANFLYF/SVETGFHHVSQ G\GLNLLTS*SAHLSLPKCWDYRRE PPRPAENLSSLTQYLECTQFEIHLGS QTALEGRLVPVTYPLGGVEISGHPV FLLTSSCGR
28	5525	A	28	506	761	DGVLLLLPRLECNSAILAHNRNLRLP/ GFKRFSCLTLLSPWDYRHLPPRLAIF FVFLVYVGFHHVGYAGLEALLTSR* SARPRPKIA
29	5526	A	29	71	425	CRRKGVNMNAPLGGIWLWLPLLLT WLTPEVNSSWRYMIATGGSCRVMC YNELGLVSRRLCQRYSPCILTLIY GEAKVLFVCGLSLLVHWPNCAPSF RDNT*LLRFLHVIIVLLRPL
30	5527	A	30	263	463	
31	5528	A	31	287	2919	MASFPPRVNEKEIVRLARTIGELLAP AAPFDKKCG\RENWTVLAPDGSY FAWSQGHRTVKLV\WSQCLQNFL \LHGTKNVTNFKQFKDLPRQNS\DG GSEKIKPREHIIDCGDIVWSLAFGSS VPEKQSRCVNIEWHRFRFGDQQLL ATGLNNGRIKWVDVYTGKLLNLV DHTGVVRDLTFAPDGSLLVLSASRD KTLRVWDLRDDGNMMKVLRGHQ NWVYSCAFSPDSSMLCSVGASKAV VAAILV*LRLCWHHSHTGAQWC*L GRKSGISGYRAGGDLYHRMK*PCIR LQGVLYVHRCWSMSTFCFSFLFFF FKVISPTVKYTDS*VN*FSSFMELGV

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						*QVKPI*CKVFGFQMVSLCYFLEFF QIPEISYVFDSI*NL YLFSFRNNVLC CRKKKNQKGLLYSKRRDCLRLNQ AHI*YNRLK*TLESCLELCTVNY*S LESKIVYELILK*LNCFIK*LMIVVS LGKIRWLNFDLLKCNCIIFIK*HFHF VMWFNILVVCQRNFIWL*IFYLLAV SVSLPRLKLVTAQYCKQVIISKGDA NGVTIC*PYVFCYIF*KSGSFWKKK EKGVCST*PYLFPYILVN*FLE*MDF SIALWLNCIAFILCLGLFLN*HLTETF EIEFACLP*LT*RLILI*L*H*AYS LNY S*FIMLNIILIKFSSFSIRCAILSSVCLN EAITFAFLQVFLWNMDKYTM MRK LEGHHHDVVACDFSPDGALLATAS YDT*VYIWDPHNGDILMEFGHLFP PTPIFAGGANDRWVRSVSFSDGLH VASLADDKMVRFWRIDEDYPVQV APVSNGLCCAFSTDGSLAAGTHD GSVYFWATPRQVPSLQHLCRMSIRR VMPTQEVQELPIPSKLLFSLYRI
32	5529	B	32	51	285	XGDEKGAAQVAAVLAQHRVALSV QLQEACFPFGPIRLQVTLEDAASAA SAASSAHVALQVFSELGFPPAVQR WVIGRCL*
33	5530	A	33	38	347	FGVAPGVSLHHPRPHPARATASTR RAWNPQALPQPSGSSAVGSPSPRC HRGRTEWQCPVMDTITWNSLGPP VLVGEVGSTFPTAGCLGRLPGGS WSLE
34	5531	A	34	331	1257	FRGCHRGKDRMAARVTHHPWAQ KHALASWSPPEASTLKGPPEADL PRSPGNLTEREELAGSLARAIAGGD EKGAAQVAAVLAQHRVALSFQLQE ACFPFGPIRLQVTLEDAALPHPPAS SAHVALQVHPHCTVAAFPGRFFSE LGFP\PAVQRWFIGRCLCVPERSLAS YGV\RDGDHAFLLYLLSA/RSRS/LQ PQDLALKNPQEDGRGTWTLVSPHIG GYPQGPTAQLPPACPSPLPA\SWSCP FRHLHSMPQKRPGCEMCSTQRPCT WDPLAAAST*QPPEVTRGEWPFPH KSDISRPLNSGDLY
35	5532	A	35	616	1017	LYWEKIIFSNLKTPELFLVMTSNIF HIFWEGNKLPHYTTQFSGFYFILWY FR\DRASL\CRPVWGA VVWS*LTAA SNSW\VRCSCLGLPSSWSLSPMPPH SANFKFY*FHLIFVGDGGLAVLFR VLNSWPQAI
36	5533	A	36	3	283	FYTQNIIFYSVESKLHTSTL*D\HYFFF FFETESYSIAQGGVQWGNLGSLOPP SPGFKQLSCLSLPSSWNYRCAPPCP ANFVFLVEMGFHWIKPG
37	5534	A	37	260	569	RENLDLGEAFISRCPLHSLAYFLH NLSFKSREMHNMFVKS*QALKFIRR IENNHLIFYFYFYFERKSL\HSPGLG NGVGLCLKKKKNNGSYKVLVWSF DSTE

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38	5535	A	38	468	849	TSEEFQQFTIHLTGVLHCHPDLETG GYKTF*WKSLEN*IAFFFFSETESPS APRLECSGSISAHCNLLPGSSDSPAP ASRIAGTTGTHHHARPFIILLVKEGF HHVGQPGCLKLLTSGDPPAPASQSA
39	5536	A	39	97	448	GSHEQPWEVVTGSRQPAR*SSR*AI MRKPRAAVGSGHRKQAASQEGRQ KHAKNNSQAKPSACD/GDVAEVTA FRGSLLSWYDQEKRDLPWRRRAED EMDLDRRAYAKWPTLQDLASASL EEVNQLWAGLGYYSRGRRLQEGA RK
40	5537	A	40	990	1812	RLPLGRRSPSEAAGAETAPSSLSAA MTPLVSRLSRLWVRWTCAIMRKPR AAVSGSGHRKQAASQEGRQKHAKN NSQAKPSACDGR*DGPGQAGICW SVHLLRA/EATLPRGPVWVGLWAR *GQVNSVL/DANPFPPVWVSKVML QQTQVATVINYYTGWMPVTPGEEG KGHGSDPR*EPLLWGGCREGLYH LHP*PCLFLPAWGYRSGPTLQDLGR AFLEEGDQLWAGLGYYSRGRMP EDTPARNGTAQRSPLQHIRPLNEWP LEWRLDACREP
41	5538	A	41	360	652	IYLAGAQWLTSVILVLWKPRVDH LRSGVRDQPGQHGETSSLLKIQKLA RRHGACL*SQLGRWRQENHSNPG DRGCSELRICTPAWATEGDSVLKKK
42	5539	A	42	1400	1823	NEKKSFLRQSL/DSVAQAGVQWC DLGSLQTPPPRFTPFCSLSPSSWDH RCPPPRPP/RFCFFLYF**RQDFTMLA RLVSNS*LQ/CDPPTLASKSAGITGM SYCTRPNQAGVQWWDLGSLQAPPP RFTPFCSLSPSSWDYRH
43	5540	A	43	227	481	KKKKELEKGNMD*IQSSRRNETIKM RAKIF*TTNTKLMKKNKTRSLVSEN FNKIGKALARLRKKEKTPITKVRNE TEDITTNFIE
44	5541	A	44	1374	1835	ILPCNKPPWNSMACTTKHLSRSQAY RSAGAFIHWTGEAGVGSALLSLAL QKPWANQGIFFPCGGRSQRGVSRN TRVWVQARNWY*VTPTHRVLWMR TAPRPALAASSAAS\PSAVGSPVAA\ PSQPGLMTQMATTATEVVVGYAV GHTLSEYSENI
45	5542	A	45	1	1470	
46	5543	A	46	62	526	EEKLKKGKSFQEYSGSLLLSIASVGF LSPTDIAIAVPRQWEEMRPLDIV*LA EPEEVEVLEPEEDFEQFLPVINEMR EDIVSLTREHGARYLNRNRSKLWRL DNMLNIQIKTQVEASEESALNHPPNP GETAEGRAAKRCEKAEKARELQ KAK
47	5544	A	47	721	1030	MGPWEPRPQMRT*CLLPLKPNSPPP TPSEE/PGHLPK*PLEVI*WPSPPSGF P/PAFRGQ*ARGHPPPPQWNTPFSP PQ\PLSAGKT*PLTPFPALPYLGTG

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						RK
48	5545	A	48	66	386	PMEIFVDDEANLTLHGVQYYLKL KDNEKNRKLFDLLDVLEFNQGVIFV KSVQRCIALAQLLVEQNFPALAIHR GMPQEE/QFKDFQRRILVATNLFGR GMDIERVNI
49	5546	A	49	434	858	CLSHTMDPYSPNLRPPTPPHNRWVI FVKSQRCIALAQLTSGSRNFPALAI HRGDGPREGGGFFRVFRQF*RFNG RIFVGYQPILGRGMGHSRRVNIAFN YGHAWRVFDTYLAFGVGQRQGRF WATKGFGFLTFCVPMED
50	5547	A	50	1	660	LALARNKSLNLKHIKHFILDECCKM LEQLDMRRDVQEIFRMTPEKQVM MFSATLSKEIRPVCRKFMQDPMEIF VDETKLTLHGLQQYYVKLKDNE KNRKLFDLLDVLEFNQVVIFLKSQV RCIALAQLLVEQNFPALAIHRG\MP Q\EERLSSVFSSFKDFQRRILVATNL FGRGMDIERVNI\AFNYDMP\EDF\D TYLHRVARAGRFGTKGLAITFVS
51	5548	A	51	143	387	QPCLTRY*DTRCTNQ*ETTS*RLCKE PFRPGSFRPNWHLANVVENIERLQL VS\TLRLIEEDSSLN*YSIIFHSESYR YN
52	5549	A	52	2	1360	VCVCVCVCVCVRQSLAPLPRLEGS VSILTHCNLRLGLSDSPASARGA GTTGMCHHTWLMFLFLVETGFRHV GQAGLELQTS\DPALPFPKCWDYR\ VNHARP*HSFYRSLGDQNVMA GQRPASMPCPVFLVQMSPAAVSTS VREWAPDSQRGHRDGHAKLWGVA DSPAPACPCTFGVTHETGWGSHLPS PKRQS/CYKGSQRPTQPQVIKQAPSS MATIPIHQGDVEGGASWFTPPSAET DPRSGPRTLCREGKCR*LSPYSSIKP GLKMG*IRDFHSTKEKF*WGQNIDL LIFESLLTRRERANDFVVEGPTQL*L V*SIMNANLNSRKAELPNNGTSTA MGSASSFSVCLFYERETPRKAAAH* ENVWELTRRFFIFFEMEFCIVAQA GAQWCHLGLSLQPAHHEFK*FSSA/S LPSGCDYRHPPPCANFFYF*RDGV PSRCPGWPR
53	5550	A	53	218	380	RKMKNSSYPAPFAPRIYSSPPPPQE/P Q*GGRDMAAIW*GALSIPPPVDDL PLG
54	5551	A	54	76	376	YKIFVLETCMYKVICRFANNTMHL SYTVIHKDPGKGRGIISPNLFYFIYFE MEF/SLMPRLCNGT\AILAHRLNH LPGSSNSPASAS*VAEITGMCTMP
55	5552	A	55	97	437	WTRTHRASTCHVAYQEDGLLHLRN TNDPENFPKSYHYHRIIGGASG*QA TAREATHYDGDVIDLDFVTPTPLG TTWGLEGTCENGDSLPAADLMHQSP LVGQPTEDFRNTGGH
56	5553	A	56	22	424	ALGMAHITLFFFFLLLFCDLSPR

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						LQCSGTISAHCNLPVPGFKQFSCLSL LGSWDYRCMPPC/RWLTFFVLVET GFHHVQGAGLELLTSGDPPALA/FP KC*DYRRDPRAWALFVFLT*FFSKL KYHKAKEKWS
57	5554	A	57	514	835	QFIFNVNKINSKTIKDRWGPVGVF TPVIPQHFGRPQQANHLRSGVRD\H PGQQGETPSLLKIQK*AGHGRGHL* TQLLRRLRQENHLNLGGGGCSEPRS RHCTPAW
58	5555	A	58	234	457	SKTENIKYWL VHGELETALHRWRN SKMAY*L GK\QFLNLR TQLPYDSAI PFIGCIPFKYECWTYNKDLFTHVYI
59	5556	A	59	1	336	
60	5557	A	60	192	432	FDNLSPTWAGHGGSC*SQHFGR LRRVDHLRSGI*DQPG*HSKTPFLL/ KNTKISWAWWRTSEIPAAREAEAG ELLELG
61	5558	A	61	81	439	CEHHKAHPPPVSPYQSMAPSFTQRL RPKEQVSPTMPFSLVSTPIHLTSGTP AGLPASIPGPLQSPWSTTTGTDPKI QGSPARPAQNSPVASS*ATSSPWP ARPPWTPLHSSLPALAA
62	5559	A	62	297	561	SQHFGPRQVDHLQSGVQDHPVQ RGETPSLLKIQKLARGGGARL*SQL LRLRLRQENHLNPGGGGCM\PI*HR CSPA WAI E*DSVSKK
63	5560	A	63	3	808	FFWEPEKAFIEEFEGVSSSSPSQL GQQRKQDAGVLHSWNSALKNLNV PPPPGGWCLWGTAALSSSQAGRG SGIGRGGGESGGTG/ASSAEGEAPG GIVSCA*GPGCRSSGAKGLRLRAS SLQAPAAALIQAAPGVR*TGLGPYL SAVHAGPAAAAAALPGCLS\SPASP AAPVGATPRA\GPLNSENHRCPPGP PGPQFGLGPLGPGPGSGPWA\AHSQ NMRAAESAAAAWLSVPSQSPRLSP SSSSSSSPTAWNFSPPRDMAGLR
64	5561	A	64	1005	1150	AWAWVCVSSGLGAPCGDGCCRGR GVASKCC\CAGGGCVSVG*GNVCA RA
65	5562	A	65	3	230	LVEMGFHQPGQHGETPSLQKI*NKK \LAGHGGTCL*S*LLRRLSQEDGLSL GGRGFSEPLCHCTPA*TTEQGLKK
66	5563	A	66	317	503	KKPKPPKPPWEPTTFG/TPAFIPPRGI WFLIAPCGWV*EEGGPSGGPWPWC PLGKTHGEGGKP
67	5564	A	67	523	741	ERGFFFGPHPGGRGKKLG*WGPPFP GLKEFSPLRPP*EGGLRGPPPLPG/SF LGFLRKGGFKHGGQGQGNPGG
68	5565	A	68	498	778	VTINMMTGIVPYISILMLNVNGLSA/ PLERRRLAEWIKIHKPNICCLQEIH LTHKDSYRLNVKEWKIFHTNGNSK *AGVAIVMSEKTDFAKATTV
69	5566	A	69	187	488	KRFGKNGFYPCGPGGLKPRALKEPP PLTPQRGGITSSPPPPQPKTLFFGY WPKKSL*INPQGGLNPSQGGKPWGW

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						GFPFLDNYGGCWNRPPGGPWGGYK
70	5567	A	71	1006	1979	GLGASILDSTTSTWSWNASRLIGL KNSLFFEME/FSLLLPRLECSGTISA QVNLRLPCSSDSSASASRVAGITGM CHHAQLIFVFLVEKGFHHVGGAGL ELTASGD/PTCLGLPKCWDYR/R*AT APGLFFFLRQSFTLVAQAGVQWR DLGSLQPPPPRPFKQFSCSLPSTWS WVYRHAPPCPANFVFFFFFFFFLVE KGFASMLRLVLNS*PHDPDPASAS QSAGITGVSHHTRPMSFKNIYFFFF FFETESRSVAQAGVQWRDLSSRQP PPPGFKRFSCLSLSSSWDYRRVP/PM PG*FCIFRRDGVSPRWSGWSQTPDL K
71	5568	C	72	126	472	MADCCAKQEPERNECFLOHKDDNP NLPRLVRPEVDMCTAFHDNEETF LKKYLYEIAARRHPYFYAPELLFFAK SSMNFGMKGRLRLPNRDSSVPVSK NLEKELSKHVARLSQRFP*
72	5569	A	73	3	873	HELLSTPLAFGTMKGVTLNLSLLFLFS SAYSRGVFRDAHKSEVAHRFKDL GEENFKALVLIFAQYLQCCPFEDH VKLVNEVTEFAKTCVADESAENCD KSLHTLFGDKLCTVATLRETYGEIA DCCENKEPERNES/CFCNHKKDNP N/LPPIG*GPEVGCGCGTGFFMDNG RRTFLEKILIMEIGQEGHPYFLWPRE LLFLLLKRVLKLLFTGMLAKLAGL KLACLLAKARWDFRNEGKASSAKQ RLQCASLQKFGERAFAKAWAVTRLS QRFPKAEFAEV\SKLVTDLTK
73	5570	A	74	849	1277	YNTTKLVPLYLCKMIFLLFCYVYVL RQCLA/SVAQAGMQWHNHSSLSK* PPGLK*SSHLSLPSSWDYRCVPQRF SLLFIFCRRKGFFPILA*AGLEQLGSR NHLALASHLSVGIGVSYHTQPVL AAIAMVLYFVNKLSVLL
74	5571	B	75	120	323	ITRRYAEFSSALVSINQITIPNERTMQ LLGQLQVEVENFVLRVAAEFSSRKE QLVFLINNYDMMLGVLM*
75	5572	A	76	154	432	QLPEAGGPGLQEPLQLGELDITSDEF ILDEV DVHIQANLEDELVKEALKTG VDL*LHSGERTTRD*QLPEAGGPGL QEPLQLGELDITSDEFILDEV DVHIQ ANLEDELVKEALKTGVDLRHYSKQ VELELQQIEQKSIRDYIQESENIASL HSQITAC
76	5573	A	77	2	630	FFVSGPAAHDLFHAVMGRTLSMT LKHLD SYLADCYDAIAVFLCIHIVL RFRNIAAKRDVPALD/RVTEFWSLM PNRPRTLLVLHDSALTDSY*PGIIN LYSHSFAPEAVVLLFDSFSPSNHCPT PTTSY*PLN*MMPHSLSPSPNIPCWL TSDSD*AHRYWEQVLALLWPRFELI LEMNVQSVRSTDPQRLGGDLTRPH YVREGKGNKG

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77	5574	A	78	175	2385	QLPEVRLRGMAAAATMAAAAREL VLRAGTSDMEEEGPAGGVPGLQE PL\QLGELDITS\DEFILDEV\DVH\IQ ANLEDELVKEALK\TGVDLRHYSK QVELELQQIEQSIRDYIQESENIA LHNQITACDAVLERMEQMLGAFQS *PSGSIKL/CRFRTLQEQSGAMNIRL RNRQAVRGKLGELVDGLVVPALV TAILEAPVTEPRFLEQLQELDAKAA AVREQEARGTAACADV\RGVLDRLR VKA\VTKIREFILQKIYSFRKPMNTY QIPQTALLKYRFFYQFLGNERATA KEIRDEYVETLSKIYLSYRSYLGR MKVQYEEVAEKDDLMGVEDTAKK GFFSKPSLRSRNTIFTLGTRGSVISPT ELEAPILVPHTAQRGEQRYPFALF RSQHYALLDNSCREYLFICEFFVVS GPA\HDLFHAVMGR\TSM\TLKHL SYLADCYDAIAVFLCIHIVLRFRNIA AKRDVPALDRYWEQVLALLWS\RF ELILEMNVQSVRSTDPQRLGGLDTR PHYITRRYA\EFSSALVSINQITPNER TM\QLLGQLQVIEVENFVLRVGSW SFSFKGREAACVFWIQQ\WTWMLG VLME*ERA\ADSKEVESFQQLNA RTQEFIEELSPFPGVLRWHL*KEAE ALIERGQAERLRGEEARVTQLIRGF GSSWKSSVESLSQDVMSFTNFIN GT\SIQGALTQLIQL\YHRFHRVLSQ PQLRALPARA*AHSTFHHL
78	5575	A	79	1333	1561	PLFIQLPGLPRMLTQFN*YTNHS*SK CQD/HSVCSWVKAFWR\VAHAC NPSTLGG*GMRITRSGVRD*TDQHG ETH
79	5576	A	80	132	356	KDKIHIIISILKKFDKI*YSLIK\TL*K LGME*TYLNIKVIYDRPTASILSGE KLKSFPLKSGR*QECPLL
80	5577	A	81	108	335	NKDKIHIIISILKKFDKI*YSLIK\TL* KLGME*TYLNIKVIYDRPTASILSG EKLKSFPLTSAR*QECPLL
81	5578	A	82	3	6742	
82	5579	A	83	499	1018	PTRVFSITAKLINGGVAGLVGVTCV FPIDLAKHSPQPALGKPCYKGMIR LPDRRLGRRASSAMYRGAAVNLT LGTPEKAIKLAANDFFRLLMEDG MQRNLKMEMLAGCGAGMCQVVV TCPME*PTRVFSITAKLINGGVAGL VGVTCVFPIDLAK\TRRSNQHWES VTKE*SDCLIEDGSGGG/PSSAMYR GAAVNLT\LTPEKAIKLAANDFFRR LLMEDGMQRNLKMEMLAGCGAG MCQVVVTCPMEMLKIQLQACWTP GRPSSGLGLSTLHLQVLHNWFGFHP QAPLCHPHCLG
83	5580	A	84	3	305	GTRQGCPLSPL*FNTVLEILVRHS/RS SSSSSSSCLTADP/MVLHIENPKGSIK *VLELINEFSQVAGYKINM/QKTVA LYTNN*LSKKEIKKTIQFIASKRT

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84	5581	A	85	39	281	KPRCIVSFFSMVVEA*ASIVK*EKEK IGNQGTKL**FEEMI/LYIGNSRASA DTLLEIKDFSKISGYRFNIHQSVMLF YFSC
85	5582	A	86	456	712	NIFTYLFIFVTECTVVQAGVQWCD LGSQPPLPG\SSDPHASTS*VAGIT GVSHGAWLIFFSFFPLRRSLPLSLQ FGQQSETLF
86	5583	A	87	218	468	NNFFSSRVLLSPRLECN\SRI*AHCN LR/LPGFKRFFCLSLPSSWDYRLLPP RPANFLYF/SV*TGHHVQASLELL TSDDPPAL
87	5584	A	88	372	666	NVCFIRTGTDCHI SEHNGMKLAITKE KLEHLQ/YVWK/LNRFNNQGVKEE ITREIRKYFEMNENKNTKYQN*ECV MTTVCRGKFIAANVHIKKQDSNYV R
88	5585	A	89	36	350	KLQLHNLKARIAAIHQAA*LTPIPT LWEAKAGRFLEPREVKASLGQ/P** GTHVHKTYKIARAWVAKHLWVPS YFKRLEVRRVALSPRGV/NGCS*RLI LPLPSQP
89	5586	A	90	58	375	VFYNKTTFKVFHAIICSLIYFVCLHSI VI*FFIL/CYCRVSEIFGYRCFIKLLL KSLL*L*FVPLFILFACILLF/WLNC YFLRLSTIVFF*KLLIVLTFFFLYRS IIFS\CFYLLLSFFCFGCTL/CSCLC LQLCLFFSFSYFLIHVLR
90	5587	A	91	107	355	DMILYIENPKDSSKNPLGLINKYSK VAGYKINTQKSA AFL*TNNYLKN*P /MRTIPFTIAASSYLETYLTMEVKD LYTENYKM
91	5588	A	92	31	358	NVKSGQNLTMGEGSVSQGSIFSSLG GHRTVS\VTMVRRCRPAHRLSR WLPST\SSGTQ*GP*NC*PNPPITLLR PPRPRQRCPSLCQFP*TSRQRPSQ PPQGPPEFP
92	5589	A	93	1	1253	MRIPSFLNLQDFEDKMEIKRYRPE GPLATSAQSHVSTAPLISTQIPPHVP PLFLDCRHLPASLFDQTLIPKKAPS NCVTDSYRKTSEIHPSLFLILNLQF RTSTSNCCFSGSGKEALTGSIGRERS PLLAQTPFPTLKKSQRSATLECEE ASLWENPLRDHGLFPASEHRLPLPL NQQKGPLRTSPA AHSPNFAG\MP PVASSEGLTSIYSQLSPIG\PPGRRRQ RGCPY*VQLHGDWPLCTAVYT*AR RSVAL*SRFCG*QTRR*TRWQRNPP VCSG/HKLREFPLKLELFPQIQDP HGFVISVGQVRGH*STQKLYGPIRS ASPGAD\GGARGRRGFDGSPPPAP NLHPGARALPGSCWSHLPGVRSQE VSFLDSGSGSRVNPPTAEDEA WESG LCSSHPACQEHTKDL
93	5590	A	94	216	1374	RPQGMVSSPPPKLLLDPLAQLFS GQQDPQPLEKPHLQCLGRELGSGR RGGGWSPGVENRSQTLFFPGHRAP



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						APGDAEGSGP*SFSGDARPTGHLLP PRKG\HL*SSGELRPGRCONS\QAAG/ HRGLGVPRGALGVSLAGSSFPSPPR RRPSG*AANNSVASEGAR*ALGRG/ GPEAMP/DEFVRGVSSG*GPRGRSR LLIEW*TEAMFADPTRTAGGVGTD GKLLPVPGQDH*ARPWKPREIRAVS RAGHVG/LPAC*EIPAQSLSGPRGA SAAIFGSCVPHGGSTRAGMVVRVA RGSPRGEQGLVLTR\GTTRTCGMNS SSPLAFSPLKSPG/MGGQLAGP/PGA PSARWSHGGSAGRWCGRGVVGQE LVSWIHRSVTGPSHKFVGCWRQTS
94	5591	A	95	282	612	
95	5592	A	96	19	1153	DLTPGKWDQEPGRARAPGWRLG AGGGEPQSNPLFPAPRTCPRGCR NWPIKLLCNGKKPEAPGGARGASL SEPSPLPGWPWSTGSEEDLEDRTE\ ERPKGFDSDHVEMLKP*NPKVPNCE GERGCSRAGSTLEPSGESSAQVQE KKDYAQWF/SNRGQLRPHMPLPT PLGH*AAAGGSGRENVPLGMCLVS GGDRCC*TPCNPRWEGPSPTPK*PF RQRWRNSRVSIAHGILADGIHFG DQLDLGSEEKAPASEGTLEVLPRAN GGVALPVA*RWEDGRRHRLQGKV GDQLSAP\GLPGKSFLSSPPRFPHP DSL*C*GCRGLGPL*CRGCPRLTSG ASPLPPPPGNLVGGSGPGDPRPSCQ LLPPGKGHL
96	5593	A	97	429	945	KSVLSTLNWAQPRHWPETLPWVPS *PETSLPPPGGS/APPTPDMD*LNSAS PNSAPPAC*NPSACRLSSLPAITPVS QDPT\PSTEQAPKPAFTPWLPPAASP FKAQTASKG*PSHMWLPLPLLTFP KPV\PSALLP*APSQPPKGVPPQAPS QHPLTPSHRTCSPAGLLTP
97	5594	A	98	178	603	SQHFGPRWTNHLRS*IQDHPG\QHG KTPSLLKILKKLAGHGG AHL*SQL LGRLRHENHLNPGGGGCSEPR\CHT AAWMTE*DSVSKKKRPGTVAHAC YPSTLGGQGGRITRSRDRDHPCQYG ETPSLLKMQKLAGHGGTRL
98	5595	A	99	405	689	GSFLFFCFFF*DRVPPCSP\GWSAVV QQPQLTSALTSGSHLSLLSSWEHR DV\PPCPG*FFIFCRDGV/LTVLHRLV SNFWAQSLPPWPPKVLGL
99	5596	A	100	3	307	FFFLEPSLACRQAECNAHLAH/CKL NSWFTPFSCLSLRNSWNYRCPPSRL GNFFVFLVETGFHCVSHDGLDLLTS *SVRLSLPKCWDYKGESLHRAQNY LDL
100	5597	A	101	279	469	PKMAQTQKGYLHLILALMCFYFRN TQAKKNLKRDC*RPSRMPKDLACC KSIQNKIKQKIGRKK
101	5598	A	102	265	446	
102	5599	A	103	283	398	NWQEKCTFQIIGGRKRMSFRILINF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FHN*DRTVCYVP
103	5600	A	104	283	397	NWQEKCSFQIIGGRKRMSFRILINF FHN*DRTVCYVP
104	5601	A	105	2	1012	AEALVESFWKAKQHTKEELKSLQA KDEEKNENEKAKAACSAAMEEDS EASSSTGDSSQGDNNLQKLGDDV SVDTSIRRVYTRLLSNEKIEIAFLN ALVYLSPNVECDLMYHKVYSQDPN YLNLFIIVMENRNLHSPEYLEMALP LFCKAMSKLPLAAQGKLIRLWSKY NADQIRMMETVQQLITYKVISNEF NSQNLVNDDDAIVAASKCLKMIYY ANAYAVTKNLGLYYDNRIRMYSER RITVLYSLVQGGQLNPYLRLIVRCD HIIDALVRLEMITMENPADLKQFY/ RGI*RRTRWVAAFWDRASEPKANSI GFGGSQLWMPTPVASYT
105	5602	A	106	966	3172	
106	5603	B	107	1	2271	MAGKASESWRKVKDTSCMAVTR NEKDAKAETPKTIRSRETYHHKNS MWETAPMIQIISQGVPTTHENYGS TIQDEIWCLTNFCLDDMLSFVLESC TNHCAYCLNVWYRKRAAAKHLIER YYHQLTEGCGNEACTNEFCASCPTF LRMDNNAAAIKALELYKINAKLCD PHPSKKGASSAYLENSKGAPNNSCS EIKMNKKGARIDFKDVTYLTTEKV YEILELCREREDYSPLIRVIGRVFSSA EALVQSFRKVKQHTKEELKSLQAK DEKDEDEKEKAACSAAMEEDSE ASSSRIGDSSQGDNNLQKLGDDVS VDIDAIRRVYTRLLSNEKIETAFLNA LVYLSPNVECDLTYHNVYSRDPNY LNLFIIVMENRNLHSPEYLEMALPLF CKAMSKLPLAAQGKLIRLWSKYNA DQIRMMETVQQLITYKVISNEFNS RNLVNDDDAIVAASKCLKMVYYA NVVGGEVDTNHNEEDDEEPIPESE LTLQELLGEERRNKKGPRVDPLETE LGVKTLDCRKPLIPFEFINEPLNEA LEMDKDYTFVIVETENKFSFMTCAF ILNAVTKNLGLYYDNRIRMYSERRI TVLYSLVQGGQLNPYLRLKVR RDH IIDALVRLEMIAMENPADLKKQLY VEFEQEQQVDEGGVSKEFFQLVVE EIFNPDIGMFTYDESTKLFWFNPSSF ETEGQFTLIGIVLGLAIYNNCILDVH FPMGCLQEANGKRNFSVTWETLT QFLYQSLKDLIGV*
107	5604	A	108	264	378	
108	5605	A	109	297	353	
109	5606	A	110	1034	1195	MQKKMIFQQTAPLNPVQTV*RHP TPKRKECPSLRRQSTLLRMMWYLP CDQWS
110	5607	A	111	1075	1826	LGLQNRNFGYKKHFWVLT DSEPA VGGGEWFFSLGSRTRDRSGAISPLI TLRTLAAKGAHQALTKTMEMMSD KKRI*VTFLFEFKMGRKAVETTCNI

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						NNAFGPGGTANERTVRWWFT\KLCK GDEGLEDEEP*WPDPLEVDSDLLAR TIKAD\PLTT\TREVAEEFNIDHSMV FP\HLKQIGKVKKLNK*VPHEPSKN KL\FLEASSLILCNNNEPFLSRIVTW DENWILYDNH*QPAQLLD*EAPKPN LHQK
111	5608	A	112	540	724	EAMFYTWEGEWAQEIVGLKKIRL GN\AHAYNPSTLGG*GGQIA*AQEF DTSLDNIARPV
112	5609	A	113	1	370	QRSRGRGSLRIGQTCLRRDMLSQEL PRLEFPLLLLLMLLMP\PPCPAHRA TLFDPTWESLDARQL\PAWFDQAKI GILIHGVLGTGPSYCIERV*RNWQM EKIPKNVEFMTDDYPPRYTHEDF
113	5610	A	114	151	379	PFYVENP**YTLKNFLELISNYNKV AKYKINIQRSIYFLYASHKQVDFKV QTQ/LPFTLA/SL/RMK*FSISLTK*VQ D
114	5611	A	115	17	214	KQRLSYCIYKTTKYATYKEIHR/LE VNGCKRIYHANTNQKKAGVAILISD KKHLRQEYYQG*KEML
115	5612	A	116	249	675	QYISVTRCHISMLTLNLNGSNAPLK RYSLTE*IFLNDTTV/CIPRHTDRLKV KG*RKTCYTNRKQKQ*/GIAILMPD KTDVMSSSSSSSRK*IIVKGSILQED MTIQNIYTPNTIAP/R*VKLILLGLK G*IHSNTIMVGKFSIR
116	5613	A	117	67	373	FCDCHHFILMFKSPHIWPVGIFSSWL LCFFWACLHHSLSIALLSCTKRYSG LILYFLCSSFEITVSSKSSVSF*RRMV FRNQVLGSRCACCC*GVAAPRPPF
117	5614	A	118	366	795	AWVEQSKVLIKEGGIQLLLTIVDTP GFGDAVDNSNCWQPVIKYFDSKSQ D\YLNESQVNRQCMPGNRV\HCCL YFIAPSGHGPHN*RLPPSGRIG*YM FVTTWHCLLLRLKPLDIEFTKHLHE K\NIPLIAKADTLMPEEC
118	5615	A	119	105	702	AGSSVSLGFCPAAAAHKPRGGALR LPVFRRRAQQGPDYALAGVARQPA GTCRRRCNRSHCRAEDPQWPTPAA APAAHSPHMSLGESGLGKLILNSLF LTDLYSPEYGPSQRIKKPVQVYILV FLIDDKLE*Y*YTQSTCCNFHYASIQ SWQPAINYIDSKFEDYLNESRVNR CQMPGNRVQGCLYFIAPSGHGPH N
119	5616	B	120	7	177	MSVSARSAAAEERSVNSSTMVAQQ KNLEGYVGFANLPNQVYRKS VKRG FEFTLMVVE*
120	5617	A	121	2114	2945	KSVAFLCTNNVQVQAENHIRNVVIS VTIAPHIKIKYQRMYPKEVKEL YR ENYKTLMEIHD DTKKWKNI P/C*W VGRK/LIYRYNTIPIKLSTSFTELEK KILKFIWNQK/HSRIAKAIL/AQKYK AGGITLPDFKLYYKTTVTKTAWYY WYKNRHRDQWNR TENPEIKPYTCN

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						QLIFDKINKNKQ*GKDILFNK*CWK NWLPICRMTLGPYLSPTYTKITSRW ITDLNVRLQTLNILEENLGKNLMDIS /VGKEFMTRP/PKAYATKTIDK*DL IKLSFC
121	5618	A	122	3	113	GLDLLAS*SARLGLPKCWDYRSDW GPGPVCGLHLCRG
122	5619	A	123	145	540	FFVFFVEMGFHCVAKAQAYNIFFFF LRWSLALSPRECCGAISVHCKLRL PGSRHSPCLSLPSSWDYRRLPPRPA NFFFVFLVETGFHPC*PGMGLDLLT S/SIRPASA/FPKCWDYRA*AIAPGK MRLFNSL
123	5620	A	124	739	835	LAKISNSDVLKLSMLHKSSENSISHK TGAERNKYLLIKLKI*LLTL*VNIC FFQLQFYVK*SFQIYVAWKVLIRQS Y*FLPVIFSIYFFYL*LIFV/CDTFCF *SHFLLFIFYVYFNLVTRITYNILEL *HFNLNLFQLKFNHIPKFYCYIYIAL L/CFMLLM*QISLFIVYHVTDLLITF YAFAF*IM*KIKSRVTNQNYNRTVF MFVYYLPLPESFVYSYSLIYLHSY CLEFIYFNLKDLTLPECQFRDKWIF FQF*KKIRKCLNFS/CHF*RI SFPAIYF SIDRFLHYFKYIIHCLLAFKVSAREIS C
124	5621	A	125	48	492	HPTGPGRRSHPRPCPRRSLTSLAPSP WPPGSLQRSLLDPQRSPWRPRTQAC TRSAHALRHTIPRSTLGVTVGLEAA PPPQHLRAKGT/PPVPGAQPPPGPRP WPTQLRERPSPEPPPPGLGLPGSKTP ALPARPRVG*MGPKAQPHTPF
125	5622	A	126	536	669	YLNVGWVVG/PMHTSNPSTSGG* GGWST*GQELKTILTSLVKHS
126	5623	A	127	793	829	GRCHLAHGGVQGSRIKQQGLGAWG RRQRDIGNRGSRLWGEKEEKAGE RKDEPALARSTSQAPSRLHPCIFNPL GVRYPRAWALHPQLCAPP*AHVSVS TQIPRQRPQVAVTLSPVPIG*FRAP QGKLPNGQMLYGRHPHPLQAPPTA RASPSHVLTLGTEQPPRA*THSPEK W*GVPAWLRTSPRPRPVGREQVT LIWKPKQN*SAESPPSHRAYPEIPFR LLCLQPRTPVLLGP*SSKCPEPPC\ TKSKPGWGKACSPLTGPCLPSP/PDL PSVPSPSPVLPDPNRTATASRNPTV TERYLNASLCWSQPDLPQGPIITDM PSAPAVPLTSDNCPSMSPAPSGKAV RQMPPGTWWGSG
127	5624	A	128	322	386	IRCFALRFSSLLSFIHLY*DT*HPDT* HPDIQTPGHL/HTQTPDTRTPGHPDT ETPDTQTLRRLTPRHLDT*HSDTQT PDTQTPGHSTPRNL
128	5625	A	129	323	516	AGGRFPSPWDPFSSRGSQASKPVRMP PTR*MRR/RGRQPCPGHRRRTQLFA VSAPSRDLQNCSSRERF
129	5626	A	130	238	583	MADKQISLPAKLINGGIAGLIGVTC

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						VFPIDLAKTRLQNQQNGQRVYTSM SDCLIKTVRSQGYFGMYRGAAVN TLVTPEKAIKLAANDFFRHQLF*GR AEA*PCLKRLGFGWG
130	5627	A	131	3	492	SSGLGCAGTRDSQLSIRRLSSTRRS GGGGDGDGTPARDLQLGWLHLLH GSGDRRGIECAIKRKDQGVNQKK KKKRTSKLGRMSSCSNVCGSRQAQ AAAEAGGYQRYGVRSYLHQFYEDCT AS\WEHEDDFHILRSPTRRS/SYIFE GVDSFSGTLL*YLAWTG
131	5628	A	132	1	245	GPGTGPEPWTPYS*EGDPRGRPRPR PLGPPP/TAHAADGSYRHSASGPGS WTSPPSPGGGEGKSGRTGQRVWKF GFWSWLCH
132	5629	A	133	554	1049	GRTGGGLGLLHGHTRLADTDLLDR GMLKDTLAQAPPPPLGEAYCHQGP GPWAGGGALSPGTRLQAGIQG/P/PE PQLPQLRPEPRP*PP/AQVVAGCGPA DLPPGGCPGCSGCSPHR*TAFIKTSA NPATLAGVGWG*GHPEGVPHTASE TGSDLQL*PTAIGHTGGPW
133	5630	A	134	798	1083	DPVGKGNVELPGRIAHCFHCLPVLH VCLSLSVLCVCFVLFWCFSTSLF*RII VFERYLTFLVCVLCC*GLCFICTCF YCSLVF*LFASCFLYSS
134	5631	A	135	71	484	EIFCYCVKYTYIQTTHAPFKFFRIYL FRDRVSL*PRLECCGVVLAHCNLR/ LPGPK*SSHLSSLSSWDYRRTPPMPS WFLCFS*RRGPHHVIQVGLELLGSS SLPALASQCWDYRREQPWPG*KVF LSSAYCLFHLTY
135	5632	A	136	186	434	SQHFGRRQLDAPRSGI*DQPGQHG ETPSLLKIQKLAGHGRRRL*SQLLE RLRQENHLKPGGGGCSEPRSRHCIP AWVTERD
136	5633	A	137	1638	1904	GGWITRSGDRDPSLAKHGETPSLLK IYKKLAGRGGRL*SQLRRLRQEN GINPGGRACSKPRSHCTPAWATG DSASKK*KIKKKVV
137	5634	A	138	421	1155	KICGSYYPLFLATFSEESFQSMLIK TTLSLNVGLVLSWKR/VQGAS\GKL QGLSEFCESQGAQNLTLRALRLHLD LQIGEKLLVKVDAKTKAQLDEWK AKKKAS\NGNARPRNCHLMTDEEA LDEETKRRDQMIKGAIEVLTREYSS ELNAPSQESDHPARKKKKEKKEAIF RRFPVAPLIPYPLITKEDISAEMED DYIDLISREISIFRDTHKRSYGD*CK MKLSAWKVTRNRINWKKRK
138	5635	A	139	338	395	
139	5636	A	140	340	1248	RPLVLANCIEVIKRVDMQVPLISG MQ/AWFNIVKQINVIYHLNIMKDN HIIHGEKAFHKIQHPVIMEILNKIE REGVYLNNTKTIHEMTTAEITSQK WNAFPVGSMMQE/CLSPLLFN/LIL AVLARAMK*/QKEIKLIEIRKKEVKL

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						YLFVDDMIFCAENHKESTKILLELS NIFSGFAQYSISTKN*LNHFTFNKQ L*KKILK/QLPLAGELK/RKKYLKIN VKRSEVFTLKSTNIDAND*KHI*RH NPY*WFGKINIVK*LYNNPM*FRFN MISIKIPISFC*RNKKQAGKMAHVC WPG
140	5637	A	141	47	411	
141	5638	A	142	1	343	GRLQAITDKRKIQEEISQKRLKIEED KLKHQHLKKKALREK WLLDGISSG KEQEEMKK/RKSTKEEAILKKLSIE RTTEDIIRSVKVEREERAEESEDIA NIPDLPKSYIPS
142	5639	A	143	460	976	LLRIGKEAELGGRGRLPGHSQIKRK LQEEISQK/RV*KLGEDKLKHQHF DK/VPLREKWLPRWNPASGKEPGR D*RSQNQPRPSTQIPGS*NKVSRL KEIQDLEKAEQISTKEEAILKKLS IERTTEDIIRSVKVEREERAEESEDI YANIPDLPKSYIPSRLRKEIN
143	5640	A	144	79	533	SSIMTFLESSAVPPHWTGQDGRVC WTGWIPQCQAGSAPE/RS*VFINSAG QKSADTGWSSSKPQN*HLSSFHQA VVGMIQPSHSQFLMKRKAASPRKL EWEH/LQPLHPMTLLYR*DGKPF VLLSTYTYCSSRDRPKSSGKNARRF PAHGSS
144	5641	C	145	354	416	MKESPGGELPQTGKKPVFLF*
145	5642	A	146	3	145	SSSSDFAGQTL*STQTVQN*FKKVL KPGRLYPVIATMGIKEPLIS
146	5643	A	147	214	464	FCGLLLLHPVSADF*PAELINTQEPQ ERCQLDTGESSRVQHTLPSCPVCQ GTAELSRNVMIGASELKCLHPSPKL EYILPGN
147	5644	A	148	246	730	SSIMTFLESSAVPPHWTGQDGRVC WTGWIPQCQAGSAPE/RS*VFINSAG QKSADTGWSSSKPQN*QLSSTGAAL PLASLSRERAWVDDGKHRLTTPMT VPQRAVQQL*ETSG**DWRQKVQIF QQAVVGMIQPSHSQFLQREDVIML RPFGLHLSWEENG
148	5645	A	149	12	288	FGGGYIPTWGKGEGILALELNHDIS REFCSAPALASRPPPTPPPLPPT/PP LPAPRSPADATPRRVGGPLR*ALKP RAPGPGWSRRRCRSWW
149	5646	A	152	106	344	KQILLPPRLEG/NGQNSG*WKFPLP GPSLFCSPSFQTSNGYGPQQARAIF WKFKIKTGFGVTRGLNFLTSGSA PLGS
150	5647	A	153	38	349	RTAKSGSTKFSLSNKGTVLAVLF MKKILVLRSPKKNDQTVKYIKRPL TSLKIREIHIKTALLYLLE/*KLLKF DDTCH**A\WRNYCWRVCVLIQPL WRQMW
151	5648	A	154	220	970	ESRTRGAEAAAGLAPSCCTSPQAHGPA PLPTHVCCGVAIGMEPGHTAISPVV ELAVHLTGLVSSHDA LGMMPSQQG

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						*QWGRQRLASGN*GRMSFPNSWP VTPICAAARLPGLLLICGFDGAGHSD RSEGF*GLRFPFCFKRQ/RSHSVSA RV*WCDHGSLQPPSSGLK\HPPVSA SQVAGTTGMWHRAWLVCLFETES CSVAQARVQWRDLGSLQPLRPQFK QSSCLSLSSWDYRHHVAPCLASLFV CLRRS
152	5649	A	155	193	369	HLN**FSNLIFFETESPSVTRGIIAH RNPRLPGSSDSPTSASRVAGTTDT
153	5650	A	156	626	1017	FDSCLFLFCFVCLRQISSVAQAGVK WHGLSSLQVPPPGFTFPSWLSLRSS WDYRHPSPHLANVFCFLGFFVFLVE RGFTVRLARIVSIS*PHDPPTASQN AGITGVSHCAWPTLVCLNAKFSIVV FVHKD
154	5651	A	157	1	336	TVSQAPSPESNPHGRRGDYHRKLIG QTFEWW/VRRHGGRAGPRLSRVTK AAGARPPEPKDFGFPEAARRVMGIT PVLDLGRQPVRGALVELRGAHGWR AGGGTGSCGIPARL
155	5652	A	158	2	320	VVAVSQAPSPE/SEP*FPVTRGHHGR HGDYHRKLIGQTFEWW/VRRHGGR AIGPRLSRVTKAAGARPPAGAGEG/ LDRVGFDLINARIPPAKGANGSSPPR GACDRPEVI
156	5653	C	159	177	380	MPTGADPLRGGDACIYQIKTNPVSP SPAPAGGRAPAALVTLNGLPIARP PWRRRPIRTSAPINFRW*
157	5654	C	160	1	417	MDATCHGCLQFQIMRNKKFQLLSP SSQHFRCMASGGKQLLCRTGQKM EHPIPXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXGRPV *
158	5655	C	161	1	403	MDATCHGCLQFQIMRNKKFQLLSP SSQHFRCMASGGKQLLCRTGQKM EHPIPXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXX*
159	5656	A	162	513	1086	QPQVASSYSAGQRRWNTPSLGKIT RSGDRDPG*HSETPSLLKIQKLAG CGGRHL*SQLLRRLRQENGVLGG GGCSEPRLRHCTPAWATE*DSISKK REKKKKKKRKKKKRKKKKWKKKE RGRGEAGEEQGEEGERRRDKKKK EKKEREETREEGRRRRRRRKKKRR RRKKKEERTTKRRRRTRKKK
160	5657	A	163	2	935	WRRSTPAPSATSASPSRRCL*SQLLG RMRQENRLNLGGGCGSEPRSCHCT LASPAGTQSCSRCTSQGGVQSDIPC TAAAPETAPRRGSAGGTWCRRRAP P
161	5658	A	164	34	1026	LLALGQSSCL*SQLLGRMRQENRLN LGGGCGSEPRSCHCTLASPAGTOSC

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						SRCTSQQGVQSDIPCTAAAPETAPRRGSAGGTWCRRRAP
162	5659	A	165	45	69	RKNQRIYQIARKRLNEMARISPLRS MILNVSGLNFPLKRCRLAEWTISSP DPIICCL/QKTHFTG/KDIYRLKIKGW KKIFHANGSQ*QTAMMNTNRERTK GYTK
163	5660	A	166	48	72	RKGQRISEIAIKRLNKMARISPLISII LNVSGLNFPLKRYRRAEWTISSPDP IICCL/QKTHFTG/KDIYRLKIKGWK KIFHTNGSQ*RTAISQSAMCENNRE RVKGFPK
164	5661	A	167	118	639	ATVPSQQLIFDKDSKAIQWRDTLFN KWCY*IN*ISTCKKLIDSYLAPRIT KINPKRILDNLVVKPTIKCLQENTGE NCWDFGSGKHFLDMTPKMQSTK*Q ISKLIKI*NFSSKTQHFALLIIRIF*KTL LTGSKYKATTWKK/VFVNHIPDKRL ISQIYQELFRTQTKNPTSDW
165	5662	A	169	435	808	KNLCNNKKFHRDEGWAQCLTPVIP ALSEARSRLYHLRISGVRN*PGQHG *KHGLYWIMQNLAGRGGTCL*SQL LGQLRQENSLNLQGGGCSEPRSRHC TPAWVTERDSVSTTTTKIFTRMNLN R
166	5663	A	170	167	197	VKFHKIKLDGEDTTYGGFDGPGLM YVYLISSDGH*FTQLHQEL
167	5664	A	171	45	259	ARMNSKLALAA*ALQKRSLRHQSNV FSMFDQSQIQEFKEAFNMIDQNDRG FIDKEDLHDMLASLGELGQGQG
168	5665	A	172	90	468	IMKLLTRAGSFSRFYSLKVGPKAK ATAAPAGAPPQPDLEFTKLPGKW LIAPLENYPPG**IGWFIKAGT*SEDF NALGTTHLLSTTCSVTNGASSFTIT RGIESADGPLTVTASREYMDHTVE
169	5666	B	173	89	186	XLKYFQTVTDYDGKDLMEKVKSP ELQAEAKVLL*
170	5667	B	174	85	298	XLEGALVRRQAKEPCVESLVSQYF QTVTDYDGKDLMEKVKSPQLQAEAK SYFEKSKEQLDTPDQEGWERELV*
171	5668	C	175	279	533	MAKDLMGEGPRTPELHAERQVFTF EKFKGSSLTPLDPRKAWERELGLTS LELIFRGNFGNHSLATPVESFPRTIW SFQTPGWAF*
172	5669	C	176	260	389	MDFFAQKKKKKVCMYVHMSTQR WLPNETNQINVLGFLNFLSC*
173	5670	A	177	84	1008	KVCCRIRKANGGKGSVPQEVDPDG APEGAPLQQGP/PGWLPLTTQSVS APPGGESPTENQPMFKQTDPMKMS FWTKMGSPTLSPNSV/AVSHFSPH FISN*EWEQNQPLSLVLSGRGDELH SDGGQKTQGLDKQQLPRGWHGLV SFGRAACSKLGKNLRPQEIKWSSKL HLPIPESQC*SPLVGVEQWGGKLS VGLLLQPKGGIPTALSPCALPAGHP TLPYGNNAGTDLRLHTEPEGPHGEP GLPARWGQDGMERWAAAGLGKG



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						YLLQASRGVVGSETGQVGFLLFGKKT KSNRLIAVNDVHFL
174	5671	A	178	79	336	NCCNTIKSISEKP/LANSIR*AKKQEG FFQISGIRQGCLLSSFLFIILEVLARG NR*D/IKCIQIGKKKVKLSLSETMR FNIWKRLR
175	5672	A	179	3	370	SVCVRAHESVVKSEDFSLPAYMDR RDHPLPEVAHVHLSASQKALKEK EKASWSSLSMDEKVELYRIKFKESEF AEMNRGSNEWKTVVGGAMFFIGFT ALVIMWQKHYGLASKWDYKNE WKK
176	5673	A	180	24	1173	RAVAAGSGGRMLATRVFSLVGKRA ISTVCVRAHESVVKSEDFSLPAYM DRRDHPLPEVAHVHLSASQKALK EKEKASWSSLSMDEKVE/LWVLKG PTGAPSSSRKRVCDRASAHFWAYC LESSLAQEGCSAGVSGHCARAPVY VLTSHLALPADRIFC*APFSVLGGGS LSAYLLGKT*LTVNY*KKLITMHSV WDERGRKITGLNRP*YCNSKK*FC SFNLHLKRTVCIFFLPCPVTCLRGHV CARMCVNMMWPGLVYPSALCFL HKCGFGEKWLNVAAEEGAADLCAC KWLSSLPVYRIKFKESEFAEMNRGS NEWKTVVGGAMFFIGFTALVIMWQ RHYVYGPLPQSFDEKWEVAKQTKR MLDMKVNPIQGLASKWDRV
177	5674	A	181	1	738	RRSQRYPFPLHGDRLAAGCGRSLPR SRGAPRRGLALFRSRDTGCRGRSRQ GSGGRMLAYQGYFTLVGKRAINSTS V\CVRA\HESVVKSEALFASQPYMH RR*HHPCPE\VAHVK\HLSCQPEGT* KEKEKAFLEASLSMDEKVEVVFAL KFKE\SA*RLNKGAPNRVVGKDRFV WAGAIVSFNRVFTALRLSCWQK\H YV\YGPLPRKSF*QKSLAKQTQEG CLDNEGEPPSQGLASK\W\PEKNE\ WKK
178	5675	A	182	82	395	ICSFAPSSIFWGSFTGTCSSTSVRA AAPPPTPQRPSMDAHMTGRKGRLS *TSFTWMTALLGVWTSVSVVW FDLADYDD*L*ALAIYD\ADGDVRF LRGLSH
179	5676	A	183	134	594	VITLTIVSPALVANNSARGLTLPAP/P LPTGSRRTGEPSPWEPDGLGSSSLASC *NPPGAPGPKS*SQTGRPAPALASR LSGPLLQLPCFLSVPRSPERAPGPRH KLLLLQSLMAVSFISQFKCHLPGEV LPDRAAPGGSWPGDSRALTKSPCT
180	5677	A	184	3	404	
181	5678	A	185	2	851	AAAPAPAPAPTPTPEEGPDAGWGD RIPLEILVQIFGLLVAADGPMPLGR AARVCRRWQEAASQPALWHTVTL SSPLVGRPAKGGVKAEEKLLASLE WLMPNRFSQLQRLTLIHWKSQVHP VLKLVGECCPRLTFLKLSGCHGVTA DALVMLAKACCQLHSLDLQHS MV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ESTAVVSFLEEAGSRMRKLWLTYSST QTTAILGDLLGSCCPQLQVLEVSTGI NRNSIPLQLPVEALQKGCPQLQVLR LLNLMWLPKPPGRGVAPGPGFPSLE ELCLASSTCNFVS
182	5679	A	186	2	568	EFGKDSCGNISAALPPLSAQVFTAPE ADPHPLEVSGTTPRVEGESSRL*LHIT CDTLGLVSTLGSSTLGAQRCSVG MSACLPGLFLLFPAGRYQRRGHP SRPGMGRKEVTAKAVRVGLAPATL SVSLVDLSLSPNPSCPSVSPQLVGE CCPRLTFLKLSG\CHGVTCLTLWSC LAKACCQFHKPW
183	5680	A	187	2	333	ARDSTSTTEMNPQVLFQRV**QFLLI TTSWRKVISQTFGRVLDTGSKL/TV QMPRISSPSVRVAACGGQVIDGVLL KVQLTVDP*T*WTDLVIFS/SAFE*VI GIDILGSECS
184	5681	A	188	2	363	AREVFTQHSWLTYYH*TIHTGEKPYK CIECGTAFGVRSCSLIHLVVHTG*LP YRCHECGMVFMNRNTHLVRHQLIHT GEKPYMCNECGRAFIAHSNLATHQ AIHTGEKPYICTECGTVFTQN
185	5682	A	189	361	1026	RKYLPPRPTFNAEALPLKVRIWGRG LISKLYH*LYQEL*L*LYQGLITILLE KKLI*KLDKNLNRHFSKEDIQMANR HMKMYSTSLNIREMQIKTTMRYPSP PQLKYLLSQKTGNNKC*RGCGEKG TLVH/WWKCILVQPLWRTVWRYL/ RKCLKIPLYNPAIPLVGIYPKERKSV Y*R*ICSMFTVALLAIAKIWKQSKCP SADEWINKIWAYAYTTEYYSAIK
186	5683	A	190	158	366	FIISMNFVFLYFVFDLSINEILLGLKE WSIYLSS/DHSLSSLCSFYLLLLMFFL CMLLLLLLCSSIIIS*P
187	5684	A	191	10	284	
188	5685	A	192	3	438	LFISLLSISEKIIENCWV*LSAARS*A LRKLAF*ATRSFF*ARDILGRFHLF F/CNFFLGLLFDWILSYSSMSFLIHL LHPAGQQASTICCSIIICQANLHTIF WQFVCIRCADYHIPLYTGISNLNDI SVCHTNYHPVIGVW
189	5686	A	193	497	752	DGVLLLLPRLECNSAILAHNRNLRP/ GFKRFSCLTLLSPWDYRHLPPRLAIF FVFLVYVGFHHVGYAGLELLTSR* SARPRPPKIA
190	5687	B	194	922	2057	YPNRFPLVMDSEKQRNFNAESTIGS HIHGPRIVAGLHAPTLMEEDDALQ ETVRASIRKEQRNSRHDGGDGIRKA HAAIPRESRSMKRSRKEVKKRW NRPKMSLAQKKDRVAQKKASFLRA QERAAES*
191	5688	A	195	1492	1790	SQTLGGRGGQITKSGDREHPG*HSE TPSLLKIQK\LAGHGNGCLWSQLIRR LRQENDMNPGGRGCSSEPRSCHCTP AWVTEQDSISKKKKQKQKEGLGGS A

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192	5689	A	196	178	572	QAGSCTRTSQPRDSRGSDIQPVGLA FGRTPAELQELHLSSPRPGRGAVWA CGSLEPGPLPLLSITSGSQPSLQLSSL PQSPLFCPLPPF/PPRPPPRVGLVPPP *LTHVPGLQPTGRPPSPSRSPAPPP Q
193	5690	A	197	209	684	PWDCVHACLRGGWHSANRGHFRI GGPGRPKAPFLPFPASLKVQALIPYP GVHPGRPLHPCVPRRMQRLCGTRD PEKLASCDIVVDVGGEYDPS\RHRY DHHQRSFTETMSSL/DPLGSRGKTK LSSAGLIYLHFGAQ\VLAQLLGTSEE DSMVGTLYDKMY
194	5691	A	198	2	720	IPGCMIRHELLPPCRELLMGHRFLR GLLTLLPPPPPLYTRHRMLGPESVPP PKRSRSLKMAPPRIGTHNGTFHCDE ALACALLRLLPEYRDAEIVRTRDPE KLR\SCDIVVNVGGEYDPS\RHRYD HPQRSFTETMSSLSPGKPWQTKLSS AGLIYLHFGHKL\VAQLLGTSEEDS MVG\TLYDKMYENFVEEVDAVDN GISQWAEGEPRYALTTTLSARDARL NPTWNHPDQDTEAGFKRA
195	5692	A	199	209	684	PWDCVHACLRGGWHSANRGHFRI GGPGRPKAPFLPFPASLKVQALIPYP GVHPGRPLHPCVPRRMQRLCGTRD PEKLASCDIVVDVGGEYDPS\RHRY DHHQRSFTETMSSL/DPLGSRGKTK LSSAGLIYLHFGAQ\VLAQLLGTSEE DSMVGTLYDKMY
196	5693	A	200	2	720	IPGCMIRHELLPPCRELLMGHRFLR GLLTLLPPPPPLYTRHRMLGPESVPP PKRSRSLKMAPPRIGTHNGTFHCDE ALACALLRLLPEYRDAEIVRTRDPE KLR\SCDIVVNVGGEYDPS\RHRYD HPQRSFTETMSSLSPGKPWQTKLSS AGLIYLHFGHKL\VAQLLGTSEEDS MVG\TLYDKMYENFVEEVDAVDN GISQWAEGEPRYALTTTLSARDARL NPTWNHPDQDTEAGFKRA
197	5694	A	201	94	660	LHLKNSDGYCLIVYQKRFPVTFIHF CFLILSLKFNNIPLNIFANGEKYFVY KFTYSY\YVVKFLT\CFVELPVNCLFI FSHFFLMSFVIFL**ILGMLYVLVL LIFNFTYICIVIAFY*LFVVIQTFLHFY LLKFNLFL*SFSGFCVLLRRVIPRI YICFIRILYNTSITLFTYLEE*FSFDM
198	5695	A	202	3	347	FFEMEF/SLLLPRLECNVILVHCNL RLPGSNDSPASAS*VAEIGVCTASS *IFVFVGTLTQ*KSRLVDQAGLELL\A PASSDPILTSQSAGITGVTTDIQPPF FLSSFANTEWT
199	5696	A	203	32	403	APIPDAMGHFTEEDKATITSLWGKV NVEDAGGETLGKLLVVYPWTQRFF DRFGNLSSASAIMGRR*VKAPG*NV \LTSLGDALMHLDDLKAPLANLRER T/CDQGCWVNPENF*LLGNVLVTVL AI

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200	5697	A	204	94	361	FCQLDSLYTESQSLDSTVL*LAEHM KFIKTSKY*GALDTFTKHLQMSVDA YE**MISILNPSSLSERQSLLLFIVLD LSLVPYLLIFE
201	5698	C	205	265	408	MTLSCSNLVFFFLFKITVFIMTMVTP QCKGGPDSVCFSTLFFVNKCPV*
202	5699	A	206	10	419	MRRGHSWARKGGMRLIRNERES GGGEQTD*ASKLKRGNRNITPFAY MDTY\ASSSSSSSSSSSSSSSSSSASKLE AELGQTGLLPIPLGGGGGAFSTKTV RSGESEGGLWKQRKRWSEGRGCR VSGWECGGAEMK
203	5700	C	207	165	248	MDTYXXXXXXXXXXXXXXXXXXXXX FQARS*
204	5701	C	208	337	428	MILRVDDFVPLALLQSFPHRSHYD PNPAA*
205	5702	A	209	531	1860	PSKPPNQCFLSLSQATSAGTHLSQD TESLTQVAKGIS*GSQGHGGGTLM RGGHSWARKGG/H*EGSSGMGRGA VEGNKQTRLLN*NGEIQTELPLLHT WTLTVQMRKVTPREGELSCPRASK LEAELGQTGLLPIPLGGGGGALSTK TVRSG\GVRGVFGSRENDGLWKVD VEGSVAGSRAGA*AMKGEPKQIPK LTL*S*P*ENPNGNAVFS*ARGKL*/ SFTKTLGAPAGAPAPPPP\GPRWPP PA/DCGHTRPPLPSESLEALKAGDS PSLALDSLSP*PPPTPPAGPRRSQGP GAPAGALGSRCPQQVKQTTLGS* RGRAGAGNTRRRGSGPHAAPIGSV DLRSGAPATAGPCG\RAASVGAGPR RGRGGRGLPAPPWGT*GAPKGPRR RGPAGWSQTGSARPCGPWASRGGP KPRPCVHGGRRPGDAPGVVTAPRC GR
206	5703	A	210	32	452	
207	5704	A	211	38	618	APSPDAMGHFTEEDKATITSLWKG VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSS\PSAIMGNPKVKAHGK KVLTSLG\DAIKHLG*SQRAPFAQA* SELALVTKLHV\DPGGTFKLLGEML LVTRFWAIPFAKEFHPWRLQA\SW QKQKMAEDGDLELASALVPSRLPL SSLAHECRAFQGYGFILASNYK
208	5705	A	212	137	368	DGVYLVWTHRPYCGLGSLNFGSVIIV LP*VKAYGWMVLTSLGDAIQPLAD PECSF\GQLRELRCMDLHVDPEDFR LLGK
209	5706	A	213	60	317	FPCLVCCTLQENSGKPILCPRRTTAQ LGPRRNPAWSLQAGRLFSTQTAED KEEHLHSIISS*SVQDYTSKHKFQA STYKH*SIA
210	5707	A	214	3	406	HEDKLCTVATLRETYGEMADCCAK HEPERNECFHQTDYNANLSRLMR PEEDVMCTAFHDNEETFLKKYLYDI ARRHPYFYDPELLIFANRHKAAFTD CSQAGD*AOWLVPKLDLYEL*A

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211	5708	A	215	1	2953	TSCIIISKCANL MKWVTFISLLFLFSSAYSRGVFRRT PLGPASSLPQSFLKCLEQVRKIQGD GAALQEKLCAATYKLCHPEELVLLG HSLGIPWAPLSSCPSQALQLAGCLS QLHSGFLYQGLLQALEGISPELGPT LDTLQLDVADFATTIWQQMEELGM APALQPTQGAMPAFASAFQRRAGG VLVASHLQSFLEVSYRVLRLHAQPG GGGDAHKSEVAHRFKDLG\EEDFT ALVLI AFAQYLQQ*PFEDHV KLANE ATEFAKTCVADESA\ENCDKSLHTL FG\DKLCTVATLARETYG\EMADC\C AKQGT*GEMECFFATQRMNDPNLP PIGWRTGWMWMLHCFHHDNEGD IF*KKYLLWKLPGRTSFTFYGPPELL FLWLKR/RIKAGFLQEC\CQGWLD*S WPACLA KGSDEL SGMKGKAS\SAK QRLKCA SLQKIWEKELSKPWAVAR LSQRFPAEFAEVSKLVDTLTKVHT ECCHG\DLLECADDRA\DLA\KYICE\N QDSISSKLKECC\EKPLLE*FH\CLA EVENDEMPADLPSLAADFVEN\KD VCKNYAEAKDVFLGMFLY EYARR HPDYSV VLLLRLAKTYETTLEKCCA AADPHECYAKVFDEFKPLVEEPQN LIKQNC ELFQ LGEYKFQNAL LVRY TKKVPQVSTPTLVEVSRNLGKVGS KCKKHPEAKRMPCAEDYLSVVLNQ LCVLHEKTPVSDRVTKCTESLVNR RPCFSALEVDETYVPKEFNAETFTF HADICTLSEKERQIKKQTALVELVK HKPKATKEQLKAVMDDFAAFVEK CCKADDKETCFAEEGKKLVAAASQA ALGLTPLGPASSLPQSFLKCLEQV RKIQGDGAALQEKLCAATYKLCHPE ELVLLGHSLGIPWAPLSSCPSQALQ LAGCLS QLHSGFLYQGLLQALEGI SPELGPTLDTLQLDVADFATTIWQQ MEELGMAPALQPTQGAMPAFASAF QRRAGGVLVASHLQSFLEVSYRVL RHLAQP
212	5709	A	216	1060	1259	TKFGQH GKTPSLLKI*KL AGHGGAH L\KSQLPGRHENHLNPGGGGCSEPR LCHCTPAWVTKRDCLKK
213	5710	A	217	2	354	SAAAGQGEENQLEASLDALLSQVA DLKNSL/EEFHLQVGERVWPADLLN TLNKVLKHEKTPFRNQVIPLVLS DRDEDLMRQTEGRVPVFSHEVVPD HLRTKPDPEVEEQEKQLTTV
214	5711	A	218	90	329	
215	5712	A	219	2	632	QPSFLCVILVYLGDPVPIGAEKRRS TLEASLDALLSQVA*SEELSGEFHL QVG\DEYGRLTWPSVLDSICLAFLD SMNTLNKVLKHEKTPAVP*PGHHSS GCCLQDRR*KISCRQT*KDGCLFSA H*GKSLDHLEKPSLDP*KLEE QEKQ LTTDCSPAFGADAAQKQIQSFE*NV

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						FQTF LGENQQRGSEDSWRFSGRT SRLLTPTDT
216	5713	C	220	309	479	MIHYSSSYSFKSSRELHIKFKFPVST SCGAFGSKIKWKVLSEVVEETQESE QPEVL*
217	5714	A	221	76	525	PQPLGPQPQQRPSRLASCCGAAAPC SWVEGAIGHAPPHGLPIMSNGYRTL SQHLNDLKKNFSLKLRIYFLEERM QQKYEASR\EDIYKRNTLKVES LKRELQDKKQHLDKTWADVENLN SQNEAELRPQFEERQQETEHVYELL EK
218	5715	A	222	534	1310	PRNEFTQQFCFIDSFFLVTLKIEALQ CSHRSSRGKVPFVQTYSLRAFEK PPQVQTQALRDFEKHLNDL\KKENF SLNVRIYFLEERMQQKYEASREDIY KR\NTLKVESLKLRELQDKKQPS GLKPWA\DVENLQPVQNEAELRRQ FEEP\QQETEHVYEL\LENKMQLLA RRNSRLATE*TMRGWQLLVERQRK GV*TWKLSGET*RESPKNWGRCP EPQVKPDPLHLRPLAQKGKDLKKI MLGSPNHIKNASDQ
219	5716	A	223	32	360	TGSKIRNIKGIIHIGREEMKLILFTNYI LVCRE/NPKIMFKLLALISRY*ATVA GCNIYIPPTPKLNFDIVG*ILLAKKLF TNANNIRYLGINLIINDGHLSKEI YIISL
220	5717	A	224	2	761	APTPTGQRVVRATPAQSAPVRLRRR SYDVNNPIPSNLKSEAKKAAKILRE FT\ETSRNGPDK\NPGSTVIKAK\G LANSCLLNQSPGSLVTFQGGPGVL VARL\PDGK\WSSPFS\ALGIAGFG\G GFEIGI*GIQTLVILEF/DDPCC*EAF AKGGNLTGGNLTVAVGPLGRNLE GNVALRSSAAVFTYCKSRGLFAGV SLEGSLIERKETNRKSVQVKVILIE SVMRK*YFKS*YNLQSTFIYSFYNM WF
221	5718	A	225	299	541	SQHFGRLTQADHLKS*VQDRPGQH GEIPSLQIQKLAGHGGASL*SQLLG RLRQENHLNPGGGGCSEPRTPGWA TE*DSV
222	5719	A	226	198	660	LLLALLFNTVLRFTVCLFLFQAPILK SPCCSAARVDRRKSIWVDGL*ICSR LSK*VIC*LGTFKFVVQILQHTLSN *L\HLNIEKN*GLTG*VSILCKLFYH SL*PLL*VKCSLRPGVVHTCNLSTL GGRGGRI*VQEFETSLGNIVRHRI
223	5720	A	227	1	347	GERLAGRRRKMAVESRVTREEIGN DS*KPIDREKTCPLSLR\AFTTNNGR HHRMDDFSRGNVPYSELQTYTWM DATLKDLTSLAQELYPQATLNGTH FTFAVALTHATPPGSRVND
224	5721	A	228	3	225	SCQGERLAGRWKMAVESRVITQE EIKKEPEKPIDREKTCPLLLRVFTTN NGRHHRMDEFSGRWSKAPGKQK

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						GP
225	5722	A	229	1984	2676	
226	5723	A	230	2	590	GCRNSARGKMAVESRVTQEEIKKE PEKPIDREKTCPLLLRVFTITNNGR\  HHRNGRVSPRGVNPSTELQIFPLGW MPTLKELTSL\ VKEVYPEARKKGTH FNFAIVFNRLCKVPGYR*FSFLQS* GGLASTHVWAERGLDDSHPELQSR KFQIGDYLDIA\ITPPNRAPPPSGR MRPYLNSNFTYLFIFYFFPSVM
227	5724	A	231	1	291	
228	5725	A	232	3	320	AKNRLQILKFLHFKERKTVLP SKH AVPEVIEDFLCNFLIKMGMTRTLDC L/QASEWYELIQKGVTELRTVGNVP DVYTQIMLLENENKNLKKDLKHYK QAAEYVIF
229	5726	A	233	209	461	
230	5727	A	234	104	609	RQPGTRGTRRTRWRLEGAYYLEQV TITEASEDDYEYEEVTC*F*IPDDNF SIPEGEEDLAKAIQMAQEATDTEIL ERKTVLP SKHAVP*VIEDFL/RCNFL DQNGELTRTLD CFQSEWYELIQKG VTELITVGNVPDVYTQIMLLENENK NL*KDLKHYKQAAEYVIF
231	5728	A	235	222	502	TSLIKHYISNLTFFINSVEYKQ*WFL LWLCVSLKC*LGQAWWAQACNLS TL*GPRWAADHLRSEVRDRTG\QH GETPSL/LKNTKISWAW*WVPV
232	5729	A	236	565	779	APGVRD*PGQHGENLSLQK*KLKK LAGHGGIHL CFQLRRPRQKYRLSP EGQDCSE/PMVCTLA WATEQDPVS
233	5730	A	238	656	923	VPVHRGKERGGIQDLDEIATPTLLS KSSSFFKTSYCTDFFLFTESCCVTR LECSGMISAHCSLCLPGSSNSAPTSP VSHNKDRLLHL
234	5731	A	240	171	373	AWLCANKTLFLNFYLFETRSC/SLS RLECNAIIAHCSLLLPGPSDSPTSA SQVAGTTRTCHDTQPI
235	5732	A	241	915	1283	QRQRLGLWDNEEGEIGTKYSSFKI DTVEKLFLGGGRSRVKPRGSNKAR DPPSFPSPAWEVGPQLGVPLKSPCG LHLGLAAVPLYDPRGGGPHTPPHTP P/PTPHPPHPPHPPHTKHTPPTNTQ
236	5733	A	242	555	767	NKKDLFSLRSGDQKSKVKTSEGPRL /PLRGIRENP/PPVPAPGGPRHCLAC GGITPVSACIITRISCPLYSN
237	5734	A	243	2	744	GTMAVFVLLALVAGVLGNEFTIL KSPGSVVFRNGNWPPIGERIPNVAA LSMGFSVKEDLSWPGLAVGNLFHR PRATVMVMVKGVNKLALPPGSVIS YPLENAVPFILDSVANSIHSLSFSEETP VVLQLAPTEERVYVMVRKANSLFEY LSITFLQLHNRLFQKNSVLTSLPLTS LNNNNELHLLFF/S*LQPLH*ISNFLS CDKHFTQKMIVLINNHSNLPMLPTK FGNPFLTKSFSPFNLSLKPFSA
238	5735	B	244	385	544	MTGSPEDDETGYPLRSPGQERSST

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						EKPMDNAATSGIRSPGIGQFPFRKTTDPX*
239	5736	A	245	1	449	GNEFSILKSPGSSVFRNGNWPPIGER IPDVAALSMGFSVKEDLSWPGLAV GNLFHRPRATVMVMVKGVNKLAL PPG\SVISYPL\ENVDLLFLSELQVLH DISSLLSRHK\HLAKGSILPDLYSL\AE RAGFGMEIGKRYGEDSEQFRDASKI
240	5737	A	246	2	1230	GAGRVRRARHLLTLRLSPCAGPFRV APQCCGRRGTMAVFFVLLALVAG VLGNEFSILKSPGSSVFRNGNWPPI RE\RDPPDVA\AI\SPMGFSVKEDLSW PGLAVGNLFHRPRATVMGDG*RG VNKTWLYPQGSV\SYPLE\NAVPF LDQCLQPIHFLIFLEETSCFLQLGF PVRE\RVVLWLGKANFSV*RTFSVT L\RLR\NIRLVFKENSVSSVSLPLNS LSRNNEVDLLFLSELQVLHDISSLL SRHKHLAK\DHSPDLYFTGSWAGL\A DEIGKALLGEDSEQFRDASKILVD\A ALQKF\ADDMYSLYGG\NAVVELV TVQSF\DTSL\IREGQGTYSLEGKTS GTPASPYNLAYKYNFEYSVVFNMV LWIMIALALA\VIITSYNIWNMDPG YDSIIYRMTNQKIRMD
241	5738	A	247	1547	1965	AQGRFQALCSLVAVRAWGWPLSG NSFSCGNSQCVTKNRSVTTRRTAP MGPTRRMRVWLAASWRMAGRIVG GMEASPGSFRGKPAFERTRSTSVGR HHQRQPLRS*NHRFQDPTKWVAYV VRPTSAARRPAPCGPSKKA
242	5739	A	248	403	734	MAVQAGTQCLVQQLHSGFLQHLW LDHCRPRKMLTEVLLLEVAPA*DQA LLAGWEDVCGSREAHGLD\GRPKG RGLVSSSTATSKSAVSALYRGCLTI WTTWARTVLASEPLR
243	5740	A	249	1	552	MVWSSQRCCRKHCGAAGPGTVCC LVRPLLTDRMVCAGYLDGKVDPAR PQKNTDTSVSNAGRFTDIWMPVLE EFKAVGIERQNVGPGLNGEAHPGR GRVRSCLREVPWQVSLKEGSRHFC EQLWWGTAGCCLPPTASPVSGIKA L\YESELADARRVLDETARERARLQ IEIGKLRAELDEVNKR
244	5741	A	250	63	497	LPDVEKLGRRRGRKMDSVEKGAAR LR\PNPRGRPSRGRPPKLQRNSRGG QGRGVEKPPHLAALILARGGSK\GIP LKNIKHLAGVPLIGWVLRAALDSG AFQRCACARVGGAAGVGRGSR AAGGAGASGATALGRGPSLMPGM C
245	5742	A	251	1	349	GTRAVVCGRRLLSVREQIRHFVMRP EINTNHLDKQVQVLLAEMCILIDEL DNQAYCETKKNCHLNENIEKGAAL KQTLLLSDLCRHRFAEKSTLFKEV QTSVIPYFLVGSSSFK
246	5743	A	252	2	423	LRWSL/DSVAQAGVQWGDLSLQA PPPGFTPFSCRLRPSSWDYRCQPRT



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						*RRGFIVLARMVSI*PCDPPASASQ SAGIIGM/SHRARPGFPT/CQTTQEPG GTTSHGYRIPPP*QDLC*LPQFPERG SGSQRC*DKPGSPSL
247	5744	A	253	891	1564	SPRALAANPWWMVTSVSSRVKQSC TQGGGFVPLAQQVHSPHSELYALV SLFFYFLFDICRARILSGSFILRTL LLLFLRRSLNSVTQAGVQWRDLGS LQAPPPGFTPFSLPSSWDYRRLP PRPANFVFLVETGFHRDETRIVSI S\GPRDPPASASQSAGITGVNHRAW PTFCIFCRDRVSSCWPGWSRSHTPG LKRSSCLSLPKFWDYRHKLPYP
248	5745	A	254	6	338	MEPSCGLGSEALALTQTWAGSHSL KYFHTSVSRPGRGEPRFIYVGYVDD TQLVRLDND/APSPKMPRAPWIEH EGSKIWDRETHIAKDTRQIFRVNLR TLRSYYDQIEAGD
249	5746	A	255	2	424	
250	5747	A	256	25	486	EFHRLRENPPWCLSPADKTNVKA\A WGKVGAAHVRSMCAEALERMFLS FPTTKTYFPHFDLSHG\SAQV*GATG KKV\ADALTNVAHV\DDMPN\ALS AL\SDLHAHKL\RVDPVQLSSS*SHC LLG*PWPAPHLPRPSFTPGGCTPSLG QVSWAFC
251	5748	A	257	230	358	FLIILRRSLILSPRLECNQSVPAHCSL/ RTPGFKRFSCSLSSS
252	5749	A	258	75	188	
253	5750	A	259	340	535	FRFKALFDLFLVEIASCCVAQAGV QWCDLSSVQPPPG\SSDSPTSASQI AGTT\GALQHAWLIF
254	5751	A	260	1618	1962	DRVSLSPRLECSGTL\AHCKLR/LP GFTLFSCSLPSSWDYRRLPPRAN FFVFLVEMGFHRVSQ/AMGLDLLT SGDPPASGLSKCWGLQGVSNLRPS QASPSFKGIKGPQTLRA
255	5752	A	261	3	395	
256	5753	A	262	152	514	LATLLGPWSCARVPSVPALLTPPPL AGPPPPQPLLQRLCSGPRLLLLSLGL SLLLLVVDVIGSQNSQLQEELRGL RETFSNFTASTEGPGSRALSTQGRA MWGRKMEVRLEFPVWRKQQ
257	5754	A	263	138	1072	
258	5755	A	264	1	488	
259	5756	A	265	1	2105	FRAASCAPPWRMELRSGSVGSQA VARRMDGDSRDGGGKDATGSED YENLPTSASVSTHMTAGAMAGILE HSMYPVDSVKTRMQSLSPSSQSPV PSIYGALKKIMRTEGFWRPLRGVN VMIMGAGPAHAMYFACYENMKRT LNDVFHHQGNHSLANGIAGSMATL LHDAVMNPAEVVKQLQMYNSQH RSAISCIRTVWRTEGLGAFYRSYTT QLTMNIPFQSIHFITYEFLQEQVNPH RTYNPHSHIISGGLAGALAAAATTP LDVCKTLLNTQENVSLANISGRL

SEQ-ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VVPMGPLLPNALERGGDGTAHRK AVCGDIREVWELDRLLPCDIRDGAF ITMPFH CYA QNRGEGLLRPAELAD GAAPRELGP GGGPEDGWGQPRW RRRQGP PPGREDYENLPTSASVSTH MTAGAMAGILEHSVMYPVDSVKPR ARPRLLAALRRGRSGEHRWLRRR LGSRGTRSLKLC TVLPRWPFGLAGA AHTCAVSEG VPRRGSPHHAGA EKR VALARPRALGTWC VAAAPRVISGT WGRQVFSRLVAALYRFDSGPWDPL SEG SCTSSP DFGSPSRREAMTFAFSF CLRGGRHMPSLREHYWARM SHER HKDWANVGGTITV LSEP NFLIN NTR LARNRTPWARHDN WCHHWQHVS P ESSLDCVRLQGLPWMAAAE VEMK LPAGHMHMPVSFPNRSPLGAGCIN
260	5757	A	266	882	1299	
261	5758	A	267	1	2607	MAFAWWPCLILALLSSLAASGFPRS PFRLLGVANGIEVYSTKINSKVTSRF AHNVVTMRAVNRADTAKEVSFDV ELPKTAFITNFTLTIDGVTYPGNVKE KEVAKKQYEKAVSQGKTAGLVKA SGRKLEKFTVSVNVAAGSKVTFELT YEELLKRHKGYEMYLKVQPKQL VKHFEIEVDIFEPQGISM L DAEASFIT NDLLGSALT KSFSGKKGHVSFKPSL DQQRSCPTCTD SLLNGDFTITYDVN RESPGNVQIVNGYFVHFFAPQGLPV VPKNVAFVIDISGSMAGRKLEQTK E ALLRILED MQEEDYLNFI LFSGDVST WKEHLVQATPENLQEARTFVK S ME DKGMTNINDGLLRGISMLNKAREE HRIPERSTSIVIMLTDGDANVGESRP EKIQENVRNAIGGKFPLYNLGFGNN LNYNFLENMALENHGFARRIYEDS DADLQLQGFYEEVANPLLTGVEME YPENAILDLTQNTYQH FYD GSEIVV AGRLVDEDMNSFKADVKGHGATN DLTFTEEVD MKEMEKALQERDYIF GNYIERLWAYLTIEQLLEK R KNAH GEEKENLTARALDLSKYHFV TPLT SMVVTKPEDNEDERA IADKPGEAS YQPPQN PYYYVDGDPHFIIQIPEKD DALCFNIDEAPGTVLRLIQDAVTGL TVNGQITGDKRGSPDSKTRKTYFGK LGIANAQMD FQVEVTTEKITCGTG\ RAISTFSWLDTVTVTQDGLSMMINR KNMVVSFGDGVTFVVVLHQVWKK HPVHRDFLGFYVVD SHRMSAQTHG LLGQFFQPFDFKVSDIRPGSDPTKPD ATLVVKNHQLIVTRGSQKDYRKDA SIGTKVVCWFVHNNGEGLIDGVHT DYIVPNLF
262	5759	A	268	1	1842	
263	5760	A	269	3	377	
264	5761	A	270	1	621	MTKRCLDHRGEWLP GAGGGGGHTE GTRCLHHAPVTWVGIEVDIFEPQGI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SMLDAEASFITNDLLGSALTKSFSG KKPVWLRGRHTPKGNLDSEVLGL SPCPIPLAGLTVNGQITGDKRGSPDS KTRKTYFGKLGIANAQMDFQVEVT TEKITLGTG\RA\STFSWLDTVTVTQ DG*APLQGLQGGLQGEGDHSGPQP NPGALSEPELV
265	5762	A	271	3	2722	FSDGLCMVALSHLGSALQLGSLCFP RSPFRLLGKRSLPEGVANGIEVYST KINSKVTSRFAHNVVTMRVNRAD TAKEVSFDVELPKTAFITNFTLTIDG VTYPGNVKEKEVAKKQYEKA VSQ GKTAGLVKASGRKLEKFTVSVNVA AGSKVTFELTYEELLKRHKGYEM YLVKVPKQLVKHFEIEVDIFEPQGIS MLDAEASFITNDLLGSALTKSFSGK KGHVSVFKPSLDQQRSCPTCTDSL N GDFITITYDVNRESPGNVQIVNGYFV HFFAPQGLPVVPKNVAFVIDISGSM AGRKLEQTKEALLRIEDMKEEDY LNFILFSGDVSTWKEHLVQATPENL QEARTFVKSMEDKGMTNINDGLLR GISMLNKAREEHRIPERSTSIVIMLT DGDANVGESRPEKIQENVRNAIGG KFPLYNLGFGNNLNYNFLENMALE NHGFARRIYEDSDADLQLQGFYEE VANPLLTVGEMEYPENAILDLTQNT YQHFYDGEIVVAGRLVDEDMNSF KADVKGHGATNDLTFTEEVDMKE MEKALQERDYIFGN YIERLWAYLTI EQLEKRNKNAHGEEKENLTARALD LSLKYHFVPLTSMVVTKPEDNEDE RAIADKPGEDAEATPVSPAMSYLTS YQPPQNPYYYVDGDPH/FSIIQPEK DDALCFNIDEAPGTVLRLIQDAVTG LTVNGQITG\DKRGSPDSKTRKTYF GKTGASPMAMQMGFPGEVTEKIT LLEQARCRAFFSWLDTVTVTQDGH FLASSRRLSMMINRKNMVVSFGDG VTFVVLHQ/VCWKKHPVPTVDFL GFYVVDHRMSAQTHGLLGQFFQP FDFKVSDIRPGSDPTKPDATLVVKN HQLIVTRGSQKDYRKDASIGTKVVC WVHNNGEGLIDGVHTDYIVPNLF
266	5763	A	272	1168	1626	RAGRGGEHKLNSYGGRRARSQG HLLSSALSPFVSAASYQPPQNPYYY VDGDPHFIIQPEKDDALCFNIDEAP GTG\RLRIQDAVTGLTVNGQITGDK RGSPDSKTRKTYFGKLGIANAQMD FQVEVTTEKIT\CGTG\RA\STFSWLD TVTVT
267	5764	A	273	534	690	FVIFSPCSIAMATKENMTSQRGML KSIH\SKMNTL\ANRFP\VNLSIQRV NL
268	5765	A	274	3	946	TTKMAAGTSSYWEGEARRPPDLRK QARQLENELDLKLVSFKLCTSYSH SSTRDGRDRYSSDTTPLLNGSSQD RMFETMAIEIEQLLARLTGVNDKM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AEYTNAGVPSLNAALMHTLQRH RDILQDYTHEFHKTANFMAIRERE NLMGSRVKDIESYKSGSGVNNRRT ELFLKEHDHLRNSDRLEETISIAMP TKENMTS\QRGMLKSIHSMNTLA\ NRFPVNSLIQRINLRKRDRSLILGG VIGICTILLLLYAFHLMGHLQGLLTA TAFTPWSGIRKHRREKLTVLIISLTS RMNARLTVMDSVTWSG
269	5766	A	275	269	476	VMAVLPSGTALKTNWEPGRDLQC NGSSLLSGAPHIVSLLGFRIRAKTG RARC\HACNPNTLGGRGGRI
270	5767	A	276	2	424	
271	5768	A	277	3	452	
272	5769	A	278	3	498	PTLLVPTDSERTHHGSCFLPDKTNV KAAVWGKVGAGHAGEYGAEALERM FLSFPTTKTYFPDFDL\SHGSAQVK GHGKKVADALTNAAVAHVDDMPN \ALSALSDLHAHKL\RVPDFNFKLPS HCLLVTL\AAHLPAEFHPLRWHALP GTSFLGFLSTVADLPNTR
273	5770	A	279	333	538	IFSSLWLFILSIKDFILFYFLAQS SVTRLECSGTISAHCNLCNPSSDF RVLRLGNRLRLKIKK
274	5771	A	280	192	607	GRLWGCVSKKSVCGLPHPGCLWA AFLTLDACGLPSSPWPVGSPLPHG CLWAAFLTLDACGLPSSPWPVTVW FPWGLPKLRDPKPPSNLMTRPVSEP PVLSPSPSPTPSATRPTHFPSLKGP HRAHVFPFNPFCFVP
275	5772	A	281	17	363	GLESEFLLRGLLRPGEQDSALASAV PGSLAQTLFPWS/PLW/TMSFPAHA APHACCHCLSY/PVSCPVSVPSSLP LGCPQLLLPSCPNSCYPSPAVPTYCP AGKEEKRRSPSCQACS
276	5773	A	285	96	389	QGPAAENMAAKMFEFIGKFGALV DAGGVVNSALYSVDAGHRAVVFD RFRGVQDIVVGKGTWLPWLQKS/ IIFDCRSQPRNVLVFTGSKDLQIGNL H
277	5774	A	286	1	390	FFYFFFLERDFLFLFYFIFFAVLLLLP NLECNCAISAHRNLRLPG\SSDSPAS ASQVAGITGMQHHAWLSFVFLVKT GFVHLGHAGLKLPTSDDPPTAASDI VGITGMIPPVAGPKQRHFCARSVLV PFI
278	5775	A	287	16	546	QLNGRSIRHEVMSHRKFSAPRHGSL GFLPRKRSSRRHGKVKSPKDDPSK PVHLTAFLGYKAGMTHIVREVDRP GSKVKNKEVVEAVTIVETPPMVVV GIVGYVETPRGLRTFKTVFAEHISDE /CRLPLRQKKAHLMEIHVNGGTVA EKLDWARERLEQQVPVNPVFGQDE MIDVI
279	5776	A	288	1	625	CKFIRVMAHTRLRLPLRRKKAHL MEIQVNEGTVAEKLDWARERLEQQ VPVNVVFGQDEMIDVIGVTKGKG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KGVTSRWHTKKLPRKTHRGLRKVA CKDGLIKNNASTDYDLSDKSINPL GGFVHYGEVTNDFVMLKGCVVGT KKRVLTLRKSLLVQTKRRALEKIDL KFIDTTSKFGHGRFQTMEEKKAFM GPLKKDRIAKEEGA
280	5777	A	289	1	903	
281	5778	A	290	38	482	
282	5779	A	291	1	1131	
283	5780	A	292	1	1329	STHASDGVMSHRKFSAPRHG\SLGF LPRKRTS\RHGRGVKSFPKDDPSK\P VHLTAFLGYKAGWTHIVREVDR\P GIHRCNKKERWWRAVTHCMRPPP MVVGGLVGVYVETPRGPPGPFT CLLEH\SDELPRGVFYKEFGH*NL KKKAFTK\YCKEIGKDED\GKKPAW KKDFQQH*KKLLAQVHPCSIQTQ\ MRLPLARQK\KAHLMEN\QVNGGT VA\EKLDWAREKLE\Q\VPVNPVS LGRMRMID\VIGGDQRAKGYKGS PS\RWHTKKAAPAKTH\RG\LRKVG LVLGAWHP\ARVAFSVG\RAAGQK GYPSTALEINK\KIYKIGPGVTLRA GSLIKEQCLHLNYDLSDKSINPLGGF VHYGEVTNDFVMLKGCVVGTGKRR VLTLRKSLLVQTKRRALEKIDLF DTTSKFGHGRFQTMEEKKAFMGPL KKDRIAKEEGA
284	5781	A	293	238	326	HTYKSDTRYERHACWGALL\CNYM RQECLDSRFVFDPRMPVFRVSVIG TSILYMKAFMHMPFK
285	5782	A	294	2	358	GWGMSLGGAGVEGMEVGTSDLGF FSGQRALSPWVSPVPGLCAWRKD SPVEQKPQGPSLPLSALPYLWG/AP WPPAGPQTRGLGPFRGTGSPSPIS RAQKDSWPWPVPSTPACFSAPG
286	5783	C	295	56	175	MASXNRQFFXNTPXKLLKSPHCNI YRLLSAKSQKFWK*
287	5784	A	296	1178	1515	KKFMKILEHMFEGFFSFLNFFIFSG GRRSALTARGGSEVAANLGLTCNL HPPGFKRFSCRLRSSWDYRRPPPR PANFVFSVETGFCYVGQAGLKLLT SSDPPASAFPKC
288	5785	A	297	136	251	IHQEKPPNIFSVKKRHYD*PGQHDP LASASQSAGITGV
289	5786	A	298	118	337	IHQEKPPNIFSVKKRHYD*PGQYGK TSLLLKIQILAGYSGTCL\KSQLLRR VGREVIQLALKIRAPIWKIECL
290	5787	A	299	160	437	KRDITSLGQYGNP\SLKIQILAG Y\SGTCL\KSQLLRRLRHQNRNLG GRG\GSEQRSCHLSWGHHSETVSK KKKKRERQQWRQIGTCMP
291	5788	A	300	61	1302	FSGSCVPPRTCGLCWISTGQSGVVS VSSTRLEESEGTQPPSPSSDTGSEGE EDDEGEEHGLGGQNEVGIIPTTLEFL ENHGNILLNSGNRTVTRVASYNQ GIVVINQPLVPQLLVQVRIDFLNRQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WTSSLVLGVITCAPERLNFPAACAP SNGQPGCCGAVGSSTTSQAGLSSQI CEKFGPNLDTCEGTILGLRLDSSG GLHLHVNGVDQGVAVPDVPQPCH ALVDLYGQCEQVTIVNPEPGAASG KSAGTQGDMEKADMVDGIKESVC WGPPPAASPLKSCEYHALCSRFQEL LLLPEDYFMPPPKRSLCYCESCRKL RGDEAHRRRGEPPREYALPFGWCR FNLRVNPRLEAGTLTKKWHMAYH GSNVAARRVLDRGELGAGTASILS CRPLKGEPGVGFEEPGTNC
292	5789	A	301	1	936	
293	5790	A	302	1	1023	
294	5791	A	303	1	867	
295	5792	A	304	1	569	SGRVAMGRRRAPAGGSLGRALMR HQTQRSRSHRHTDSWLHTSELNDG YDWGRLNLQSVTEQSSLDLFLATA ELAGTEFVAEKLNIKFVPAEARTGL LSFEESQRIKKLHEENKQFLVVYRG DQTNQNTTPEELKQAEKDNFLEW RRQL\VRLEEEQKLILTPFERNLDFW RQLWRVIERSDIVVQIVDA
296	5793	A	306	846	1070	RVGDRSEREIVILKTNFTYFQVFPKA GCGCFSFLFSFFLSFFFLRGETESRSV A\RMKCSGVISAHCNLCPLPGSS
297	5794	A	307	118	340	KFQTEVSHFFLCNLICSYFIFLL/CS FLLIHF/LYSLFFLLFCFMFFLFIMY /LFFVLLIRYSYIKSLFLMSCN
298	5795	A	308	42	352	TRGPRVPHSGSASSPAQKSGCTG/P* NSALARPALVSFRAMPNSRGW/PQG EQR/PGSPHRSPEGHWKRVHVPPA AQRGPGAGGCHQGTGPEAQAQAHQ VRPPAQGG
299	5796	B	309	796	3180	VAEAPGLVDVPGGHPEPQSCEKLE NTGGKIGHRRKMPYSTPAPCVSPLK LDLWLSVRERTPDGSLTLLHCATS DPQGQALCPGGSPQHQLAGQLV VHELFSVLQEICDEVNPLLTLSQP LLGIARNETSAGRASAEFYVQCSL TSEQVRKHYLSGGPEAHSTGIFFV ETQNVRRLPETEMWAEPCPSAKGA IILYNRVDVVLASTPMRICPPAAMP LLPLRLCRLWPRNPPSRLGAAAGQ RSRPSTYYELLGVPAGASTEVEVKRA FFSKSKELHPDRDPGNPSLHSRVEL SEAYRVLSREQSRRSYDDQLRSGSP PKSPRTTVHDKSAHQTHSSSWTPPN AQYWSQFHSVRPQGPQLRQQQHK QNKQVLGYCLLLMLAGMGLHYIAF RKVKQMHLNFMDEKDRIITAFYNE ARARARSVPALFCSLLPVQEPHFGIP IPTTQAPVSQPDAPGHQRKVVSVID VYTRATCQPREVVVPLTVELMGTV AKQLVPSCVTVQRCGGCCPDDGLE CVPTGQHQRMQVLGTWGNQGQ MQILMIRYPSSQLGEMSLEHSQCE CRPKKKDSAVKPDSPRPLCPRCTQH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HQRPDPRTCRCRCRRRSFLRCQGRG LELNPDTCRFSCSLTAGSLLQLTDV WWLLGRLKISLVGEQAQPDHSSHE SQPRCTGRVLSICLSAVATATGAEG KRKLQIGVKKRVDHCPIKSRKGDV LHMHYTGKLEDGTEFDSSLPQNQPF VFSLGTGQVIKGDQGLLGMCEGE KRKLVIPSELGGATLVFEVELLKIER RTEL*
300	5797	A	310	61	674	GCGTLGPLQWDFPEPGCKGMMAPL AEGQSSAHISVWGNLRTFCVSTKKI PVDSGASGSPTQVSASLTCSESQAA LDIELGTGLGNNLVSFRGDAKQAG AGLRVKNRAGSPSTRSPEGHWKR VHVPPAAQRGPGGWGLPPRAHGPE AQGAHQVRPPA\QGPQPPAGSGAG RQGSRLWLVRPPPVGPPDRPAC HPSRWHPAVAA
301	5798	A	311	89	1166	
302	5799	A	312	1	2094	MGAPAVQSSSGPAGARPRKAGVER RAEPAGPLPETTRKSPQPILGFSLR AVVWDLFPGSKQIVRRKLPIPGQAV LVQADVATLTSRRVLHACGLVPLE MPCIAQYGTAPSPGPRDHLASDP LTPEFIKPTMDLASPEAAPAAPTALP SFSTFMDGYTGEFDTFLYQLPGTVQ PCSSASSASSTSSSATSPASAFKF EDFQVYGCYPGPLSGPVDEALSSSG SDYYGSPCSAPSPSTPSFPQPQLSPW DGSFGHFSPSQTYEGLRAWTEQLPK ASGPPQPPAFFSFSPPTGLS\PSLAQS PLKLFPSQATHQLGEGESYSMTAF PGLAPTSPHLEGSGILDTPTVSTKAR SGAPGG\SEGRCAVCGENASCQHY GVRTCEGCKGFFKRTVQKNAKYIC LANKDCPVDKRRRNRCQFCRFQKC LAVGMVKEVVRTDSLKGRRGRLPS KPKQPPDASPANLLTSLVRAHLDSG PSTAKLDYSKFQELVLPFHGKEDAG DVQQFYDLLSGSLEVIRKWAEEKVP GFAELSPADQDLLLESFALELFILRL AYRSKPGEGKLIFCSGLVLHRLQCA RGFGDWIDSILAFSRSLHSLVDVP AFACLSALVLITDRHGLQEPRRVEE LQNRIASCLKEHVAAVAGEPQPASC LSRLLGKLPRLTLCTQGLQRFYLLK LEDLVPPPIIDKIFMDTLFP
303	5800	A	313	858	1143	QLVPCCPPTQRTVQKNAKYICLAN KDCPVDKRRRNRCQFCRFQKCLAV GMVKEGVWL/RVRPTGARVGLSGV RPPGPPGFCPPGPTGGHVLFPPLH
304	5801	A	314	190	330	ERIKKQDLSICCLQVTHFTFKDSQRL KVKGWKK\IFHTNKNQKRIWT
305	5802	A	315	190	324	ERIKKQDLSICCLQVTHFTFKDSQRL KVKGWKK\IFHTNKNQKRI
306	5803	A	316	85	310	CAWHVNILIGKRLNTFPYRSGTRQG CMLLPFLNTILKDLVTALKNQDIK GKQIK/EEIKLSLFTMITRVDKNQS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *-Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
307	5804	A	317	33	494	
308	5805	A	318	1	612	
309	5806	A	319	113	551	LLWRESAVTALWGKVNVDVGGK ALGRLLVVYPWTQRFESFGDLST PDAVMGNPKVKAHS\KKVLRGAFS GG\LAHL\DNLKGTF\AHTVSLHCD KL\HVGSWRTFRLLG\NVLVCCWA HSLLGKEFQPHQLQACLIKIGWLG VG
310	5807	A	320	221	376	DRVSIPRLESSGAILAHCNFR\SGFK QFSCLSLPSSCDYRCVLP RRALCSSC
311	5808	A	321	32	452	
312	5809	A	322	72	570	SRRAWVSFTEEDKATITSLWGKVN VEDAGGETLGRLLVVYPWTQRFDD SFGNLTCSAIMGHPKV\HVGKK VLTSLGDA\NEHLDDLKGTF\AQLSEL HCDKLHVDPENLKLGNVLETALAI /HFS\AKQFTPEVQASWQKMGD\GV ASALCFTKHLDFMCMMSQSFQR
313	5810	A	323	35	359	
314	5811	B	324	102	431	MIIYRDLISHDEMFSDIYKIREIADGL CLEVEGKMVSRTEGNIDDSLIGGNA SAEGPEGEGETESTVITGV\DIVMNH LQETSFTKEAYKKYIKDYMKSIKGG LEEQR\PD*
315	5812	A	325	132	708	RRRRLPSV\AIMIIYRDLISHDEMFSDI YKIREIADGL\CLEVEGKMVSRTEG NIDDSLIGG\N\SAEGPEGE\GTRST\ VITGV\DIVMNHHL\AGNKFSQKEAY KKYIK\DYIEIQFKGETLKEPEDQKR VKPFYDRGLQE\QFKHILG*FSKTYQ FFIG\ENMNP\DG\MVALLDYREGWV *PHI*FSFKDG\LEMEKC
316	5813	A	326	1	5796	
317	5814	A	327	3	467	
318	5815	A	328	73	1593	
319	5816	A	329	57	1358	RRKVAMDLIPNLAVETWLLAVSL VLLYLYGTRTHGLFKRLGIPGPTPLP LLGNVLSYRQGLWKFDTECYKKYG KMWGTSSLFGPHYPSSYEALGGSC VRLLLCVTP**TRT*GCCVSYN*GT YEGQLPVLAITDPDVIRTVLVKECY SVFTNRRICATTSTIKMQTHSVTMW LPPAVLQSQHGVCFL*QSLGPVGF MKS\AISLA\EEFWKJRSLSP\TFTS GKLKEKRHHKIH\YKMSLTAPCWRK PYPSGT*VCTFNYSIFGAYSMDVITG TSFGVNIDSLNNPQDPFVESTKKFL KFGFLDPLFLSILFPFLTPVFEALNV SLFPKDTINFLSKSVNRMKKSRLND KQKHRLDFLQLMIDSQNSKETESHK ALSDELEAAQSIIFIFAGYETTSSVLS FTLYELATHPDVQQKLQKEIDAVLP NKVRG
320	5817	A	330	870	1150	HRDLFLQLMIDSQNSKETESHKALS DLELAAQSIIFIFAGYETTSSVLSFTL YGTGPLHPDVQAGNCKREIDAVLP



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NK\APPTYGAVGTDGSYL
321	5818	A	331	144	377	RRCKGISTSCHCIITNEIFIFIFFEAE SHSVA\RLCSGAVLAHCKLCLPGL RHCPASATREAEAREWLETRSRRL Q
322	5819	A	332	3	323	DRVLSLSRPLECNGMISTHCNLHF PGSSDSPDTP/SQVAEITGVHHAQL IFVFLVETRFHHIGQAGLELLTSSDL PTSASPSAGIIGVRHCAWARITFQRT KCFSI
323	5820	A	333	187	450	NYVSQKRKKLNSPINYKEIEFIVLK LPK\KKPLGPNGFTEFYQTFKKGM \TPILDHLLQKIDVTLPLYFYKTDFT LTLKPKTIQKTRA
324	5821	C	334	122	292	MMCSMTLSFISFMRKLCRSIRASS WNSPWFRVSGCPSFTEYWWKVLM MVYMLRSS*
325	5822	A	335	295	931	VLSRKCQRSLTAFSSKCPNSWFSITQ TECKTMTCGMPQHVTQQ*RPIINTS HQYSVKLGHPRHPETRGRFKELVR\ KDLQNFLKKENKNEKVIEHIMÆDL DTNADKQLSFR/EEFIMLMGEA*PG AFPRRKIARGLTEGPG\HHHKPGPG GGAPPKDHSGPRFTVGHGHGHSTW WPRPQATNHGGQATLPLPNHRPRG LLCQTVLAVGLGAGAK
326	5823	A	336	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQALSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
327	5824	A	337	3	556	HSLFGTSEVINKLRSPDA\MGHFTEE DKATITSLWGKVNVE\DAGGETLGR LLVVYPWTQRFFDSFGNLSSASAIH GQPPKSRHMGKKVLTSLGDAIKHL\ DDLKGHLLPKPEVNCTCDKAALLD PEELSSFLGEMLLG/VPVFGQSHFRA KEFHPWRLQGFPGISRRWQKMVT\ GVASALVPSRYH
328	5825	A	338	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQALSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
329	5826	A	339	38	547	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSA\SAIMGNPKVKAHGK KVLTSRGRCHKSTWDDLKGTFQAQ A*SE\H\CDK\H\VDPGGTFKLLGK MLLG*PV\LAIPFSAKEFHP*RLQAS WQKQKMAEDGDLELASALVPSRY H
330	5827	A	340	168	330	SSLGLDLVCGDMAKCTKKVRIISKY GTRYGASLRKMVK\RIAITQHTKYI CSSRA

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331	5828	A	341	2	355	ARATMVLSPADMTNVKAAWGVKVAHAGEYGAEALERMFLLTTTKTYFSHFDSLHGSAQVKGHCMMKVVDALTNAGINVDNL/PNAL/DTLIDLLTPIFCRSLNLFYLLISNLSLFIHSVH
332	5829	A	342	176	410	AGLLPDP/TITARMNVGVHSEVNPNTVRVMNSRGIWLAYIILVGLLHMVLLSIPFFSIPGGWTLTNVIHNLATYVFLHT
333	5830	A	343	469	708	
334	5831	A	344	49	351	ATSPD\AMGHFTEEDKATITSLWGKVNVEDAGGETLGRLLDGYPWTQRGFDSFGNLNYTSDVMVDPKFMGHGMKVLTYLGDALCDLDDTNGNFAHVSTVMC
335	5832	A	345	665	921	AKKKEKKTGALSARRQPNPPTQNTPHPHPPNPTPHHPPPSPTTAPHSPPPFLILQKLLLIAVTIFDPTYCVISYSWVIMTFNKL
336	5833	A	346	2	341	HEEGFVNPGARFCLPEAAAVRRPPGEATVIMSDQEAKPSTEDLGDKNEGESIKLP/VLAHRTTETHFNVKTTTHLTSLPQSYCQIQA/VPLNSLTLLFARPTTAAHHTPELPMQ
337	5834	A	347	209	397	VSLWQEAMRLPKNTPEEKDRRTAALQEGRLRPVSVPLTLAENGAF\WSDMENLSDIYWYASE
338	5835	A	348	87	356	IHFYRVKIFFHILCFYIFIQICHYSFIFYFCRQG/HLSPREGSGAILAHCNLCLLGSNDPPTSASRVAGTAGTHHHAWLIFVFFIETGY
339	5836	A	349	3	204	KMEARKQRESMRGREAREKEKGYERSSEGERVV\ERNIGHKRRRDAKREARWEKIHGAKEARRNRYK
340	5837	A	350	3	341	HERHEIPIKMSHRGPWLMVDFLSYKLSQNGYSWSQFTDVEENTTEAPERTELD\RTTPAINGNRSWHLADSPAVNGTTGHSSSDARDVIPMAAVQH\ALWEASDEFELRHR
341	5838	A	351	67	341	EAPARRALCGRVPSEAQRDGHQAPLLSRRRRRL*AFFVADGIFKAELNEFLTRELAEDGYSGVEVRVTPTRTEIILATRTQNVLGEKGRRIRELTAVVQKRFGFPEGVELYAEKVATRGLCAIAQAESLRYKLLGGLAVRRCAGNQSEDHACLG\TNW
342	5839	A	352	3	495	
343	5840	A	353	1	459	EDGYSGVEVRVTPTRTEIILATRTQNVLGEKGRRIRELTAVVQKRFGFPEGVELYAEKVATRGLCAIAQAESLRYKLLGGLAVRRCAGNQSEDHACLG\TNW
344	5841	A	354	1	885	SWSTHASVSAERGGKMAVQISKKGEFVADGIFKAELNEFLTQPLAEDGYSGVEVRVTPTRTEIILATRTQNVLGEKGRRIRELTAVVQKRFGFPEGVELYAEKVATRGLCAIAQAESLRYKLLGGLAVRRCAGNQSEDHACLG\TNW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VLGEKGR\RIRELTAV\VQKRFGFP RRASVELYA\EKVGHYRSCVAIAQG RSLCVYKLLRKGFACAGGPC\YGV AAGSIMEKWGPKA FEVCWWSGKT SEEQRA*IP*SFVEWP*WIHSGDPV* LTNVDTA VR\HVLLRQG\VLG\IKVK IMLALGTQLGKIGPKPLPDHVASIV EPKDEIL\PTTPIS\EQKGKPV TALH GPTRSPQPNRVSLAAVFWSLDVAL
345	5842	A	355	1	284	SLFLYTANSRLGPLVSPAFMPHRISC NVTKGLPHDHYACLQEIKSSYKFYR YFETQQQSV PQCLSRTHQKSRLN NVYSAVRRLQVHMKALLNE*VSPA FMPHRISCNVTKGLPHDHYACLQEI KSSYKFYRYFETQQQSV PQCLSRTH QKSRLN NVYSAVRRLQVHMKAL LNE
346	5843	A	356	1	1404	
347	5844	A	357	1	771	
348	5845	A	358	3	913	
349	5846	C	359	461	667	MRMTMMMMMIHLKLILMMMM KSMEPLLEGAYDPADYEHLPASAEI KELFQYISRYTPQLIDL GTTN*
350	5847	A	360	76	158	
351	5848	A	361	1	2313	
352	5849	A	362	788	926	PSPELPEGDFEGFFPQKLQ*SCLPTL QKKKNNNNNNNNNNNNNNNEK
353	5850	A	363	168	447	TGTPGYACNSQN LGGPTGGISRSVP *NQPGQKGETPGFLKIPKLTRGGGR ALQFQVLGRVRPENPLNL CGQNFN* PKLCPCTSTWGKIRLPF
354	5851	A	364	637	1258	VLFLRKPTPAACLGHALSHRN LGPS AANSPSVLGKPAPSWSHVPATVLP GQQTGTPCDMRVSGTVRVGSTVMST TSIPALPHLGSTSVGPPQPGHEKQ MITWCKDRLQLTHSDEGFGVGFFQ TTMYILASKMCTGAQRSGCWALRV PQEDGKNQLIRFYCMYVCIYFETES HSVVQAGVQWRDLDSL*PPSPEFKR ISCLSFLSSW
355	5852	A	365	217	481	KCSFQM*YRLKNYN NNHSHPF SISL FLISSNIQNNFGSRYN*NHLKMYKT EAQRLTCSMLHKS NPHLFILNRMFL TRNLLGPHSLVP
356	5853	A	366	1	245	PVPRGGSKLLTHHLAPLTLPKAGDS GVNPRVPPFFLSPPAIWGP KPKILGL AKTPVPRFPLGKKFFPSP*FPPFFPK NKTL
357	5854	A	367	145	196	
358	5855	A	368	120	173	
359	5856	A	369	138	321	NECLLSFFSV/PNSSLLK*KS*ASA VAHTCNPSTLGG*GGWIT*GQEFET SLANMVKPCLY
360	5857	A	370	1536	1629	KSQKACNPSTLGG*GGWIT*AQEFT TSLANT
361	5858	A	371	11498	11651	LKNNFKKCTMWA\GMVADTCNPST LGGRGGWIT*GQGFKTSLANMMKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						CLY
362	5859	A	372	15	272	RLKAATLKMPGSAAGSEL SERIES FVETLKRCGVPRSED TARV TLLM MRWIFNDHRWIPP*ELVDPYIYFPW PCSTLSCWDWS
363	5860	A	373	433	612	QAPLQKPTVRR*K*VREIRGRD*VE E*IEEWYR*RSGRETRRGRESGR*ER GEVDREERKRE*GSRVRRGRERRG RERRGRERGGEESQEGKREKRKRE RRGREKRGREERKRAKEVFKDGER PRAKVGIVLKRQ
364	5861	A	374	785	1178	ALGCPGCPLLAVSGKDHSNSTQPAT HNSRRRRERRRKEERERRGRERGEE IEEGKR*RSGRETRRGRESGR*ERGE VDREERKRE*GSRVRRGRERRGRE RRGRERGGEERQEGKREKRKRERR GREKRG
365	5862	A	375	1969	2208	GANPIHDLPHDLTTSRPHIFIIFFE MESRSVTQAGVQWHDLGSLKSPT GLKLFSCSLSPSG*NYRCTPSHLANF CIF
366	5863	A	377	171	442	GKKWSFSLQNWVQAY*LSCNRY CSLKDHDFITPSDGGPDIFLHICDVE GEYVPVEGDEVYKMC SIPPKN EKL QAVEVGITHLPGTQH
367	5864	A	378	3	775	SVHSSAHASERVAEQNLQGGQAMS SVPSPPPQPPTHQA\GVGLDTPRSR ERSPSPLRGVVPSPLPTRR\TRTFSA TVR\ASQGPVYKGVCKCFCRSKGH GFITPQLMAAPDIFLHISDVEGEYVP \VEGDEVYKMC SIPPKN EKLQA VEV\ITHLAP\GTKHETWSGHVISF LGDGGSTPCPVLVGRLCGEEAADT GDDILPHETGLQRGNPSHVSPGGK GYGGAGVGCGVFAISTAYGPLQQ PLHHLKSIKSI
368	5865	A	379	7	316	APSPDAMGHFTEEDKATITSLRGKE NVEDAGG*TLGRLLDDYPWTHRIL DS*GKLLSDYAIMGKQDDKEHA EK ELPSLEDALAHWADASASGHWP SD VPCAYR
369	5866	A	380	61	304	ARTWNSVRMASSGMTRRDPLANK VALVTASTDGIGFAIARRLAQDGAH VVVSSRKSQNVQV*VST*LASV*L IYLMCVLP
370	5867	A	381	2	281	
371	5868	A	382	2	558	HSLLERLRSLISFLVQTPIGHSTEED\ KATITSLWGKGEMWKNAGRKKPL GRPPGLSLPQWTPRG SFEQALG\NL VSSCPPAPSMGKPPQKSKGTMAKK GA*PSLGKMPIKAPLDD\LKGT FAP A*SELH\CDKLH/VLDPENFKLLG\N VLVT\VLAIHFGKEFTPEVQASWQK MVTAVASALSSRYH
372	5869	A	383	3	368	EFFCGLCVKSEISLHLFLANFFPSL KPQITSSGEMVPLLPCQS*EWRKRD ESSTLPPPPSSGAECCTWLRPSPSTS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PCPCLPHPYVQGSLCETQSHLTVNP ASSYRISPPPLISSRTRY
373	5870	A	384	179	455	EFGWGGGKSLGLPRAGLD*IGGSLG FIPLLSTPVSHSHAFSVGAILIFLL ESLAFQWLLLLSSSHFLYFSLLFFRQ SSFCFLTEEQKKKK
374	5871	C	385	22	423	MKAAVLTALXFLTGSQLRHFWQ QDEPPQSPWDRVKLHELQEKLSPLG XEMRDXRAPMWTXXNASGPLQRR VRXLWPRALRLSRRTAAQTWPSTT XRPPSILSTFSEKQGARVRGTSKA CXPLLESXKGXVS*
375	5872	A	386	1	671	SGRIQEVPHGPFMRMKA AVLTLA\VL FLTGSQLRHFWQDEPPQSPWDRV KDLATVYVDGLTEDSGKDSVTSTFS KLRE*LGPVTQ\EFWDNL\EKETGL RQ\MSKDL\EEVKAKVQPYL\DDF QKKWQEEMELYRQKVEPLRAELQE GARQKLHELQEKLSPLGEEMRDRA RAHVDALRTHLAPYSDELRLRLAA RLEALKENG GARLA EYHAKATEHL STLSEK
376	5873	A	388	24	499	HTDTYPHPHLIARPQGFPELKNDTF LRAAWGEETDYTPVWCMRQAGRY LPEFRETRAAQDFSTCRSPEACCEL TLQVRGPQKRERFMPSVCHLATCL LFPTPLRRFPLDAAIIFSDILVVPQA LGMEVTMVPKGGPSFPESLREEQDL KRLDPEMV
377	5874	A	389	109	750	HTDTYPHPHLIARPQGFPELKNDTF LRAAWGEETDYTPVWCMRQAGRY LPEFRETRAAQDFSTCRSPEACCEL TLQPLRRFPLDAAIIFSDILVVPQAL GMEVTMVPKGGPSFPESLREEQDLE RLRDPEVVASELGYVFQAITLTRQR\ LAGRVPLIG\FAGAPW\TLMTYMGFI LTWTQNMWAPLWMLCINTHVCFD RTECIPLPSSTNTDD
378	5875	A	390	1	295	PQTQREPAMVLSPADKTNVKA AW GKVG AHAGEYGAEALERMILFFTT TRTYFPRLDLSLLSDPV*FPVITEAF ARTYSGVIADLLSNTEPHMIQMAAS
379	5876	A	391	112	310	
380	5877	A	392	49	615	RAQRGCSQSCGKM NARGLGSELKD \SFPVTELSASGPLES\HDLLRKGF\S CVKNELLPSH\LELS\EKNFQLQPR LK*NFSTLEETFQGSILLPLKITGGDF QGQCRQV\QRLPFSFQAPNLSTGMV FEGGNDETIWDLEDIL**SHHKSEV HGESH TFDGWEYKPWVYCNS SAGS WKPRAAILFIVIFVL
381	5878	A	393	167	1955	LCPHVVEGMWEVPVISLMRALIPF MRASPSRVRRATPAAVTCQLSNW SEWTD CFP CQDKK/YTVM TLSAIQT IQGNILIS ETLIMSAMAGFPNKYRHR SLLQPNKFGGTICSGDIWDQASCSSS TTCVRQAQCGQDFQCKETGRCLKR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HLVCNGDQDCLDGSDEDDCEDVR AIDEDCSQYEPPIGSQKAALGYNILT QEDAQSVYDASYGGQCETVYNG EWRELRYDSTCERLYYGDDEKYFR KPYNFLKYHFEALADTGISSEFYDN ANDLLSKVKKDKSDSFGVTIGGPA GSPLLKFIFTRFTKVQTAHFMRK DDIMLDEGMLQSLMELPDQYNYG MYAKFINDYGTHYITSGSMGGIY ILVIDKAKMESLGITSRDITTCFGGS LGIQYEDKINVGGGLSGDHCKKFG RARKAMAVEDIISRVRGGSSGWSG GLAQRNSTITYRSWGRSLKYNPVVI DFEMQPIHEVLRLHTSLGPLEAKRQ LRRALDQYLMEFNACRCGPCFNNG VPLEGTSCRCQCRLGSLGAACEQT QTE/G*GAKADGSWSCWSSWSVCR AGIQERRRECDNPAPQNGGASCPGR KVQTQAC
382	5879	A	394	94	276	
383	5880	A	395	25	1876	ILQGPACTHLLLQFPEYIALFLQGN VRGLLAEMFAVFFILSLMT*QPGV TAQEKGNQRRPATPAAVTCQLS NWSEWTDCCFCHDKKYRHRNLLQ NKFGGTICSGDIWDQASCSSTTCV RQAQCGQDFQCKETGRCLKRHLVC NGDQDCLDGSDEDDCEDVRAIDED CSQYEPPIGSQKAALGYNILTQEDA QSVYDASYGGQCETVYNGEWRE LRYDSTCERLYYGDDEKYFRKPYN FLKYHFEALADTGISSEFYDNANDL LSKVKKDKSDSFGVTIGGPA VGVGVSHSQDTSFLNELNKYNEKK FIFTRFTKVQTAHFMRKDDIMLD EGMLQSLMELPDQYNYGMYAKFIN DYGTHYITSGSMGGIYILVIDKA KMESLGITSRDITTCFGSLGIQYED KINVGGGLSGDHCKKFGGKTERA RKAMAVEDIISRVRGGSSGWSGGL AQNRSTITYRSWGRSLKYNPVVIDF EMQPIHEVLRLHTSLGPLEAKRQNL RALDQYLMEFNACRCGPCFNNGVP ILEGTSCRCQCRLGSLGAACEQTQT EGAKADGSWSCWSSWSVCRAGIQE RRRECDNPAPQNGGASCPGRKVQT QAC
384	5881	A	396	2	307	QAGV**WDLGSLQPLPRLKQFS/CI LNPGNLSKEF*STKETKQIFVGHQ SQTSKFAISLIQHPINMRSGTKTFM MV*GNKQRSKFPIWTFKIFPDMLPS
385	5882	A	397	374	665	GAQGLSLSPRLECNGAILAHCNLCL PGSSNSPGSAS*VAGTIGMHHLHARL MFVFLVESGFHHVQGAGLELLTSSD PPASASQSAGIRGISRRAGLDF
386	5883	A	398	202	425	RLGGVEEGWGKGRSLVLHLKCGV QILLMTLTGKTISL*LDPSDTIVNVK ALIHDIERIPPDHEMLIFACKQLE
387	5884	A	399	202	418	RLGGVEEGWGKGRSLRLNLRGGL

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						HIYMITILDNLISLEDMPNPTI*NVK AMILSNNGIHSHE*RLIFEGMR
388	5885	A	400	144	433	
389	5886	A	401	1	3135	
390	5887	A	402	79	929	PVAQGMLRWTVHLEGGPRRVNHA AVAVGHRVVSFGGYCSGEDYETLR QIDVHIFNAVSLRWTKLPPVAPGEV CHPWASS\VPYMRYGHSSV\PSDD TVLLWGGGRNDTE\GPCNVLYAFDV NTHKWFTPRVSGTVPSARDGHSAC VLRKIMYILGGYEQQADWFSNDIH KL
391	5888	A	403	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
392	5889	A	404	50	562	APSPDAMG\HFTTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRFF FDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDA\EHDDLKGTFAQLSE LHCDKLHVDPENLKLGNVLETAL AIHFGAKILPFKGRLPGRRWQKMV TGVASALCFTKHLDFMCMMSQSFQR
393	5890	A	405	228	420	TPEADALYSHNPGGNLDRHTASKPS ALLQPGPAWQRGSACSLQILPESRV GFPTGPP*ARKVSI
394	5891	A	406	653	940	KWKKINVFFETGSRSAQAARVQWC HLGSLQP*HPRLKEPPASASQTAGT TGMHHHAWLS*VSFVKMRLGHIIQ DIRRLMDSINMPHYMHQAPPMCO
395	5892	A	407	795	1802	CRLHTQQIQRLETASGFLRMKGKNS VQLQEGWERFQDPGNHITRPRFLP SDPHPTLMCLQGPPGKPGKSRAT GTCAAEGA\DETSYF*NAFQLPLYK LIKIRKKEK*K*KSCT*KRVRWSKL CPRDWAAARTEAPPTGLESRQPV QDPPPLPTAACIPP/CWLGSF*KRM ND*QTKITPWG*FPHHPRL/PPSSSPS NSSSSPSSPSKLSSSMASPVKYST ARGTIRSRKKCPISKSEANVNSESSS SDSPSPDATDLPFNGLKLLKKDSL TCFVIVLTVPRPLCFCFFLMVLT VTF FPPFQSIVHPSQSTISGPSKEKGSALS GSDFIL
396	5893	A	408	342	515	
397	5894	A	409	3	333	AAWLLGAAATGLTRGPA/PRPSPPR ALTPA*GPLAAFTAARSDAGIRAMC SEIILRQEVLDGDFHRDLLIKVKFGE SIEDLHTCRLLIKQDIPAGLYVDPYE LASLRERNITEEKTSWRLWLPSDN
398	5895	A	410	877	1206	QGGQSSLGTAGPEPDSPGDPGSAAE QSAREGRRAHGSNV*PPPARSTDG PAPGPHIPATREAREPGPLPRSGPP SPAPLTGVRARGGEGRGPPAREPG RRPEEQPGR

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399	5896	A	411	238	326	LHSGPGVVVT*YRKMTSLWAGCSR HACNPSTLGSRGIQITRGQEF
400	5897	C	412	194	474	MWKMHMCMERHGSTVLAITYLRQQ MPQHFFSHSSQYIHILANENYLGSLP FLLKHKFFIKCCIPASSNAHADFRR ARRKETAAPQPCRRPAAR*
401	5898	A	413	1	88	
402	5899	A	414	65	191	
403	5900	A	415	131	363	EVKMAGFLDNFRWPECECIDWSE RNVVASVVAGILVSEKDWLVTCIPY LLPWKLMPVPLN*EWLSRTIYFTAV LYR
404	5901	A	416	146	567	EVKMAGFLDNFRWPECECIDWSE RNAVASVVAGILFFTGWIMIDAA VVYPKPEQLNHAFHTCGVFSTLAF FMINAVSKLLQVRGDSYGKAAVL GRTGARVWAFHWGFMLMFGSLIA SMWILFGAYVTPKYLFI
405	5902	A	417	17	369	KLTFGLGLGVPPKPIPFKNRPIGPG PWVPPVIPAPLEAQVGGSPSPEIGAP PGYKGEPPFFLKPKQKTRQCGQPPL SQVPWSFRPKKGLNPGSRAFH*LRS RPCSTWATKPNFVS
406	5903	A	418	553	673	RRIEKGQVQWLTPTVISVLWEAAAG D*LEASSRLYATPPD
407	5904	A	419	2	427	HVIKVLHDDWIFTPIQGP*SM/CSS KNESRHIGS*RVTG*LLEVLKSLL*S FGRLNALNMKSL/TSEVQEE*RKLN KTHRVQRDFDKDRKLA VGQSESPG HPTSEKPPSTSSSAGCMLCSLHISRG FQLRRKRQLNGKCCPIQ
408	5905	A	420	82	371	RRHSVACTPHPSSQVLKSLL*SFGRL NALNMKSLKAKFRKSDVN*IKLIEC KEPSTEN*LLARVKVLVIRLPRNLL QPHRLLA VCYAAYISPLAFS
409	5906	A	421	103	430	SFGRLNALNMKSLKAKFRKSDTNE WNKNDDRLLQAVENGDAEKVASL LGKKGASATKHDSEGKTAFHLAAA KGHVECLRV MITHGVDVTAQDTTG VHSAHLAAKNSHHE
410	5907	A	422	87	283	SFGRLNALNMKSLKAKFMKSDTNE WNKNDDRLLQAV*NGDAEKVASL LGKKGASATKHDSEGKTA
411	5908	A	423	2	424	
412	5909	B	424	108	395	VGAHAGEYGAEALERMFLSFPTTR TYFPFDLSHGFCPLRGHGKEGGR RADQRRGQRGTTCPTLSALS DLHA HKLSGGTRFNFQAPKATGLLG*
413	5910	A	425	2	334	
414	5911	A	426	236	649	
415	5912	A	427	76	322	TNSPCYVVFNGNSFFS*IIENKKQENK VQAGIRLYGALLTKCPRLYSKQIH PALLRRLQHGVDLVYFEDILDKLIG HGPGSV
416	5913	A	428	988	1223	RGERADHLRSGIRDQPGQHGETPSL LITQKLAGLGSACL*SQLGRLRQE NCLNAGVGGCSEP*SRHCTPAWAT



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						ERDS
417	5914	A	429	57	349	ERESPFAPRLEGKGANLG*WKAPLP GLSPFSGLSLPRGTGNYGPPQPPVNF F*F*GETGFPRLTREGLNLRPSENPA LVKPQNKVAPKHGVEKPGGK
418	5915	A	430	291	594	SWLFRLGAMAHAYNNSSLGGQSGR IVWAQEFNTQPGQHRGDPGLYK*FF FLISQCDGMHLWSQLLRRLRQKDH LNPRAGGCSEL*LHCCAPAWVTEQ DLSQ
419	5916	A	431	27	361	RGPTVTPQIMAVEDVASTGADPCD LDSGDLLEILTSPLILLGLCIFLL YLIVR*DQPAANGDSDDD*PSPLPR LKRRDFTPDDLRRFYSVDPRILMD FNCKVFDVTK
420	5917	A	432	196	555	SPSMNPRKKVDLKLIVGAIGVGKT SLLHQYVHKTFYEEYQTTLGASILS KN*SYWVDTTCLKVTDLGDGGER FRSMVSTFYKSGDCILTFDVTDL SFEALEFWPGGGLAQNGPNEA
421	5918	A	433	1	685	EIKYHSLPRLECRGEISAH*NLCLPG SSDSPATAS*VAGITGMRHYAQLIFL FLVET*FHHVGQGSRTDPSNDPPA SASQAGDYRRD
422	5919	A	434	56	335	KCSPKILLTSESTSSNPCLIDTNASDF HFLSQVLE*VVSPKGSKEALCCILR HLGYETRESCPWCPSPQFRYITFDMG SYVGPVLHHSCQALS
423	5920	C	435	24	332	MKGRTFISLLFLFSSAYSRGVFRRD AHKSEVAHRFNDLGEENFRALVLIA FAQYLQQRPFEDHVTYYAQLQLFV KPMVKWLTAVQKNLREMNASCN TXMTTH*
424	5921	A	436	130	599	
425	5922	A	437	1	404	
426	5923	A	438	3	647	FSLLSTPHAFGTMKWVTFISLLFLFS SAYSRGVFRRDAHKSEVAHRFKDL GEENFKALVLIAFAQYLQQCPFEDH VKLVNEVTEFAKTCVADESAENC KSLHTLFGDKLCTVATLRETYGEM ADCFLQHKDDNPNLRLVRPEVDV MCTAFHDNEETFLKKYLEIARRHP YFYAPELLFFAKRYKAAFECCQA ADKAAACLLPKLDELREDEG
427	5924	A	439	323	899	MMRVFLSEKALSSSYLEMYLSTPH AFGTMKWVTFISLLFLFSSAYSRGV FRDAHKSEVAHRFKDLGEENFKA LVLIAFAQYLQQCPFEDHVKLVE AKQEPERNECFQHKDDNPNLRL VRPEVDVMCTAFHDNEETFLKKYL YEIARRHPYFYAPELLFFAKRYKAA FTECCQAADKAAACLLPKLDELRE
428	5925	A	440	1	1206	SFLLSTPHAFGTMKWVTFISLLFLF SSAYSRGVFRRDAHKSEVAHRFKD LGEENFKALVLIAFAQYLQQCPFED HVKLVEVTEFAKTCVADESAENC DKSLHTLFGDKLCTVATLRETYGE

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						MADCCAKQEPGRNECFLOHKDDNP NLPRLVRPEVDVMCTAFHDNEETF LKKYLYEIARRHPYFYAPELLFFAK RYKAAFTECCQAADKAACLLPKLD ELRDEGKASSAKQRLKASLQK/PR NLGKVGSKCKHPEAKRMPCAEDY LSVVLNQLCVLHEKTPVSDRVTKC CTESLVNRRPCFSALEVDETYVPKE FNAETFTFHADICTLSEKERQIKQT ALVELVKHKPKATKEQLKAVMDD FAAFVEKCKADDKETCFAEEGKK LVAASQAALGL
429	5926	A	441	28	1587	
430	5927	A	442	1	1652	GTMKWVTFISLLFLFSSAYSRGVFR RDAHKSEVAHRFKDLGEENFKALV LIAFAQYLQQCPLEDHVKLNVKDD NPNLRLVRPEVDVMCTAFHDNEE TFLKKYLYEIARRHPYFYAPELLFF AKRYKAAFTECCQAADKAACLLPK LDELDEGKASSAKQRLKASLQK FGERAFKAWAVARLSQRFPAEFA EVSKLVTDLTKVHTECCHGDLLEC ADDRADLAKYICENQDSISSKLEK CEKPLLEKSHCIAEVENDEMPADLP SLAADFVESKDVCKNYAEAKDVFL GMFLYEYARRHPDYSVLLRLAK TYETTLEKCCAAADPHECYAKVFD EFKPLVEEPQNLKQNCLEFEQLGE YKFQNALLVRYTKKVPQVSTPTLV EVSRLGKVGSKCKHPEAKRMPC AEDYLSVVLNQLCVLHEKTPVSDR VTKCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQI KKQTALVELVKHKPKATKEQLKAV MDDFAAFVEKCKADDKETCFAEE GKKLVAASQAALGL
431	5928	A	443	1	1515	MKWVTFISLLFLFSSAYSRGVFRD AHKSEVAHRFKDLGEENFKALV LIAFAQYLQQCPFEDHVKLNEVTEFA KTCVADESAENCDKSLHTLFGDKL CTVATLRETYGEMADCCAKQEPER NECFLOHKDDNPRLVRPEVDV MC/H/YPNAAQNPW*TGDAFQLW KSMKHTEPKSLMLKHSPSMQIYAH FLRRRDKSRNKLHLLSL*NTSPRQQ KSN*KLLWMISQLL*RSAARLTIRRP ALPRRVKNLLQVKLP*AYSRGVFR RDAHKSEVAHRFKDLGEENFKALV LIAFAQYLQQCPFEDHVKLNEVTE FAKTCVADESAENCDKSLHTLFGD KLCTVATLRETYGEMADCCAKQEP ERNECFLOHKDDNPRLVRPEV DVMCTTKCTESLVNRRPCFSALEV DETYVPKEFNAETFTFHADICTLSE KERQIKQTALVELVKHKPKATKE QLKAVMDDFAAFVEKCKADDKE TCFAEEGKKLVAASQAALGLTCEA CQEPGGLVVPPTDAPVSPTTLYVED

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						ISEPPLHDFYCSRLDLVFLLDGSSR LSEAEFEVLKAFVVDMMERLRISQK WVRVAVVEYHDGSHAYIGLKDRK RPELRRIASQVKYAGSQVASTSEV LKYTLFQIFSKIDRPEASRIALLMA SQEPQRMSRNFVRYVQGLKKKKVI VIPVGIGPHANLKQIRLIEKQAPENK AFVLSSVDELEQQRDEIVSYLCDLA PEAPPPTLPPDMAQV
432	5929	A	444	2	1848	RFSLLSTPHAFGTMKWVTFISLLFLF SSAYSRGVFRDAHKSEVAHRFKD LGEENFKALVLIAFAQYLQCCPFED HVKL VNEVTEFAKTCVADESAENC DKSLHTLFGDKLCTVATLRETYGE MADCCAKQEPERNECFLOHKDDNP NLPRLVRPEVDMCTAFHDNEETF LKKYLYEIARRHPYFYAPELFFAK RYKAAFTCCQAADKAACLLPKL DELRE*LNLOKHVLLMSQLKIVTNH FIPFLETNYAQLQLFVKPMVKWLTA VQNKNLREMNASCNTKMTTQTSPD W*DQRLM*CALLFMTMKRHF*KNT YMKLPEDILTFMPRNSFSLKGIKLL LQNVAKLLIKLPACCPKLDEL RDEG KASSAKQRLKASLQKFGERAFAK WAVARLSQRFPAEFAEVSKLVTD LTKVHTECCHGDLLECADDRADLA KYICENQDSISSKLKECCEKPLEKS HCIAEVENDEMPADLPSLAADFVES KDVCKNYAEAKDVFLGMFLYEYA RRHPDYSVLLLLRLAKTYETTLEKC CAAADPHECYAKVFDEFKPLVEEP QNLIKQNCLEFQGEYKFQNALLV RYTKKVPQVSTPTLVEVSRNLGKLP SC**SC\CLLPKLDEL RDEGKASSAK QRLKASLQKFGERAFAKAWAVARL SQRFPAEFAEVSKLVTDLTKVHTE CCHGDLLECADDRADLAKYICENQ DSISSKLKECCEKPLEKSHCIAEVE NDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VLLLLRLAKTYETTLEKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQ NCELFEQGEYKFQNALLVRYTKKV PQVSTPTLVEVSRNLGKLPS
433	5930	A	445	1	3780	MKWVTFISLLFLFSSAYSRGVFRRD AHKSEVAHRFKDLGEENFKALVLIA FAQYLQCCPFEDHVKL VNEVTEFA KTCVADESAENC DKSLHTLFGDKL CTVATLRETYGEMADCCAKQEPER NECFLOH/KCFLQHKDDNP NLPRLV RPEVDMCTAFHDNEETFLKKYLY EIARRHPYFYAPELFFAKRYKAAF TECCQAADKAACLLPKLDEL RDE\ GKASSAKQRLKASLQKFGERAFAK AWAVARLSQRFPAEFAEVSKLVTD LTKVHTECCHGDLLECADDRADL AKYICENQDSISSKLKECCEKPLEK

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						SHCIAEVENDEMPADLPSLAADFVE SKDVCKNYAEAKDVFLGMFLY ARRHPDYSVLLRLAKTYETTLEK CCAAADPHECYAKVFDEFKPLVEE PQNLIKQNCLEFEQLGEYKFQNALL VRYTKKVPQVSTPTLVEVSRNLGK VGSCKCKHPEAKRMPCAEDYLSVV LNQLCVLHEKTPVSDRVTKCCTESL VNRPCFSALEVDETYVPKEFNAET FTFHADICTLSEKERQIKKQTALVEL VKHKPKATKEQLKAVMDDFAAFV EKCKKADDKETCFAEEGKKLVAAS QAALGLTPLGPASSLPQSFLKCLE QVRKIQGDGAALQEKLCAATYKLCH PEELVLLGHSGLGPWAPLSSCPSQAL QLAGCLSQLHSGFLYQGLLQALE GISPELGPTLDTLQLDVADFATTIW QQMEELGMAPALQPTQGAMPAPAS AFQRRAGGVLVASHLQSFLEVS YRVLRLHAQP
434	5931	A	446	2	2255	STPHAFGTMKWVTFISLLFLFSSAYS RGVFRDAHKSEVAHRFKDLGEEN FKALVLIQFAQYLQCCPFEDHVKL NEVTEFAKTCVADESAENCCKSLH TLFGDKLCTVATLRETYGEMADCC AKQEPERNECGTMKWVTFISLLFLF SSAYSRGVFRDAHKSEVAHRFKD LGEENFKALVLIQFAQYLQCCPFED HVKLNEVTEFAKTCVADESAENC DKSLHTLFGDKLCTVATLRETYGE MADCCAKQEPERNES/CFCNHKKD NPNLPRLWRPEVDVMC/TAFHDNE ETFLKKYLYENCPEHPLPFMAPG NSFSFAKRYKAATFECQAADKA ACL/LCPKLDLGRG*KGRLRSKQR LKCASLQKFGERAFKAWAVARLSQ RFPKAEFAEVSKLVTDLTKVHTECC HGDLLCADDRADLAKYICENQDSI SSKLKECCEKPLLEKSHCIAEVEND EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCLE FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCKHPE AKRMPCAEDYLSVVLNQLCVLHEK TPVSDRVTKCCTESLVNRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKKADD KETCFAEEGKKLVAASQAALGL
435	5932	A	447	1	477	FYNRVLLLLPRLEC*GVIFPHRNHL PGSSDSHALAFRVTGITGTCHHACLI FVLLVETRFLHVGQAGLELLTSSDP PSSASQSSGITGVGHCAIPTAHFLP HKVLRSLTKLPSGMSPETIHPRRHA EKSCLFSFSLYLFHLTSSCSFIHPFSL TFKC

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436	5933	C	448	141	390	MAKFSLCPPVKERGEKAHWEXXX XXNKATNSICEVSTFMXXXXXXXXXX XXXXXXXXXXLNIHYESDWVISKLIP GCIKMTEAITC*
437	5934	A	450	345	462	NQRSTARGKELLQDTRALKKNS*R VIKYSKQQAQTCEG
438	5935	A	451	1538	1709	SKCKLKQDPESHAGTSLQSOLLRRLR QENPLRPGFQGCSEL*SYHCTPARV TEQDPIS
439	5936	A	452	243	353	YSYHIRVHVHTHPLHACP*LHTVR YT*NSTHTHTYF
440	5937	A	453	2	366	SLPASDRPPISSPLATSGTIFSAISCF WDLPAFPLWLAPSCQPTMSSQIRQN YSTDVEAAVNSLVNLYLQASYTYL SLQDIKKPAEDEWGKTPDAMKAA MALEKKLNQALLDLHALGSART
441	5938	A	454	2	797	LIGKFAPRGPRIRQRRGGPARVWSL CFKQVFGTEQDPGILFPASGPPSDFL LRLQTSGTIFSAISCFLPAQHRFLW LAPSCQPTMSSQIRQNYSTDVEAA VNSLVNLYLQASYTYLSLGFYFDR\ DDVALEGVSHFFRELAEE\KRKGYE RLK\MQNQ\RGGRALFQDIKKPA EDE\WGKTPD\AMKAAMALEKKLN QAL/LWDLHALG\SARTDPLHCDFL ETHFLDEEVKLIKMGDHLTNLHR LGGPEAGLGEYLFERLTLKHD
442	5939	A	455	2	331	FFVFCFGKRGSLAVFRVEGKGMNPG *RNLWLPGLKNFSGTLWRGGNNK PGPPLQPKFGFLKKKGFSPPGGGGF KIPNLEIGPNKGPKGWE*RA*PPNPS PSNFFNKPWVG
443	5940	A	456	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQALSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMTGTVASALSSRYH
444	5941	A	457	38	533	APSPDA\MGHFTEEDKATITSLWGK VNVE\ DAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHG KKVLT\SLGDAIK\HLDLKGTFQAQ A*SEPAPVTKL\HVD\PENFKAPGEM LLVTR/VLAIPFSAKEFHP*RLQASW AE/MMGDLQLASALVPSRYH
445	5942	A	460	3	198	GIPGSSFCGLCGDVPKGPV*RADGS C*DGVA PRLLRPRGFRGGRCGPVLD SLAQQRGAESGCRG
446	5943	A	461	649	1185	ETCLAFMYQRTCSADSKRYIWQLF LEKGPMGYHPLHF*VFLGFFFFFET VLAVLPQAGSVGGHNHSSIASNHP RA*ANPPHLVAGDYKLTAQPGKLF/ VFLLETGFSYVCPGWVSGSLGSNGP PAPAFQRHRAKFVSFVPCHHAAQK GSIPFNELTFINWVMLGGASSLSWEI VNSS
447	5944	A	462	1	298	NKEILARPNGSSPEFPPLWGLRQVD

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						PPESGVQSPASPHGKTLFLLKKPTLT GQGGPNPVFPVLRVVKPQGPNPG GGGFH*PKSCPCPPEWGAKLDPVF
448	5945	A	463	179	351	RHVGIKHGDHEATEKFIDEFAK VIA DKHLTLEQVYNANETSLF*HYYP KTPITAAE
449	5946	A	464	1	327	PGVPMQRAEFEPYKRSRCDSPRT PSNTPSAEADWAPGLELHPDYKTW GPEHGCSFLRRGGFDKPVLLKNIRE NEITGALLACPDESSFENLGVSVLR* T*KLLNYYS
450	5947	A	465	261	452	GDLRVTGAPSVLSLSP*LGLP*VSRP* VPSPLASGTSKPLARFPEEAVGFSRP GLCLLISFPL
451	5948	A	466	362	991	PSRHLSWLWGSTGCRNAHVQLAG GAGARAGEERPCFPRPELAGTVSPG DKSLRQFGEKGGGGHERMQGPHHS SKESGGQSHGEDPSLEASPPKPESPA SQVPMKSPVIPGETAHGLP*VSRP* VPSPLASGTSKPLARFPEEAVGFSRP GLWSAMQAGVCDQGICAIRNSPQT TQGGRRP*ERRCRYMHVTEKAAF TPSAPRECLPH
452	5949	A	467	24	436	RFIVLVHYISAPGELCRGWGSPKME GWGKRTSCQSLPKAGRSPGSLRSTD EYCGHRLPDNV*ATGGGQGPAPG MGVRNPSPAPRTSPGWRVPSNTAP QLLGCFGGQTGRVPFIQDPSSSSG MRNSPPGRGCLESA
453	5950	A	468	2	424	
454	5951	A	469	3	452	
455	5952	A	470	2	467	PDSSGPHRLRENPPWCLSPADKTNV KAAWGKVGAVHGEYGAELERMF LSFPTTKTYFPHFDLSHGSAQV\KGH G\KKVADALTNAVAHVDDMPNALS ALSDLHAHKLRVDPVNFKLL\SHCL LVTLAAHLPAEFTPCGGTASLDFK LGFLKQRC
456	5953	A	471	61	346	VRARVPSPAAAMGCTLSAEDKAAV ERNKKIDRNLREDREKAAKEVKLL VLGAGESGKSAIGKPMIIEEGYIQ DEWKPFKGIVYSNTLQAIIGT*KAA VERNKKIDRNLREDREKAAKEVKL LVLGAGESGKSAIGKPMIIEEGYI QDEWKPFKGIVYSNTLQAIIGT
457	5954	A	472	828	1066	QAQWLTPCNAQHFAFRRANHLRL GV*HQTGOHGKTPSLLEKYYKKKK KVASRSHMSVIPTMWKAEAEELLE PGRQRSQ
458	5955	A	473	180	350	EPMAKGKTESPGPKRCGP*I*WVIS QRGTLRFRGAGLFFMGEFLRLGENL LEIPRGA
459	5956	A	474	1689	1856	GRCHITCVKSHGAADFDTTFILFY FILFYFILFIF*TESCSVTQAGVQRGN LGSL
460	5957	A	475	115	324	SNFQLSRKLYF*FFQGKSKHNEYFII FE*T*ILHFLNLGIVIYNYGTSFRKNR

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						MKRKWWNDKMGQQQKHG
461	5958	A	476	310	633	RFSLGEQECEVCYRLRPTPGWTPGE TAGVAGREPLVCSPPPPPPASPCAPP KVRSDMGPCPCAS*WPSGLTKGP SCFPVASHGGITPGQWPGEETS KERSSATK
462	5959	A	477	2	293	PAAERSCLRVTFASACPASMEPKRI REGYLVKKGSVFNTWKPMWVVLIE DGIELYKKNCNSP*GMIPLRGITLT RPWLDGFRRCWF TKSSIIQYL
463	5960	A	478	387	511	WDIPFISDIYIILITGYLTTY*NVLH WKKIIFYIALIVL
464	5961	A	479	130	240	KNEQDPRDL*DNDKWPNIHVIGVPE EDKDNTERVFD
465	5962	A	480	116	423	GIRCPGPREASLLSQFILSMRQAGQ DWQPEAYTLRICQLEVFSTCVSSLL HPVCRSQ*LPMEPEVIPGWNGKPRG HWPVQIFKSFTHTGTPNLAGPGCCCC VR
466	5963	A	481	64	343	QLL**LSSTWEG LQA AKELDEQRGI GC
467	5964	A	482	61	342	QPQTD TMGHLTPEEKSAVTDLWGK VNADEADGEALVTLLGVYPWTQR MFESFGDLDTPEADMGNPKVKAHG WKVL*AFIDGPAHPDQLKGNLCT
468	5965	A	483	557	816	SRHFERPWVDHLRLGV*DQPGQHG ETPSLQKIQKLARSGGTHL*SSYLG G*SGKNHLNPGSQGCSEP*SCHCTP GWVTEQNSVSKK
469	5966	A	485	277	322	FFF*VYHVWFLFSFLICRFMPFAKFG NF*PLFLEIFFHPYSFSSL*YEW*SFC YCLRGLLCFHVYPLFLVYFSLFFILV NFC*LFFSSLILFFCHMQSTVELVQ
470	5967	A	486	31	309	FLELGP GKPFGNMYDADDDMQYD EDDDEITPDLQETCWIVIRSYFDKK G*VIQQLDSFD*SIHMTALRIGEYAA PIDLQADAHHASGEKEP
471	5968	A	487	130	521	KAKFRFCFTSSFYN*DLDFKIYPSPI KVAEPS*LSGQCFSSLFFHQDLGFCF VLLFETESCSVTQVEHSGAISAHCN LRLPG*SNPVSVSLAAGTTGTHHY TQLIFVLVAEMGFCHVGQSGLELAS CR
472	5969	A	488	32	452	
473	5970	A	489	38	525	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTS LGDAIKHLDDLKGTF AQLAS ELH\CDKLHVDPENFKLLG\NVLVT VLAHFGQRIHP*RCRASWAEDG*L GVASALVLQDTTELTC
474	5971	A	490	818	947	VCFLFLFF*DGVSLMLPRLECNGTIS AHRNLCPGSSDSPVSA
475	5972	A	491	17	416	PPSSNPMGHFT*EDTATITSLWGT NAENAGGKTLRLLGAYPWTQRLF DSFGNLSSASAIMGNPQKAHGLK VLTLL*DAVKHLDDL MGTF SHPTL

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						PCYKLHLDSENKLLGYVLAIVMAI HFGKEVIPAV
476	5973	A	492	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSA SAIMGNPVKVAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
477	5974	A	493	34	548	APSPDAMGHFTEEDKATITSLWGK\ VNVE\ DAGGETLGRLLVVYPWTQR FFDSFGNLSASA\ MGNPKVKAHG KKVLTSLGDAIKHLDDLKGTFAQL\ SELH\CDK\ LHVDPENFKLLG/NMLL VTRFGQSHFRAKNFTPEGCRASWQ KQKMAEDGDLQWPVPCSSRIPLKP LGP
478	5975	A	494	527	1022	GWASAFWLWIKPGSPRGYRCNPHH VILPVSAGLELPLCSLLPSTDTCPAS QTGSGRANRATPGCRPAGVRKGR PACKRSKNFRAACGSGARSRPGRH TPGSSRPPGRQKRAPWASQARRPPA *SRPGGRGGAARPHPRRTGAPAGSA RGAQRSERARPQPRDPA
479	5976	A	495	2	379	
480	5977	A	496	3	723	VPRVCLLLQQCLDGTDPGTGLPASD RPISSPLATSGTIFSAISCFWDLAP FLWLAPSCQPTMSSQIRQNYSTDVE AAVNSLVNLYLQASYTYLSLGFYF DRDDVALEGVSHFFRELAEEK\REG YERLLRMQNQ\RGGRALFQDIKKP AEDEWGKTPDAMKAAMALEKKLN QALLDLHALGSARTDPHLCDFLETH FLDEEVKLIKMGDHLTNLHRLGG PEAGLGEYLFERLTLKHD
481	5978	A	497	1	196	GTSVTKMEAFSGRSGLWAGGPAP GQFYRITFTPDSFMDPASALYRGPI RTQNPMTGTSTVLGV*IEGGWVIA GHMLGFYVCLDRLRDFYRFRVNL STVLDASGDAE*HYL*QFYRITFTP DSFMDPASALYRGPIRTQNPMTGT TSVLGV
482	5979	A	498	1	401	GTRKWVTFISLLFLSSAYSRGVFR RDAHKSEVAHRFKDLG*ENFKALV VIAFAQYLQCCPFEDHVKLVNEVTE FAKTCVADESPDN*D*SLHTLFGDK LCTVAILPETYGEMADCCVQLEPER NECFLQLKD
483	5980	A	499	47	411	
484	5981	A	500	316	493	LLVGRALPEGDRHDQHQQGLEQS ILKLEKIQDLENAELQISTKEEAIL* KLKAIER
485	5982	A	501	27	526	LSLTSRMEEAELVKGRQLQAITDKRK IQEEISQKRLKIEEDKLKHQHLKKK ALREKWLLDGISSGKEQEEMKKQN Q\QDQH\QIVLEQSILRLEKIQDLE KAELQISTKEEAILKKLSIERTTEDI IRSVKVEREERAESIEDIYANIPDLP



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						KSYIPSRLRKEIN
486	5983	A	502	25	208	VSRIEAVSGSHGFSIHKLLTVNVITY DCVSSWCLYVSFQQKDPLVLGQRQ LKSKPAGDLNT*GKVIKCKAAIAW KAGKPLCIEEVEALPKAHEARIQV SRWFRLELSLA
487	5984	A	503	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGPNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
488	5985	A	504	52	562	APSPDAMGHFT*EDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTS LGDAIKHLDDLKGTFAQLS ELHCDKLHVDPENFKLLGNVLVTV LAIHFGKEFTP EVQASWQKMAED\ VTGVASALCFTKHLDFMCMMQSFQ R
489	5986	A	505	801	927	
490	5987	A	506	659	837	RKIKEAGHRGSQLYSQHFGRLRQE DCLSPGGQGCSEPR LHRCVPAWVT G*KKTL PKNKQ
491	5988	A	507	3	203	
492	5989	A	508	23	678	RPRVRMAEVQVLVLDGRIGHL\LGR LAA/LSVAKQVLLGRKVVVVRCEGI NISGNFYRNKLKYLAFLRKRMTN PSRGPYNFRAPSRIFWARTVRGMLP HKTKRGQAALD\RLKVFDGMPPPY D/KAPLFL*QKKRMVVPALKVVR LKPTRKF\AYLGRLA\DEVGWKYQA VTAT\LEEKREKAK\IHYRKKK*L\ MRLRKQAERNVRRIFANTPEVLKT HGLLV
493	5990	C	509	275	370	MPQGGACSPVLPGLVVSLLLTQSY LVVVPQW*
494	5991	B	510	1	1122	MVFLSGNASDSSNCTQPPAPVNISK AILLGVLGGLILFGVLGNILVILSVA CHRHLSVTHYYIVNLAVADLLTS TVLPFSAIFEVLGYWAFGRVFCNIW AAVDVLCCTASIMGLCHSIDRYIGV SYPLRYPTIVTQRRGLMALLCVWA LSLVISIGPLFGWRQPAPEDETICQIN EEPGYVLFSA LGSFYLP LAIILVMYC RVYVVAKRESRGLKSGLKTDKSDS EQVTLRIHRKNAPAGGSGMASAKT KTHFSVRLKFSREKKAATLGIVV GCFVLCWL PFFLVMPIGSF PDKPS ETVFKIVFWLGYLNSCINPIIYPCSSQ EFKKAQNVLR IQCLRRKQSSKHAL GYTLHPPSQAVEGOHKDM*
495	5992	A	511	928	1311	AMIVPTAVQGRQSKDPVSKEKKE KARKERWLGTVAHSCNPRTLGGQG GWIMRSRDRDHPGQQGETPSLLKM QKLAGRGGGHQSRLGLRLQENG NPGGGACSEPRWHCCTPAWATE*D

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SISNNNKK
496	5993	A	512	23	288	APSPDAMGHFAEEDKATITSLWGK VNVEDAGGETLGRLLVVPGLKL NSSLG*Q*FGGCILSPHHCLGKGRK CFFSIVEMLVILYFM
497	5994	A	513	20	207	LDAGTACAETMACTSRLYGLPRST WPNHPDAILPEGYFSSEI*SRPDCGL RVIYRGLTISSA
498	5995	A	514	228	375	CVALGAMRGMRRLPAGAPKMLMG V**ELDRLGYIAHPQLGKRARAGIV L
499	5996	A	515	417	573	ETPTGLRGGTCL*S*LPRRLRWENC LNPGGRCSEPRSHHCTPAWATEQ DS
500	5997	A	516	173	420	LLLANQLMSLQIRQNYSTDLEAAV NRLGNLDLQAYYTYLYLGFYYDRD DEGLEGVSHFFRELAEDKRDY*RL LTMQNQRGG
501	5998	A	517	3	415	HEGHQYAPNPDAMGHFTEEDKATI TSLWIKVNEENAG*ETLARLLAGYP WTQRIFDRFGNLFASDIMGNSPVQ AHGKNVLTSLLDATKHLDDLKGT AQLSELHCYKLHVDPENFHALANE LATALAMHFR**FTP
502	5999	A	518	3	232	
503	6000	A	519	1	2361	
504	6001	A	520	4806	5788	HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLOHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRRYVYMVVIIDFVLV SNIILPKFNHLCHTHTHTHTLTLFST YLKNDKDKTIMCKLSLIG*LAESLEF GGSGENVVDYNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELFF AKRYKAAFTCECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWDLGT LSV
505	6002	A	521	151	364	VTHDCICYLQQTHF*PKDKNRLKLR RCKKQFHENSQKRVEVALLISAQ RDLRSKIDTEGKSIQQRKKSSC
506	6003	A	522	925	1168	SQHFGPRWVDHLRSGIGDQPGQH GETPALLKIQKLARCGYMR*SLRR LRRENHLNPGGGGCSETRLHHCIPA WATEQDS
507	6004	A	523	142	329	THSLFLLWSLSHHSPTVNTTLRNLG ALHRRHGKL*AAETLDVFNLTSSCS LLFNPFFYRNFR
508	6005	A	524	108	283	KQNLILSPRLKCNGPISVN*NFNLP LTRSQA*ASREAGTTGTCYHA**IG* IFIIDG
509	6006	A	525	1	345	GTRAAPLRIQSDWAQALRKDEGEA WLSCHPPGKPSLYGSLTCHGIVLYG IP*ATSSHRFIANDPNIITSHSSRPTVF VPSSFSSILFFLAHLPLSISLPFFSLPA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FPLNFLPLRS
510	6007	A	526	3	276	HEPRRPQYSSGRRAAWLSYSLFSAG CGASAPRPLVMSDSGSYGKSDVEH LYYRNY*STRI*GYIQTSHI*SG*GM TTDSYYGINIFYKLQ
511	6008	A	527	2297	2435	LKLVSKKRVYNFILLLML*TYFLK DGLFECLWHLTCKKKKLQKNP
512	6009	A	528	123	317	QETKKEQNKENKQIK*RSTRKKHR QGTNKTKERGERQTPPVGNRQTPT LGIHARPRRRATTSPRA
513	6010	A	529	787	1069	FASHFGRLRQADPLRSGVQDQPGQ QGETPSLLKIQKFPRRDGGRL*SQLP RKLRQENCNFRGGGDCSEPRLCPFL PAWATERNVSVKGERKEKK
514	6011	A	530	110	369	CWLSCCLEVRSCLYTFLSAYNFKCV LTI*HTFFVFFWSLCVYYFFIVLCLL VLVWCLSSLYYGIHYYLYFCYSLFI VLGYGILAV
515	6012	A	531	268	331	QM*TAKCARCEGLGLITLCLDCIVA NTLLVPNGETSWTNTNHLTLQVW LKDGYIGWGLMALCTGIAPVLAGG KDCCGARRCGNR*QMLRYDFS*AL VVLGAIYWLS
516	6013	A	532	807	1060	SWHFGRLRWADYLRPGAGDQLSQ HGEISSLLKTQKLPGCGDTHL*SQLL GRLRQENHLNLGGGGCSEPRSHHC TSAWVTERDSV
517	6014	A	533	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
518	6015	A	534	38	550	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF \FDSFGNLSSA\SAIMGNPKVKAHGK KVLTSLGDAIKHLE*SQGAPFAQA *SELH\CDKPAALLDPGGTFKLPGENV AGLTVFGQSHFRAKEFHP*RLQAS WHKQKMAEDGDLELASALVPSRY H
519	6016	A	535	2	348	ARAGAGRLRRAASALRLLSPRLPVR ELSSLARLYPHRVDDHYENPTNAGS LD*TSKNVGTGLQLAPA*GDVVKL QTLVDEKVKNVDAKFCTLGCGSAI AYSSLATEWVTGKTADE
520	6017	A	536	385	536	RMSAGALFIGYCIYFDHKRRSDPNF KNRL*DGRKKQKLAKERAGLSKLP D
521	6018	A	537	123	705	AAPTALRVRGPPLLRGPCRHRPRSA FVEKMVGRNSAIAAGVCGALFIGY\ CIYFDPQKTK*TPTFKNRLRERRK\K QNLQQRRELGLASKLPDLKDAESCC RKFFL*RNTSLGEELLSFDG*/YEY*E RAVDHLDKLP\IAV\CGQ\PQQLLQV LQQT\PPPVF\QMLLT\KLPTISQRIV SAQSLAE\DDVGMNRNKCLH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
522	6019	A	538	1	430	
523	6020	A	539	42	373	
524	6021	A	540	1	430	QQLQRLVHPDFFSQRSQTEKDFSEK HSTLVNDAYKTLAPLSRGLYLVS* SS/YGIEIPERTDYEMDRQFLIEIMEI NEKLAEEAESEAMKEIESIVKAKQK EFTDNVSSAFEQDDFEEAKEILTKM RYFSNIEEKIKLKKIPL
525	6022	A	541	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDFSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
526	6023	A	542	38	547	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQ/R FFDFSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIKHLADDLKGTFQA *SELHCDKAALLDPENFKLPGGNV AG*PVFGQSHFRAKEFHPWRLQGFP GISRRWQKMVTWSWPVPCSSRYH
527	6024	A	543	328	495	NLGANNCSLLGIGLLKGSMSGRLW PKAFSAG*KQGLQNQRKHTALVKIE DVDA*GE
528	6025	A	544	154	340	PGLLKAAIWGIAYLRTYWTYVLA DLHPFADMLHAGYSITSEVEQPVLA VQLTYNPDES*WP
529	6026	A	545	124	323	EVKSVYLVYILSNRFF*CTYMHILV YYVYFIGLTI*LEEHSMLVYQNLVH YFLVFVNVGIYLLYL
530	6027	A	546	314	445	SPILLQFTVVLTRYLFTKIQFIYFFET ESCSIAQARV*WCDLG
531	6028	B	547	1	1011	MDLKFNNSRKYISITVPSKTQTMSP HIKSVDVVVLGMNLSKFNKLTQF FICVAGVFVYLIYGYLQELIFSVEG FKSCGWYLTQVAFYSIFGLIELQL IQDKRRRIPGKTYMIAFLTVGTMG LSNTSLGYLNYPTQVIFKCKKLIPV MLGGVFIQGKRYNVADVSAACMS LGLIWFTLADSTTAPNFNLRVLYSY SIGFVYILLGLTCTSGLGPVTFCAK NPVRTYGYAFLFSLTGYFGISFVLA LIKIFGALIAVTVTGRKAMTIVLSFI FFAKPFTFYVWSGLLVVLGIFLNV YSKNMDKIRLPSLYDLINKSVEARK SRTLAQTV*
532	6029	A	548	244	1408	SRHNGMDLTQQAKDIQNITVQETN KNNSEIECSKITMDLKFNNSRKYIS ITVPSKTQTMSPHIKSV*RVVVLGM NLSKFNKLTQFFICVAGVFVYLIY GYLQELIFSVEGFKSCGWYLTQV FAFYSIFGLIELQLIQDKRRRIPGKTY MIAFLTVG/TMGLSNTSLGYLNYPT QVIFKCKKLIPVMLGGVFIQGKRYN VADVSAACMSLGLIWFTLADSTTA PNFNLTGVVLISLALCADAIGNVQ EKAMKLHNASNSEMVLYSYSIGFV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						YILLGLTCTSGLGPAVTFCANPVR TYGYAFLFSLTGYFGISFVLALIKIF GALIAVTVTTRKAMTIVLSFIFFAK PFTFQYVWSGLLVVLGIFLMFTAKI WDKIRLPSLV
533	6030	A	549	66	346	IQQLPTFFHIFSIFFLIR*FFYMKGFR* LVLFIYCPHVYA*SYFSLFFCSTLI* FISFSLYFTLFLFFFTLLFICVLAMFI FFELHLSYIP
534	6031	A	550	21	337	GPEAQCPDQPPPWLSFQGLPQGT WATHSAPCSPNLTSSWCPDSEPR AGGRGRPPTLDHDAPPTTPL*PSKP HPCIPQALPSSRTLRLPLATPRQHAA TQCTP
535	6032	A	551	526	771	PPPLGVPGTLQFLRPRAAVLIGSKLL RPGRFGRWIFSPLLL VNISWLGTVV HACNPSTLGDQGGRT*G*EFETSLP TWRNS
536	6033	A	552	305	569	KKPLKGEKGGSLKTRPSFKKPD AKIYLKKS VGFL*TNPEQFKKEIRNTIPLI KGASSSSSKTNLGINLTKVVKDLN NENSRTLRLRQS
537	6034	A	553	90	339	EVSALPDLPAVMLAGPTP*PSFPRTP SYFSAPPLLLPLSCSFLLPLMPHSC PPSSSPSPSLLLLSITSPAPSPFLLF P
538	6035	A	554	1179	1408	GYPVGKRRLGEROQPRQPPTLLPCD KEAERGEHIYIYFIYILI*YIYNIYII YIYNIYIHIYIYIYIYIYIYI
539	6036	A	555	722	991	SQHFWRPQVNHVSLGVQDQHGQ HSENPVSTKIYIYIQKLARCSDRCL* S*LLRRLRHENHLNLGGGGCSELKS CHCTPAWATE*DPVSK
540	6037	A	556	1	362	GTSRQVCREHSFQSVKLSAGARSW CFLSHWDPAGEVSLTDCSEIFLPFLG MAAVYHYFSINIFFKTSFFRLILY** SYFHLYFLYYSILCLFILLFIIFYC YILFISNLFTIIFLFL
541	6038	A	557	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
542	6039	A	558	38	497	APSPDAMGHFTEEDKATITSLWGK\ VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIK\H\DDLKG\TFAQA *SELALVDKLACGILENFKAPGEML LVTRFWQSHFRQKNFTPEGCKASW AERWVTW
543	6040	A	559	1	414	FETVSLLLLRLLEHTGTISTHCNLR LPGSNDASASAS*VAGTTSVCHHTGLI SVFSIETEFHHVGQTGLELLTSSDPL TSASPGAGIKGGSHCAQSPICFRGN NEMNYQATGIYSKSEIFFCLGYVTM SRCLTSQSGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
544	6041	A	560	178	334	NVCRLPVTNAESDAMINDAIRPINF TGFLTMFA*NLTGADPADVIIAAFD VL
545	6042	A	561	322	649	
546	6043	A	562	3	452	
547	6044	A	563	24	587	GIPQTQREPTMVLSPADKTNV\KAA WGKVGAHAGEYGAEALER\MFLSF PTTKTYFPFHDLSHGSAQVKGHGK KVADALTNAVAHVDDMPNALSAL SDLHAHKLRVDPVNFKLLSHCLLV TLGA\HLPAEFTPAVHA\SLDKFLAS VSTGLTSKYPLSWSPRWPCFLAPW ASPQPLLFPAPVPPWSLK
548	6045	A	564	3	474	
549	6046	A	565	1099	1243	
550	6047	A	566	425	943	MGRSAPVEISYETMRFMTRNPTN ATLNKFTEELKKYGVTTLV\RVCD TYDKAPVEKEGIHVLDWPFDDGAP PPNQIVDDWLNLLKTK\FREGARVC CVA\HVCVGRVGE GAPVL/VLALAL DWNVGMK\YEDAV\QFIRQKRRGA FNSKQL\LYLEEYRPMRLRFRDTN GHC\CVQ
551	6048	A	567	1	441	
552	6049	A	568	1	890	MSKSESPKEPEQLRKLFIGGLSFETT DESLRSHFEQWGTLTDCVVMRDPN TKRSRGGFV\TYATVEEVDAAMNA RPHKVDGRVVEPKRAVSREDSQRP DYFEQYQKIEVIEIMTDRGSGKKRG FAFVTDDHDSVDKTVIQKYHTVN GHNCEVRKALSKQEMASASSSQRG RSGSGNFGGGRGGGFGGNDNFGRG GNFSGRGGFGGSHGGGGYGGSGDG YNGFGNDGSNFGGGGSYNDFGNY NNQSSNFGPMKGGNFGGRSSGPYG GGGQYFAKPRNQ/GGYGSSSSSSSY GSGRRF
553	6050	A	569	579	2102	SPKEPEQLRKLFIGGLSFETTDESLR SHFEQWGTLTDCVVRFG\RD KAVKQ PISLAYLGAVFSECL*K*LIAL*LELC WQRNVLL*F*KLTS*I*G*WETGRTF YKRLV*SFLLPYSK\K*QKLLRSD VLHKLTLFSG\MRDPNTKRSRGFGF VTYATVEEVDAAMNARPHKVDGR VVEPKRAVSREVS\GFFFFFLNLLG YVLL*T*DSGVF*TYQNFLFEYRLC* SKPMVFLLL\DSQRP\GAHLT/V*KKI FVGGIKRRHLKEHHLRDYFEQYQK IEVIEIHDLTRGSGKKR\GF\AFVTFD DHDSVDKIVSKYQIVAFSGSTICM AF*TLIPCCIVVFLVQKYHTVNGH NCEVRKALSKQEMASASSSQRGML VA*LNLKGNFELLQYE\FNA*TSCL KV/ESGSGNFGGGRGGGFGGNDNF GRGGNFSGR/GYVWFIYM*F*LLTIF AMKILQYGNCIQNVTLSPSHT*NLK LFLTGGFGGSRGGGGYGGSGDGYN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GFGNDGKFFRNK
554	6051	A	570	250	381	
555	6052	A	571	249	468	PNQRLKWKS*LMGQGRG*KWKLL VLFYHKA*RMWPA\C\CLDLGLGTG \CTC\CLLVYANWLHLLFLCLCPYP WLS
556	6053	A	572	2	488	QEPADLRMYGKIINFVLLSEIVSIS ALSTTEVAMHTSTLLPSSHKRVTSS S\QTNGETGTTCPVSLYPAPCSDNT HYFVCDGWYYWNDPLNFLLYSMT DKGMRMWPAACCLILPRTSCTCCSL AYANWLHL\LFL\CLCPYPWAILNS LFSWPSLITGILYF
557	6054	A	573	7	412	
558	6055	A	574	3	479	NWELLWLLVLCALLLLVQLLRF LRADGDLTLLWAEWQGRPE/WEL TDMVVWVTGASSGIGEELAYQLSK LGVSLVLSARRVHELERVKRRCLE NGNLKEKDILVPLDLTDGSHAA TKAVLQEFGRGFFNGLRTELATYPG IIVSNICPGPVQSN
559	6056	A	575	1	321	
560	6057	A	576	2	1243	GAASAEPGAPEPLLLPACSLGGAGA VRLWAGRRGGAAIPQGSATLVRA VFFPPSWACAAAMNWELLWLL\V LCDVLLLLVQLL\RFLRADGDLTL LWAEWQG/RDRPEWELTDMVVW VTGASSG/LGEELAYQLSKLGVSL VLSAR\RVHELEKGEKERCL\ENGQF LKEKDITLFLPLDLDTLGS*SRLT KAVLQEVLRIDILGSTMVGM\SQR SL\CMDTSLDVYRKLIELNLYLGTVS LTKC\VLPHMIERKQKIVTVNSILG IISVPLSIGYCASKHALRGFFNGLRT ELATYPGIIVSNICPGPVQSNIVENSL AGEVTKTIGNNGDQSHKMTTSCV RLMLISMANDLKEVWISEQPFLVT YLWQYMPPTWAWWITNKMGGKRIE NFKSGVDADSSYFKIFKTKHD
561	6058	A	577	175	354	
562	6059	A	578	2018	2182	
563	6060	A	579	140	287	MVKRNQCPSLPPN*KMRSQGSTCQ PHCQRWLPSTRSYTHPLKARPWSA S
564	6061	A	580	357	760	
565	6062	A	581	182	459	
566	6063	A	582	1	382	
567	6064	A	583	3	406	
568	6065	A	584	173	415	
569	6066	A	585	2	424	
570	6067	B	586	108	395	VGAHAGEYGAEALERMFLSFPTTR TYFPHFDLSHGFCPLRGHGQEGGR RADQRRGARGTTCTPSLSALSDLHA HKLSGGTRFNFQAPKATGLLG*
571	6068	A	587	379	579	
572	6069	A	588	2	366	SLPASDRPPISSPLATSGTIFSAISCF WDLPAFLWLAPSCQPTMSSQIRQN

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						YSTDVEAAVNSLVNLYLQASYTYL SLQDIKKPAEDEWGKTPDAMKAA MALEKKLNQALLDLHALGSART
573	6070	B	589	220	480	MSSQIRQNYSTDVEAAVNSLVNLY LQASYTYLSLGFYFDRDDVALEGV SHFFRELAEEKREGYERLLKMQNQ AWRPRSLPGHQEAS*
574	6071	A	590	142	383	
575	6072	A	591	1	308	
576	6073	B	592	195	326	MMGVLDGVLMEQDQCALXLLKDV IATDKEDVAFKDLDAVAILVV*
577	6074	A	593	5	1199	PDSLRLILHLFKLSQFSIMSEPIRVL VTGAAGQIAYSLLYSINGSVFGKD QPIILVLLDITPMMGVLDGVLMEV RLCPSPPERCGNGSVFGKDQPIILVL LDITPMMGVLDGVLMEQDQCALPL LKDVIAITDKEDVAFKDLDAVAILVGS MPRREGMERKDLLEY/ADVKIFKSQ GAALDKYA\QKSGKVIVGGNPANT DCLTASKPAPCIPKENFSCRLTDH NRAKAESGLRLVVTADHGQNGIIV GNHSSTQYPDVNHAKVKLQKQEV GVYEALKDDSWLKGEFVTTVQQR GAAVIKARKLSSAMSAKAICDHV RDIWFGTPEGEFVSMGVISDGNSYG VPDDLLYSFPVVIKNTWKFEGLP INDFSREKMDLTAKELTEEKESAFE FLSSA
578	6075	A	594	46	298	
579	6076	A	595	982	1193	
580	6077	A	596	69	399	VSNYPTVGCCIFLQIRARNPAFQPQT LMDFGSGTGSVTW*VTFSPILVNF SSRKPYLHHSKINRLNQRNRQVG NL*CFHQRQRRRYMDWGQNLK EMSSKKRRMY
581	6078	A	597	600	887	
582	6079	A	598	813	973	
583	6080	A	599	166	437	ADHLKSGV*DQPGQHGEILSLLKLQ *FPGRGGAHL*SLLGRLKQENHLN PGGGGCSEPRCHWTPVRATVGDS VQKK*KSQDGPRAKLG
584	6081	A	600	3	238	SGDRDHPG*HSETLSLLKIQQIAGR GGGRL*SRLLRRLRQENGVSPPGG ACSEPRSHHCTPAWETERDSVSKK KKKKL
585	6082	A	601	4005	4345	SQHFGRRPRADHLRSGVQDQPDQH GETPSLLGRRGGRTKSGDRDHPG* HGETPSLLKMQ/EKLAGRGGGRLW SLLGRLRQENGVSPPGRACSEPRS CHCTPAWLTEQDSVSKK
586	6083	B	602	1	9234	MGAPTLPPAWQPFLKDHRISTFKN WPFLEGCACTPERMAEAGFIHCPT NEPDLAQCFFCFKELEGWEPDDPI EEHKKHSSGCAFLSVKKQFEELTLG EFLKLDREKAKNKIAKETNNKKKEF EETAKKVRRAIEQLAAMD*
587	6084	A	603	1577	2233	SGCLLSPPSVGRQNSPVELGGAGLS



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RAGWAPQERGRAALLISPGPNVR GGPDWLPSVLQMRGLPLWDLGGRP DVGRMSPGGRPGSCWATQLRFHIS LAPLFSWAGRSGSRLNPSTLGGRGG PITRSGDRDHPG*HGETLSLLKIQKI SQACWR/CACSPSYGRLRQENGVP GGGACREQRSGHCTPAWATEQDSV SKKKKKKSGSTIRLKHILHKII
588	6085	A	604	151	454	FQKIGPGAVAHACNPSTLGGRSRRI TRSGGRDHPG*HSETPSLLKIQKLA GRGGGCL*SLLWRLRQENGVPNG GGACSEPRSRHCTPAWVTERDSVS KKK
589	6086	A	605	1362	1647	
590	6087	A	606	10289	10708	SQHFGKLRQEDHLRSGVREQPGQH GKTPYLLKIQKLARRSGACL*SLL RRLRQENRLNPGGVGCSEPRLHHC TTAWTLQ*DPVSKKLLKKYIERQR YHQHMKHPWSTKIQYVCMGDG*HR SVEKQIIQTLCMFVFTHTY
591	6088	A	607	709	980	
592	6089	A	609	234	381	PPWTQFSLSCVCLL/CSRPA/VSAWR QARENESQAKGETAYETITSCENRS H
593	6090	A	610	1	1755	
594	6091	A	611	1128	1321	
595	6092	A	612	650	800	
596	6093	A	613	149	475	
597	6094	A	614	1	801	
598	6095	A	615	1284	1386	
599	6096	A	616	20	3888	
600	6097	A	617	204	411	
601	6098	A	618	1	1468	
602	6099	A	619	48	178	
603	6100	A	620	79	1953	LQVGTASSLLDSRVFGDRGYSPET RKCPKPINVRVTMDAELEFAIQPN TTGKQLFDQVVKTI RPSRQVWYF/G LHYVD\NKGFTWLKL\DKKVSAQ EVRKKNPLQFKFR/APKFYP\EDVA\ EELIPGTFTQKLFFLQVEGRESLSDE DLLAPLETGRALWGSYACASPRLG DYNK/EKLHKSGVPSASERLIPQRV MDQHKLTRDQWEDRIQVWHAHR GMLKDNAMLEYLKIAQDLEMYGIN YFEIKNKKGTDLWLGVDALGLNIY EKDDKLTPKIGFPWSEIRNISFNDKK FVIKPIDKKAPDFVIFYAPRLRINKRI LQLCMGNHELYMRRRKPDTEVQQ MKAQAREEKHKQQLERQQLETEK KRRETVEREKEQMMREKEELMLRL QDYEEKTKKAERELSEQIQRALQLE EERKRAQEEAERLEADRMAALRAK EELERQAVDQIKSQEQLAAELAEYT AKIALLEEARRRKEDEVEEWQHRA KEAQDDL VKTKEELHLVMTAPPPP PPPVYEPVSYHVQESLQDEGAFTG YSAELSSEGIRDDRNEEKRITEAEKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ERVQRQLVTLSSLSQARDENKRTH NDIIHNENMRQGRDKYKTLRQIRQ GNTKQRIDEFEAL
604	6101	A	621	269	361	
605	6102	A	622	210	367	ISQSGDCCSVWLSLQGPPKGC PKP/I PSPGLQPRATPPA*VQQR TSHPMSC SN
606	6103	A	623	1792	1935	
607	6104	A	624	9	326	
608	6105	A	625	250	381	
609	6106	A	626	155	457	NQKELGNTPRYPLEASNWLQPVKD WPVTNQRLKWK*LMGQGRG*KW KLLVLFYHKA*RMWPA\C\CLDLGL GTG\CTC\CLLVYANWLHLLFLCLC PYPWLS
610	6107	A	627	2	488	QEP AHDLRMYGKIIFVLLSEIVSIS ALSTTEVAMHTSTLLPSSHKRVTSS S\QTNGETGTTCPIVSLYPAPCS DNT HYFVCDGWYYWNDPLNFLYSMT DKGMRMWPA CCLILPRITSC TCCSL AYANWLHL\LF\CLCPYPWAILNS LFSWPSLITGILYF
611	6108	A	628	2	364	
612	6109	A	629	946	1142	LSGIIHYSFFTIRNIKALFSLC*VFQF GFLRDFPFIFPFIFRKPILTKGPTSVA M*WKGGIH FIA
613	6110	A	630	946	1193	LSGIIHYSFFTIRNIKALFSLC*VFQF GFLRDFPFIFPFIFRKPILTKGPTSVA M*WKGGIH FIA*SAFPVQGLLFRS WNL
614	6111	A	631	946	1142	LSGIIHYSFFTIRNIKALFSLC*VFQF GFLRDFPFIFPFIFRKPILTKGPTSVA M*WKGGIH FIA
615	6112	C	632	294	710	MVRSRQMCNTNMSVPTDGA VTT S QIPASEQETLVRQES EDYSQPSTSSSI IYSSQEDVKEFEREETQDKEES VESS LPLNAIEPCVICQGRPKNGCIVHGKT GHLMACTCAKKLKRNKPCPVCR QPIQMIVLTYFP*
616	6113	C	633	822	1149	MLVLHICLLLTIRGFRAW SRGSLKT PQFPSRGLTTAEARRPGRGSFHS PG QGTGRSYALIRGGTVLLA AKAAGS RSEGSRPPLGLGFLHLSDTQGH TG PRSSQARAV*
617	6114	A	634	5	76	
618	6115	A	635	269	354	
619	6116	A	636	184	299	FFCTFSTDGVSPC*PGWSRSPDLVIH SPRPPKVLGLQA
620	6117	A	637	3	307	ESCSEAQAGVQGAQSWLTATSS FQ VHAILLPQPK*LGLQVPATTPG*FF VFLVETGFHCVSQDGLKLQTS*SAH LGLPKCWDYRHEPLRPAKQLFKN VP
621	6118	A	638	2	131	SKAALTGSGPGP/IPLCFVSAVLAPFI RPS*SLLAGRGLDGGQD
622	6119	A	639	1	822	
623	6120	A	640	1258	1454	LSGIIHYSFFTIRNIKALFSLC*VFQF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						GFLRDFPFIFPFIFRKPILTKGPTSVA M*WKGGIHFA
624	6121	A	641	248	386	SARLSLPKIWDYRREPLHPARSFFIY SSSSILY*S*LVSIEETALLF
625	6122	A	642	132	243	LGLQVPATAPG*IFFVFLVETGFHH VSQDGLDLLTS
626	6123	A	643	397	954	
627	6124	A	644	1	1388	
628	6125	A	645	2285	2409	
629	6126	A	646	36	224	
630	6127	A	647	242	933	YGESKDOWNQKDLLSALVLTVNCL PTPIMAKSAEVKLAIFGRAGVGKSA LVVRFLTFRFIWEYDPTLESTYRHQ GNHSMMEVVSMGGY*DTAGQEDTI QREGHMRWGEFVLVYDIT*PRKF LKEVLALKEHLDEIKKPKNVTLILV GNKADLDHSRQVSTEEGEKLATEL ACAFYECSACTGEGNITEIFYELCRE VRRRRMVQGKTRRRSSTTHVKQTI NEMLT KISS
631	6128	A	648	596	709	
632	6129	A	650	1	367	
633	6130	A	651	135	307	
634	6131	A	652	170	372	
635	6132	A	653	3	320	
636	6133	A	654	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDFSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
637	6134	A	655	52	518	APSPDAMG/HFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF DFSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIHLDDLKGTFQAQLSE LHCDKLHVDPENLKLGNVLETAL AIQFRRKNSPL*GQASWQKMVTGV ASALSSRYH
638	6135	A	656	123	219	
639	6136	A	661	413	545	
640	6137	A	662	4	350	
641	6138	A	663	1034	1091	
642	6139	A	664	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDFSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
643	6140	A	665	38	602	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF DFSFGNLSSASAIMGNPKVKAHG KKVLTSLGDAIKHLDDLKGTFQA A*SELHL*QSCNVDPENFKAPGEM LLVTR/VLAIPFSAKEFTPEGCRASW AERWVTCSPVALFLQDTTEAQLP MNAELFKDKAFILASNYK
644	6141	A	666	24	452	APSPDAMG/HSLWGKVNVEDAGGE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMTGVASALSSRYH
645	6142	A	667	38	536	APSPDAMGHFTEEDKATITSLWCK VNVEDAGGETLGRLLVVYPWTQR FFDSFGNLSSASAIMGNPKVKAHG KKVLTSLGDAIKHLDDLKGTFQA A*SELHC*QAGMWDPENFKLLGE MLLVTRFGQSHFRQKNFTPEVARL SWAERWWTWSWPSALVPSRYH
646	6143	A	668	132	357	
647	6144	A	669	1	89	
648	6145	A	670	136	594	LNRVAFPLGAAVILIGHLHTHTGPS GVCNVSMRGFSSPAGWPTGSHRG KERPAGRLMHRRMGWSAVEWTG\ AQGIPCISTCPTERTGGDAATRSRPP VLPPPPRPPQRRCRHLVSRAGTPRC ACAGLTSTKRGTHWRSTELLRRSP LRSSQ
649	6146	A	671	400	696	
650	6147	A	672	120	352	
651	6148	A	673	276	401	
652	6149	A	674	139	470	
653	6150	A	675	136	1058	GVVGAAASGAGSRKAGLAGVPGPP GRANRESPPGPVAMGRVIRGQRKG AGSVFRAHVKHKRGAARLRAVDF AERHGYIKGVKDIHDPGRGAPLA KVVFDRDSYRFKKRTELAFIAAEGVIH TGQFVYCGKKAQLNIGNVLPVGT\ MPEGTIVC/CALEEKPGRGKILAR ASGNYATVISHNPAETKKTTRVKLPF RVQRRRLSPSANKSLWLVLVAGGWP ECDKPILKAGRAVPQI*RQKRCNW \PRVTGVWAMNPFEEFLKGGNPPA HRQSPPIRRDAPAGRKVGLIAARR TGRLRGTKTVQKEN
654	6151	A	676	21	340	
655	6152	A	677	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMTGVASALSSRYH
656	6153	A	678	38	529	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSASAIMGNPKVKAHGK KVLTSLGDAIKHLDDLKGTFQA DVNLHC*QACMLDPE\NFQASWGN VL\VTRFWAIPFSGKEFHP*RCQAF LGRKMGDLELASALVPSRYH
657	6154	A	679	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFQQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EVQASWQKMVTGVASALSSRYH
658	6155	A	680	3	545	HSLFGTSEVINKLRSPDA\MGHFTEE DKATITSLWGKVNVE\DAGGETLGR LLVVYPWTQ\RFDSFGLSSASAIH GQPPKSRHMGKKVLTSLGDAIKHL \DDLKGHLLPKPEVKLH\CDKAALL DPEELSSFLGEMLLGDPFLGNPIFGQ KNFTPEVARLSWAERWVTWSWPS ALVPSRYH
659	6156	A	681	1	432	
660	6157	A	682	334	845	AVRVRYVAFRYRAPRAVCLRLWSC RREVIHVPVRGKQGGKVRAKAK\S RSSPRGPCRFPVGPSCTELLRK\GNY AER/MSGAGAPV*LGGRCLKYLTA IPEAWLANAAA*QRRPRIIPRHLAS SPIRNDEGS*TKLLGQKLTIAQGGV LPNIQAVLLPKKDGESEGRRSK
661	6158	C	683	392	445	MQPAVQVRVGNLSRYFPS*
662	6159	A	684	183	481	
663	6160	A	685	253	385	
664	6161	A	686	256	374	
665	6162	C	687	354	416	MKESPGGELPQTGKKPVFLF*
666	6163	A	688	2	171	
667	6164	A	689	320	584	TRLPFDRPRATGCHQVPSPERRSPIS QDRLTHVQLLFTWNPSPRLRPSKFSF EYLL\PPRSCTCGGSHPGPKP*ASR LTAAALLLVAA
668	6165	A	690	33	494	
669	6166	A	691	1	522	PLKRS DGCNDGRPTRPPTRPD TTVF TSNLKQTRMVHLTPEEKSAVTALW GKVNVDVGGKALGRLLVVYPW\ TQRFESFGDLSTPDAVMGNPKV KAHS\KKVLRGAF\SDGLAHL\DNLK GTFAHTEVSLHCDK\LVDP*RTFR LLGQRAW SVVAGPIHFWQKNFNPT SCRLA
670	6167	A	693	241	1104	
671	6168	A	694	95	462	
672	6169	A	695	33	494	
673	6170	A	696	1	523	PLKRS DGCNDGRPTRPPTRPD TTVF TSIAHTDTMVHLTPVE\KSAVTALW GKVNVDVGGKALGRLLVVYPW\ TQRFESFGDLSTPDAVMGNPKV KAHS\KKVLRGAF\SDGLAHL\DNLK GTFAHTEVSLHCDK\LVHRSGLKNFR LLGQRAW SVVAGPIHFWQKNFNPT SCRLA
674	6171	A	697	318	515	
675	6172	A	699	2	648	
676	6173	A	700	137	507	
677	6174	A	701	118	375	VAVVQIIFLPVFIAEKYKDLVPD NSK TADNATKNAEPLINLDVNNPDFKA GVMALANLLQIQRHDDYLVM LKVA IRILVQERLTQD
678	6175	A	702	1	969	AATVLT TIGEAPSRSDSAPARPLAA SPVPAPPAPPRFFSPGRGPVDQSEKR WTMFRRLTSLDYHNPAFNC KD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ETEFRNFIVWLEDQKIRHYKIEDRG\ NLRNIHSSDWP\FFEKYFKRC*TCP FKIQDRQESYLTGFFG\LA VRLEYG DNAEKYKDLVPDNSKTA*QLQLKI AEPLIN\LDVNNP\DFKAGVVGFG*T WLQIQRH\DG LPGQMLKANS GFVW QERLDHQGCQFA*GQIKQKRGLPV A\LDKHILGFD TGDAVLNEAAQILR LLHIEELRELQTKINEAIVAVQAIIA DPKTDHRLGKSLEDEHLRTSASHLL
679	6176	A	703	105	1591	
680	6177	A	704	110	431	
681	6178	A	705	171	1577	GGNRATIQAGQCGNQIGAKFWGR* SVNEHGIRPHRHP THGSDPAAWT RNPPVYYNESHKVGK\YVPRAILG GI*EPGEPWDSVR\SGSFLGPPKGEKI FPPFRPDNFVFGQSGAGNN\WAKRP LAQEGAEL\VDS\VLDVGTEGRQRS CD\CLQGFP A*PTSLGRGGTSGMG TLLYQQGFEKEYPD\RIMN\TFSVVP\ SPKCLDTVVQPYKATLSVHQLVEN TDETYCIDNEALYD\ICFRTLKLTTP TYGDLNHLVSATMSGVTTCLRFPG QLNADLRKLAVNMVFPRLHFFMP GFAPLTSRGSQYRALTVPELTQQV FDAKNMMAACDPRHGRYLTVA AV FRGRMSMKEVDEQMLNVQKNSS YFVEWIPNNVKTA VCDIPPRGLKM AVTFIGNSTAIQELFKRISEQFTAMF RRKAFLHWYTGE GMEFTEAES NMNDLVSEYQQYQDATAEEEEDFG EEAEEEA
682	6179	A	706	1	558	
683	6180	A	707	1306	1459	LASMCMCWIESHF CPPGPTGGSRRG PP/HLWLPGRSSGRSQRRLAESTEAP R
684	6181	A	708	1073	1324	
685	6182	A	709	1	797	
686	6183	A	710	1	3210	MVKGSIQQEELTILNIYAPNTGALRF IKQVLRDLQRDLDSHTIIMGDFHTP LSTLDRSTRQKV NKDIQELNSALHQ EDLDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEIITNC LSDHSAIKLELRIKNLTQNRSTTWK LNNLLNDYWVHNEMKAEIKMFFE TNENKDTTYQNLWDTFKA VCRGKF IALNAHKRKQERSKIDTLTSQLKEL EKQEQT HSKASRRQEITKIRAE LKEI ETQKTLQNINESRSWFFERINKIDRP LARLIKKKREKNQIDAIKNDKGDIT TDPTEIQT TIREYYKHL YANKLENL EEMDKFLNTYTLPTLNQEEVESLNR PITGAEIVAINSLPTKKSPGPDGFTA EFYQRYKEELVPFLLKPFQSIEKEGI LPNSFYEASIIIPKPGRD TT KKENFR PISLMNIDAKILNKILAKRIQQHIKN LIHHDQVG FIPGMQGW FNIRKSINVI QHINRAKDKNHMIISIDA EKAFDKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QQPFMLKTLNKLDDMIVYLENPIVS AQNLLKLISNFSKVSQYKINIQKSQA FLYTNNRQTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFK\ENHKPLL EIKEDTNKWKNI PCSWVGRINIVKM AILPKVIYR/FNAIPIKLPMTFFTELE KTTLKFIWNQKRARIASILSQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSERTPHIYNLY IFDKREKNKQWGKDSL FNKWCWE NWLAICRKLKLD PFLTPYTKINSRW IKDLNVRPKTIKTLEENLGFTIQDIG MGKDFISKTPKAMATKAKIDKWDL IKLKSFCTAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCPSLAJREM QIKTTMRVYH LTPVRMAIKKSGNNRCWRGCGEIG TLLHCWWDCCLVQPLWKAVWRFL RDLELEIPFDP AIPLLGIYPKDYKSC CYKDTCTRRKQLDCAEPVEPRKVG DGEWSLTKWTRPGSRALPWPPEQA KPYPPTLPTLAQDF
687	6184	A	711	1	2666	MVKGSIQQEELTILNIYAPNTGAPRF IKQVLSDLQRDLDSHTLIMEDFNT LSTLDRSTRQKVNKNTQELNSALH QADLIDIYRTLHPKSTEYTFFSAPHH TYSKIDHIVGSKALLSKCKRTEITN YLSDHSAIKLELRIKNTQSRSTTW KLNNLLNDYWVHNEMKAEIKMF FETNENKDTTYQNLWDAFKA VCRG KFIALNAYKRKQERSKIDTLTSQLK ELEKQEQTHSKASRRQEITKIRAE KEIETQKTLQKINESRSWFFERINKI DRPLARLIKKKREKNQIDTIKNDKG DITDPTIEIQT TIRESYKHLYANKLE NLEEMDTFLDTYTL PRLNQEEVESL NRPITGSEIVAIINSLPTKKSPGPDGF TAEFY/PESYL*QTHRQYHTEWAKT ASIPFENWHKTGMPSLTTPIQHSVG SSGQGNQPGEGNKGYSIRKRGSIQV PVCRRHDCLSRKPHRLSPKSP*ADK QLQQSLRIQNQCTKITSILIHQQQT NREPHE*TPIHNCFKENKIPRNPTYK GCEGPLQGELOTTAQGNKRGHKQ MEEHSMMLGRKNQYRENGHTAQG NLQIQCHPHQATNDFLHRIGKNYFK VHMEPKKSPHRQVNPKEQSWRH HTT*LQTLQGYSNQNSMVLVPKQR YRSMEQNRALRNAA YLQSLD*LQ T*EKQAMGKGFPI**MVLGKLASH M*KAETGSLPYTL YKNQFKMD*RF KR*T*NHKNPRRKPRHYH*GHRRG QGLHVQNTKSNQNSQN*QMGSN* TKELLHSKRNYHQSEQATYNMGEN FRNLLI*QRANIQN LQ*TQTNLQEK NKQPHQKVGEQHEQTLLKRRHLCS QKTHEEMLIITGHQRNANQNHYEIS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SHTS*NGNH*KVRKQQRQNS
688	6185	A	712	1	4371	
689	6186	A	713	1	1849	MVKGSIQQEELTILNIYAPNTGAPRF IKQVLSDLQRDLDSHTFIMGDFNTP LSTLDRSRRQEVNKDTQELNSALH QADLIDIYRTLHPKSTEYTFFSATHH TYSKIDHIVGSKAVLSKCKRTEITN YLSHSAIKLELRIKLTQNRSTTW KLNNLLNDYWVHNEMKAEINMF FETNENKDTTYQNLWDTFKA/EIQA TIREYYKHLTYNKLENLEEMDKFL DTYTLPRLNQEKVESLNRPTGSEIV AIINSLPTKKSPGPDGFTAIFYQRYK EELVPFLLKLFQSIEKEGILPNSFYEA SIILIPKPGRDTTKKNFRPISLMNID AKILNKILANRIQQHIKKLIHHDQVG FIPGMQGWFNICKSINVQHINRTKD KNHMIISIDAFAFDKIQQPFRKLT NKLGVDTYTKIIRAIYDKPTANIIL NGQKLEAFPLKTGTROGCPLSPLLF NIVLEVLARAIQKEKARDVKDLFK ENYKPLLKEIKEDTNKWNIPCSW VGRINIMKMVILPKDSTWAEVLVG DRRSGRLTEMLVIFLVFQSFHSFLN TLMSPSIFSSWPCFCSSQLVSLCRT CRSVCLSSAAGVSRVASLGNQKKR DLGSENL
690	6187	A	714	1	1825	MVKGSIQQEELTILNTYAAHTGAPR LIKQVLSDLQRDLDSHTIIMGDFNTP LSTLDRSTRQKVNKDTQELKSALH QADLTDIYRTLHHKSTEYTFFSAPH HIYSKIDHILGSKALLSKCKRTEITN YLSHSAIKLELWIKNLTQNHSTTW ELNNLLNDYWVHNEMKAEIKMFF ETNENKDTTYHNLWDTFKA VCRG KFIPLNAHKRQERSKIDTLTSQKE LEKQEQTTHSKASRRQEITKIRAEK EIQTKTLQKINESRSWFFERINKID RLARLIKKKREKNQIDAIKNDKGD ITDPTEIQTIREYCKHLYANKLEN LEEMDKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPDGFT AKFYQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIIIPKPGRDTTKKN FRPISLMNIDAKILNKKLAKRIQQHI KKLIHHDQVGFIIPGMQGWFNIRKSI NVIQHINRAKDNHMIISIDAFAF DKIQQPFMLKTLNKLGIKYLGIHLT RDVKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPKNLI TLQLLLVLPELSTLIPLWLPALAGQ
691	6188	A	715	1	3552	
692	6189	B	716	1	3786	MVKGSIQQEELTILNIYAPNTGAPRF IKQVLSDLQRDLDSHTLMGDFNTP LSTLDRSMRQKVNKDTQELNSALH QVDLIDIYRTLHHKSTEYRFFSAPH HTYSKIDHILGSKALLSKCKRTEIT NYLSGHSIAIKLELKIKNLTQNRSTT



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						WKLNNLLNDYWIHNEMKAEIKM FFETNENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLTSQ KELEKQEQTHSKAGRKEITKIRAQ LKEIETQKTLKKLMNPGAIEQTIRE YYKHLIYAKKLENLEEMDKFLDTYT LPRLNQEEVESLNRPIGAEIVAINS LPTKKSRTTRWIHSRILPEEASIIIPKP GRDTTKKENFRPISLMNIDAKILNKI LAKRIQQHIKKLIHHDQVGFIPGMQ GWFNIHKSINVIQHINRAKDKNHHIS IDAEKAFDKIQPFMLKTLNKLIGID GTYFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLFNIVLEVL ARAIROEKEIKGIQLGKEEVQLSLFA DEMIVYLENPIVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTRDV KDLFKENCKPLLNEIKEDTNKWNI PCSWVGRINIMKMAILPKVIYRFNAI PTKPPMTFFTELEKTTLKFIWNQKR ARIAKSILSQKNKAGGITLPDFKLYY KATVTKTAWYQNRDLQWNR TEPSEITPHIYSYLIFDKPEKNQWG KDSL FNKWCWENWLPICRKLKLD FLTPYTKINSRWIKDLNVRPKTIKTL KENLGITIQDIGMGKDFMSKTPKAM ATKDKIDKWDLIKLSFCTAKETTI RVNRQPTKWEKIFATYSSDKGLISRI YNELKQIYKKKTNNPINKWVKDMN RHFSKEDIYAAKKHMKKCSSLAIR EMQIKTTMRYHLTPLRMAIHKSGN NSASPTARNKTARNQRTKMIAVTA PRNRAPLELELILYRQNRQSKTHILE TNNTSAELLVPFEEDYLIEIRTVSDG GDGSSSEEIRPKMSMIDHILPKSPE ELQNGEGFGYIIMFRPVGSTTWSKE KVSSVESSRFVYRNESIPLSPFEVK VGVYNNEGEGSLSTVTIVYSGEDD GYVFLWMVEPQLAPRGTSLSQSFSA SEMEVSWNAIAWNRNTGRVLGYE VLYWTDDSKESMIGKIRVSGNVTT KNITGLKANTIFYASVRAYNNTAGTG PSSPPVNVTTKKSRYLITTAYLEVPE I*
693	6190	A	717	2	3155	
694	6191	B	718	1	3414	MVKGSIQEEELTILNIYAPNTGAPRF IKQVLSDLQRDLDSHTLIMGDFNNP LSTLDRSMRQKVNKDTQELNSALH QVDLIDYRTLHHKSTEYRFFSAPH HTYSKIDHILGSKALLSKCKRTEIT NYLSGHSIAKLELKIKNLTONRSTT WKLNNLLNDYWIHNEMKAEIKM FFETNENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLTSQ KELEKQEQTHSKAGRKEITKIRAQ LKEIETQKTLKKLMNPGAIEQTIRE YYKHLIYAKKLENLEEMDKFLDTYT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LPRLNQEEVESLNRPIITGAEIVAINS LPTKKSRTTRWIHSRILPEVQGGTEK EGILPNSFYEASIIIPKPGRDTTKKE NFRPISLMNIDAKILNKILAKRIQQHI KKLIHHDQVGFIQGMQGWFNHHSI NVIQHINRAKDKNHHHSIDAEKAFD KIQQPFMLKTLNKLIGDGYFKIIRA IYDKPTANIILNGQKLEAFPLKTGTR QGCPLSPLLFNIVLEVLARAIQEKE IKGIQLGKQEVQLSLFADEMIVYLE NPIVSAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKENCK PLLNEIKEDTNKWKNI PCSWVGRIN IMKMAILPKVIYRFNAIPTKPPMTFF TELEKTTLKFIWNQKRARIKSILSQ KNKAGGITLPDFKLYYKATVTKTA WYWYQNRDLQWNRTEPSEITPHI YSYLIFDKPEKNKQWGKDSL FNKW CWENWLPICRKLKLDPFLTPYTKIN SRWIKDLNVRPKTIKTLKENLGITIQ DIGMGKDFMSKTPKAMATKDKIDK WDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKQIY KKKTNPNPINKWVKDMNRHFSKEDI YAAKHKMKCCSSLAIREMQIKTT MRYHLTPLRMAIHKSGNNSASPTA RNKTARNQRTKMIAVTAPRNRAPL ELELILYRQNRQSKTHILETNNTSAE LLVPFEEDYLIEIRTVSDGGDGSSE EIRIPKMSTGGEEGMAAVFKNKCRC SWSRVVIA YHSSSGNQMGTNPEQD PGQHAIPLEGTLTHTRTHSDWDHLD TAMN*
695	6192	A	719	1	5127	
696	6193	A	720	965	9275	
697	6194	A	721	3	376	
698	6195	A	722	1	380	
699	6196	A	723	104	462	
700	6197	A	724	762	902	
701	6198	A	725	78	747	LRRGRSRETNEEPPPTVQVQGGPGP QREEKQKTKMAKFVIRPATAADCS DILRLIKELAEYEMEEQVILTEKDL LAEDGFGAEHPFYHCLVAEVPKEHW TSEGHSIVGFAMYYFTYDPWIGQ VICILEDFFVMSDYRGSGIGSEILK NLSQVAMRCRCSSMHFLG*PEWVN EPS\NFYKRRGAS\DLSS*RRGWRL FQGSCKGVIWLKNGPTEGVEGVAC C
702	6199	A	726	149	460	
703	6200	A	727	1	501	
704	6201	A	728	1	391	SPLNKVQLINELNEREVQLGVANK VSWHSEYKDSAWIFLGGLPYDLTK GDII CVFSQ\QRSTIVADNFNGIKIK GRTIRVDHVSNYRAPKDSEIDDVT RQLQEKGC GARTSPSLSESEDEK

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						PTKKP
705	6202	A	729	18	240	
706	6203	A	730	254	1223	SPLTRVKLINELNEREVQLGVADKV FWHSEYKDSA WIFLGGLPYGLTNEG DIICVFSQYGEIVNINLVRD\KKTGK SKGFCFLCYEDQRSTILAVDNFNGI KIKGRTIRVDHVS\NYRAPKDSIEDID DVTRQLQEKSGGARPPSPTLSSESSE DEKPTKKHKDKK\EKKKKKKEKE KADREVQAEQPSSSSPRRKTVEKD DTGPKKHSSKNSERAQKSEPREGQ KLPKSRTAYSGGAEDLERELKKEKP KHEHKSSSRREAREEKTRIRDRGRS SDAHSSWYNGRSEGRSYRSRSRSR DKSHRHKRARRSRERESSNPSDRW RH
707	6204	A	731	2143	2346	
708	6205	A	732	2016	2206	
709	6206	A	733	90	401	
710	6207	A	734	276	488	
711	6208	A	735	186	537	IWFPLRRRKARQEEKSGLGAPRSPS HNYPGPGYLGCLGKTNTS*TYILDQS NIGKRVA\AILN*ILGGRKLRLEKSL SCQPKVEELYERVAW/IP*KPGCLLL VSVKVRNVFDWCTWVY
712	6209	A	736	3	318	
713	6210	A	737	1	280	REPTMVLSPADKTNVKAAWGKVG AHAGEYGAEALERMFLSFPTTKTP VNFKLLSHCLLV\TLAAHLP AEFTP VHASLDKFLGVSSTVLTSKYR
714	6211	B	738	34	264	MVLSPADKTNVYFPFHDLSHGSAQ VKGHGKKVADALTNAVTVDDMP NALSALSDLHAHKLRVDPVNFKLL STACW*
715	6212	A	739	3	190	EPTMVLSPADKTNVKAAWGKVGA H/AGEYGAEALERMFLSFPTTKIQIP LSWSLGGHASCPLG
716	6213	B	740	12	298	MVLSPADKTNVKAAWDLLPALRPE PRLCQVKGHGKKVADALTNAVAH VDDMPNALSALSDLHAHKLR LAW*
717	6214	A	741	2	392	QTQREPTMVLSPADKTNVKAAWG KVG AH/AGEYGAEALERMFLSFPTT KTYFPFHDLSHGSAQVKGHGKKVA DALTN AV/AHVGGPVNFKLLSHCLL VTAAHLP AEFTP\AVNASLDKFLV SVSTVLTSKYR
718	6215	A	742	623	1235	SNLVELSNTLSWSSGGKVGAHAGE YGAEALERMFLSFPTTKTYFPFHD SHGSAQVKGHGKKVADALTNAVA HVDDMPNALSALSDLHAHKLRVDP VNFKLL\SH\CLLVDPGPAHFPAEF TPAVHASLDKSTKTYFPFHDLSHGS AQVKGHGKKVADALTNAVAHVDD MPNALSALSDLHAHKLSVDPGNFK LP SHLPAGDPC
719	6216	A	743	117	403	
720	6217	C	744	62	370	MKSMRKQAPIITAFILTSRSGKNWIP

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						KLSASVNASLKIPVQCLEILPTTHCS SRDLIFQKFNNLMNQYLIYLGMLSV DTEEDTQLASLFPGEKHSSVSFVCP*
721	6218	A	745	3	1242	AAPQAGLSPVAIAAAIQLHLHSTQC SSPNTCCCLPRRTRATIIYSRWSYHP LGSVP*SP*PFQEAS/ALTLPACSFY GPLT*FQPKP*GSFPLSQ*MEYTIGL YT*TFHCPGTSRRQIPSSYLNCKDAF LPLL/SNPPQCRPFTGVGLVDVLTGF ETNNKYEIKNSFGQRVYFAAEDTD CCTRNCCGSPRPFTLRIDNMGQEV TLERPLRCSSCCCPCLQEIKSLDEQ CVVGKISKYWTGILREAFTDADNFG IQFPLDLVKMKAVMIGACFLIDRN CSPAMEQSWMENYFDEMTEIGFRR SVITNFSELKEHVLTHCKEANKNLD KMLDEWLTRKNSVEKTLNELMEV KTINEKLTIGKISKYWSGFVNDVFT NADNFGIHPADLDVTVKAAMIGA CFLFAFRLGSELHN
722	6219	A	747	129	1235	EGCAAAPDSLEAQKRKPSPGPSL DLVSLGSGNSGSQRTVLIMDKQNS QMNASHPETNLPVGYPPQYPTAFQ GPPGYSGYPGPQVSYPYPAGHSGP GPAGFPVPNQPVYNQPVYNQPVGA AGVPWMPAPQPPLNCPGLEYSQI DQILIHQQIELLEVLTFETNNKYEI KNSFGQRVYFAAEDTDCCTRNCCG PSRPFTLRIDNMGQEVITLERPLRCS SCC\CPCLQEIEIQAPPGVPIGYVIQ TWHPCLPKFTIQNEKREDVLKISGP CVVCSGCGDVFEEKSLDEQCVVG KISKHWTGILREAFTDADNFGIQFP LDLDVKMKAVMIGACFLIDFMFFA ESTGQPGNKNSGVWVVGFS
723	6220	A	748	647	797	
724	6221	A	749	2	424	
725	6222	A	750	2	460	ARATHREPTMVLSPADKTNVKAA WGKVGAGHAGEYGAEALERMLLSF PTTPTYFPHFDLNHGSAAHVKGHGK NVDDALTNAVTHVYMPNSLYALS DLHPHNLRMDPVNFMLLSHCLL*T LVVHLPAELTPAVHASLNNVLESER TELTSSTS
726	6223	A	751	1	456	RPRRPQREPTMVLSPADKTNVKAA WGKVGAGHAGEYGAEALERMFL/SF PTTKTYFPHFDLSHGSSQVKGHGKK VADALTNAVGHVDDMPNALSALS DLHAHKLKRVDPVNFKLLSHCLLV LAAHLPAEFTPAVHAFLDKFLASVS TVLTSKYR
727	6224	A	752	1	594	PRLFWSPTQREPTMVLSPADKTN VKAAGKVGAGHAGEYGAEALER MFLSFPTTKTYFPHFDLSHGFAQVK GATGKKVDDIALTKRRGAPLDDMP NALVRPLKRPCTTHKAFGVEPGSTS KLLASHLPCLGEPWAAHLPRPSFNP WRLQRLPWGQSFLGFLVEEPLLEPS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KIPVKA WKPSVGHCFAPWGFPPAP SSL
728	6225	A	753	2	386	
729	6226	A	754	33	476	
730	6227	A	755	5	417	
731	6228	A	756	1	412	
732	6229	A	757	2	446	
733	6230	A	758	3	713	
734	6231	A	759	87	236	
735	6232	A	760	181	322	
736	6233	A	761	213	427	
737	6234	A	762	213	422	
738	6235	A	763	1	732	
739	6236	A	764	31	1074	TLILSGFTVKQVY AIDQIFSSRLTIT IKMFCGDYVQGTIFPAPNFPIMDA QMLGGALQGFCDK DMLINILTQR CNAQRMMIAEAYQSMYGRDLIGD MAREQLSDHFQDVMAGLMYPPPLY DAHELWHAMKGVGTDENCLIEILA SRTNGEIFQMREAYCLQYSNNLQE DIYSETSGHFRDTLMNLVQGTREEG YSDPAMAAQDAMVLWEACQKKTG GHKTMLQMLCNKSYQQLRLVFQE FQNISQDMVD AINECYDGYFQELL VAIVLCVRDKPAYFAYRLYSAIHDF GFHNKTVIRILIARSEIDLLTIRKRYK ERYGK\SLFHDIRNFASGHYKKSTG LPIC
740	6237	A	765	613	926	
741	6238	C	766	79	405	MIGGTPQMFFISGAKGQWSPSLQPP PRAHRSPWAPSSKSTSGGTAALGS LGSKDYFPRTGDGVVELRRSDQRR AHLPGCPTVLR TLLPQQRGDRDLQ QLRHHELRL*
742	6239	A	767	1	321	
743	6240	A	768	110	431	
744	6241	B	769	756	1533	MREIVHIQAGQCGNQIGAKFWEPW KASSIELSQCRNSPSKVFRSKEHDGL PVTPTTR*
745	6242	A	770	20	453	GIPGSTISLFCSEKKLREVERIVKAN DREYNEKFQYADNRIHTSKYNILTF LPINLFEQFQRVANAYFLCLLILQLI PEISSLTWFTTIVPLVLVITMTAVKD ATDD\ILQNEKWMNVKVGDIKLEN NQFVAADLLLLSSSEPH
746	6243	A	771	1	1014	
747	6244	A	772	128	2654	LVQDHKAGEHQVGAMARLGNC SL TWAALIILLPGSLEECGHISVSAPIV HLGDPITASCIKQNC SHLDPEPQIL WRLGAELQPGGRQQLSDGTQESII TLPHLNHTQAF LSCCLNWGNSLQIL DQVELRAGYPPAIPHNL SCLMNLTT SSLICQWEPGPETHLPTSFTLKSFKS RGNCQTQGSILDCVPKDGQSHCCI PRKHLLLYQNMGIWVQAENALGTS MSPQLCLDPMDVVKLEPPMLRTMD PSPEAAPPQAGCLQLCWEPWQPG L

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HINQKCELRHKPQRGEASWALVGP LPLEALQYELCGLLPATAYTLQIRCI RWPLPGHWSWSPSLELRTERAP TVRLDTWWRQRQLDPRTVQLFWK PVPLEEDSGRIQGYVVSWRPSGQAG AILPLCNTTELSCTFHLPSEAQEV VAYNSAGTSRPTPVVFSES RGPALTRLHAMARDPHSLWVGWEP PNPWPQGYVIEWGLGPPSASNSNKT WRMEQNGRATGFLLENIRPFQLYE IIVTPLYQDTMGPSQHVYAYSQEMAP SHAPELHLKHIGKTWAQLEWVPEP PELGKSPLTHYTIFWTNAQNQSF SAILNASSRGFVLHGLEPASLYH IHLMAASQAGATNSTVLTLMTLT PEGSELHIILGLFGLLLLLTCLCG TAWLCCAPTGRIPSGQVSQTQLTAA WAPGCPQSWRSCDPDRDSGWGRHLK *AVLSPHILVCRMPSSCPALARHPS PSSQCWRRMKRSRCPGSPITAQR PVASPLWSRPMCSRGTQEQQFPSP NPSLAPAIRSFMGSCWAAPQAQGGQ GTISAVTPLSPSWRASPPAPSPMRT SGSRPAPWGPW
748	6245	A	773	123	2486	
749	6246	A	774	128	2573	LVQDHKAGEHQVGAMARLGNCSL TWAALIILLPGSLEECGHISVSAP IVHLGDPITASCIHKQNCSHLDPE PQILWRLGAELQPGGRQQLSDGTQ ESIITLPHLNHTQAFSLCCLNWGNS LQILDQVELRAGYPPAIPHNLSCL MNLTTSSLICQWEPGPETHLPTSFT LKSFKSRGNCQTQGDSILDCVPKDG QSHCCIPRKHLLLYQNMGIWVQAEN ALGTSMSPLCLDPMDDVVKLEPPML RTMDPSPEAAPPQAGCLQLCWEPWQ PGLHINQKCELRHKPQRGEASWAL VGPLPLEALQYELCGLLPATAYTLQ IRCI RWPLPGHWSWSPSLELRTER APTVRLDTWWRQRQLDPRTVQLFW KPVPLEEDSGRIQGYVVSWRPSGQ AGAILPLCNTTELSCTFHLPSEAQEV ALVAYNSAGTSRPTPVVFSES RGPALTRLHAMARDPHSLWVGWEP PNPWPQGYVIEWGLGPPSASNSNKT WRMEQNGRATGFLLENIRPFQLYE IIVTPLYQDTMGPSQHVYAYSQEMAP SHAPELHLKHIGKTWAQLEWVPEP PELGKSPLTHYTIFWTNAQNQSF SAILNASSRGFVLHGLEPASLYH IHLMAASQAGATNSTVLTLMTLT PEGSELHIILGLFGLLLLLTCLCG TAWLCCAPTGRIPSGQVSQTQLTAA WAPGCPQSWRRMPSSCPALARHPS PSSQCWRRMKRSRCPGSPITAQR PVASPLWSRPMCSRGTQEQQFPSP NPSLAPAIRSFMGSCWAAPQAQGGQ GTISAVTPLSPSWRASPPAPSPMRT SGSRPAPWGPW
750	6247	A	775	151	273	

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751	6248	A	776	785	920	
752	6249	A	777	332	473	
753	6250	A	778	264	387	
754	6251	A	779	257	354	
755	6252	A	780	101	290	
756	6253	A	781	21	215	
757	6254	A	782	158	955	KMTSSSEQEEDKNNQSATPRQTGP ATTMNSKGQYPTQPTYVQPPGNP VYPQTLHLPQAPPYTDAPPAYSELY RPSFVHPGAATVPTMSAAPPGLASL YLPMAQ\SVAVGPLGSTIPMAYYP VGPIYPP\GST\VLGGKGGYDAGARF GAGATAGNIPPPPPG\CPPNAAQLA VMQGANVLVTQARKGNFFMGGSDG GYTHLVRNQGHLCAREKTSHTLQH FSQCNCFSHINLKLQFRHMLLGCLS GAQTRHFSNLIRNHVMVAVPP
758	6255	A	783	167	342	
759	6256	A	784	368	525	
760	6257	A	785	311	487	
761	6258	A	786	148	298	
762	6259	A	787	164	314	
763	6260	A	788	232	382	
764	6261	A	789	2	390	
765	6262	A	790	3	376	AQKAGLGTIFIMTCSPLLLTLLIHCT GSWAQPVLTPPPSVSAAPGQKVTIS CSGSGSNIGNNYVSWYQQLPDLFH AHK*LLPGSRDSGLEAR*QPRQGS GDHHTLQTKQQQVRGQQLPEPDA
766	6263	A	791	2	353	
767	6264	A	792	2	382	
768	6265	A	793	3	654	
769	6266	A	794	9	885	
770	6267	A	795	1	412	
771	6268	A	796	2	616	WPIDIDIQCGGIPRDNLHDDLPSPP HPSHCPTTPRAVSAEGRTRDQSSM TCSPLLLTLLIHCTGPWAQSVLTQPP SVSATPGQRTVISCSSGSRNIGDNYV SWYKQLPGTAPQLLIYDNNKRTSGI PDRFSGSKS\GTSATLGITGLQTGDE ADYYCGTWDTILSAGVFGGWTKLT VLGQPKAAPSVTLFPPSSEELQANK AT
772	6269	A	797	489	715	
773	6270	A	798	20	371	
774	6271	A	799	181	382	
775	6272	A	800	353	479	
776	6273	A	801	3	368	HEAASSSSASPFQTKIEKMVDLTQV MDDEVFMAFASYATHLSKMLMS TATAFYILTRKVFANPQHCVTFGKG ENAKKYLRTDDRVRVRAHLNDL ENIIPFLGIGLLYSLSGADPSTAI
777	6274	A	802	246	363	
778	6275	B	804	55	366	MGHFTTEEDKATITSLWGKVNVEDA GGETLGRLLVVYPWTQRFFDSFGN LSSASAIMGNPKVKAHGKKVLTSL GDAIKHLDDLKGTFAQLPHRLVIVA

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						LSSSVK*
779	6276	A	805	129	409	
780	6277	A	806	24	253	
781	6278	A	807	32	433	
782	6279	A	808	15	468	
783	6280	A	809	25	1404	APSPDAMGHFTEEDKATITSLWGK VNVEDAGGETLGRLLVVYPWTQRF FDSFGNLSSA\SAIMGPNPKVKAHGK KVLTSLGDAIKHL\DDLKGTFAQLE *TCTCDKL\H\VDPENFKLLGNVLV TVL\AIHFGKEFTPEVQSFLGRKMV TGVASALSFPDYH
784	6281	A	810	113	387	
785	6282	A	811	1330	1465	SECCGLSRPGHWPHFI*WLPSL/CL DVPT*QRKGLVRNWVLP*NLWE LLP/ALAGSGEGHLKNMTGSKLSRM PNRISDSESE/GVNTARIHGEMFWR GDNWACTCCRGARSLAADSADPA TGLTSFPLASASSA\TRASIPKRCN SWFSTRP
786	6283	B	812	17	718	MVVVAAAPNPADGTPKVLLLSGQP ASAAGAPAGQALPLMVPAQRGASP EAASGGLPQARKRQRLTHLSPEVPS LPRKLKNRVAAQTARDRKKARMSE LEQQVNQKLLLENQLLREKTHGLV VENQELRQRLGMDALVAEDFCLLQ SDILLGILDNDPVMFFKCPSPEPAS LEELPEVYPEGPSSLPASLSLVGTS SAKLEAINELIRFDHIYTKPLVLEIPS DTG*
787	6284	A	813	464	714	
788	6285	A	814	349	581	
789	6286	A	815	223	513	DHEEPQAREGDQSVHRPHAERTGQ PGMWRHPRLDECQPQELL/TKHSTS PSQEKEVHTPHP/RPLESCWASLNR DPQHHSSPTPGKTSKSRENKEIISQ
790	6287	A	816	384	464	PLPQLLRFAQPKPEAHLTPARPQPK RTCHGLTCRRGVSPGWRRDGPWRT HRSAGATRRPIQETASVPQPEAAPP HRARGSGKMRDGKPGAGNTERRD PQSRTVGLNKKNSTPHQSPQPPADV *TSAGG
791	6288	A	817	1	255	IVMGHSMLPHF*IWSPPPGAAARL APLSGAGHSGPRLAPWT*AGQLQT QSLVR\*PELGKSELSAPSLVIGSW MDM*PKPGQ
792	6289	B	818	191	1072	MWRSLRLRXRGTPSPESAGGWPQ RFYESGANHPVSSPGLRPADRKEEV LFRMFSIHTGEALAI\AVATEWDSQQ DTIKYYT\HMLTTL\CNTSLDNPTQRN KDQLIRAAVKFLDTDTICYRVEEPE TLVELQRNEWDP\IEWAEKRYGVEI SSSTSIMGPSIPAKTREV\LVSHLAS NTWALQGIDGSRPCCCSRL\EEYQI PEVGGNIEWAH\DYELQELRARTAA GTLFIHLCSESTTVKHKLKE*
793	6290	A	819	1518	1891	



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794	6291	A	820	217	491	
795	6292	A	821	1789	2411	KTYWRKKVEKVVVSNR\LVTSPCVC IVTSTYGTANMGENH*KLQALKE TTSTMG/YMASQRKHRGIKPLTL IEYLKAKRPEGLIRTDKS\VKDLVIL LY\ETALLSSGFQSWKIPRHH*QVS YRMIKL\GLGIDEDGPYLLDDTSAVA VNLKELPPLEGDDDTFTHGKEVG LLGLRGWTLPVSVLYNSSDNIFFQG CFPLFLVNI
796	6293	A	822	592	1122	
797	6294	A	823	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
798	6295	A	824	38	531	APSPDA\MGHFTEEDKATIT\SLWGK VNVEDAGGETLGRLLVVYPWTQR FFD\SFGNLSSASAIMGNPKVKAH GKKVLTSLGRCHKSTWDDLKGT AQA*SELHL*QSCNVDPENFKLLG\ NVLVTRFGQSHFRQKNFTPEGCRAS WAE/MMGDLQLASALVPSRYH
799	6296	A	825	1	278	
800	6297	A	826	80	591	RGCKREGLSMSSLIRRVISTAKAPG AUGPPTVQAVLVDRTHLHFRDQIG HGPLPSWTSLCPGGVAGRSLNKL KNMGEIPESLPGCDFTNVVKTTCS GLDINDLQLLFNEILQTVFSRSNPPA RAAYPSWLLLPQKGSRIEIEA\VAIQ GPLTTAFILSGDPCCVWDC
801	6298	A	827	1	396	
802	6299	A	828	1	346	
803	6300	A	829	3	720	RGIPASRWARKAVVLLCASDLLLLL LLLPPAG\SGRAEGSPGTP\DEFTPP RKKKKDIRDSNDADMARLLEHWE KHDD\EEGDLPEHKRPSAPVDFSKI DPG\KPESILKMTKKGKTLMMFVT VSGSPTEKETEEITSLWQ\SLFNAN YDVQRFIVGSDRAIFMLRDGSYAW EIKDFLVGQDRCADVTLEGQVYPG KGGGSKEKNKTKQDKGKKKKEGD LKSRSKEENRAGNKREDL
804	6301	A	830	349	567	
805	6302	A	831	1098	1684	
806	6303	A	832	2	441	PCRNSRVENFVSMWVCSTLWRVRT PPGSG/GLLPASGCHGPAASSYSA SAEPARVRALVYGHGDPKVVET VIPGHTWQLRNVA*PTLRR*FERNT HSSLDDMNISVWLCA*LNLELAA VRGSDVRVKMLAAPINPSDINMIQG
807	6304	A	833	3	421	ASMWVCSTLWRVRTPPGSG/GLL PASGCHGPAASSYSASAEPARVRAL VYGHGDPKVVVEGITRELFQRF WIFLQLITAVISSASTVLKNLELAAV RGSDVRVKMLAAPINPSDINMIQGN

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						YGFLPELPAVGGNEGV
808	6305	A	834	2	611	ILQLGRGRAVRVCSTLWRVRTPA\G SGG/GLLPASGCHGPAASSYSASAEP ARVRALVYGHGDPKVVVELKNL ELAAVRGSDVRVKMLAAPINPSDIN MIQGNYGLLPELPAVGGNEGVAQV GAEGSNVTGLKPGNWVPA\NAGL RTWRNRG*VHPKEALIQVPSDIPLQ SAATLGVPNCTAYRMLMDFEQLQP GDSVIQNAS
809	6306	A	835	159	312	
810	6307	A	836	637	974	
811	6308	A	837	240	419	
812	6309	A	838	20	283	
813	6310	A	839	508	715	IPGNFEPSRLGRG*KTQACSPSLLWE FWLTQYLPALGAGHILKNFTTFPVI\ SCVSKLSTLFGGKMPEN
814	6311	A	840	3	362	
815	6312	A	841	7	479	GAIMGVDIANKDRRVRRKEPKSQD IYLRLLVKLYRFLARRTNSTFNQVV LKRLFMSRTNRPLSLSRMIRKMKL PGRENKTAVVVGTTDDVRVQEV KLKVCALRVTSRARSRLRAGGKIL TFDQLALD/SPYVRSKGRKFERARG RRASRGYKN
816	6313	A	842	2	723	CAVNSAEQRGAIMVSGHLFITKDRK VR\RKEPKSDIYLRLLVKLYRFLA RRTNSTFNQVVLKR/LFMSPHQPGP PLSLS\RMIPED*SFPGPGKQRRVV VG\TITD\DVVRVQEV\PKTERVCCTC AVDQAGAPQAAILRAGGQDSFTFR PSLALGTSPKGLVGTCSWLFRRFP RGPRRWYPAIFGKGPGQTAPAQATP KPYV\RSKGPKEFERARG\RRASRGY KKLTLDPSTLLKKFLPKKK
817	6314	A	843	1221	2238	EPLIVCVCFCLCPPLFFFSFLGSAEK AVLEQFGFPLTGTEARCYTNHALSY DQAKRVPRWVLA\EHIFQKAR*MG DADRKHCKFKPDNPIPTTFSFNFEN YVGSGWSRGHMAPAGNNKFSSKA MAETFYLSNIVPQDFDNNSGYWNRI EMYCRELTERFEDVWVVSGLTLP QTRGDGKKIVSYQVIGEDNVAVPS HLYKVILARRSSVSTEPLALGAFVV PNEAIGFQPQLTEFQVSLQDLEKLS VLVFFPHLDRTSDIRNICSVDTCALL DFQEFTLYLSTRKIEGARSVLRLEKI MENLKNAEIEPDDYFMSRYEKKLE ELKAKEQSGTQIRKPS
818	6315	A	844	1	306	
819	6316	A	845	216	339	
820	6317	A	846	425	553	
821	6318	A	847	190	334	
822	6319	A	848	241	435	
823	6320	C	849	280	450	MLEKNWCPSLQVPIILNWAQPCGKI LTECCTLGYSLIQGDWTFIRKHAR TRLVKR*

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824	6321	A	850	1	301	
825	6322	A	851	2	3484	
826	6323	B	852	225	326	MAFKDTGKTPVEPEGAIHRIRITLTS RKRKSFEK*
827	6324	A	853	348	515	AFKDTGKTPVE\PELAIHRI\IRITLTS\ RNVKSLEK\VSASFVMRGGGGIGRK ATSFTR
828	6325	A	854	42	529	SARSLLHDSPHVRSRRGTSVRKPA RNRPLAFKDT\GKTPVEPEV\AIHRI RITPNKAANVK\SLEKVVCLTLIRRA QKEKNFQS*KGPVS/RLPYPRFLRIH FQKTPCGLKVFKDVGVRFPRWRI HK\RL\DLHSPS\EIVKQITFHQYLSP GVEVEVHHLQML
829	6326	A	855	14	345	
830	6327	A	856	1	396	
831	6328	A	857	3	718	RGIPASRWARKAVVLLCASDLLLLL LLLPPAG\SGRAEGSPGTP\DEFTPPP RKKKKDIRDSNDADMARLLEHWE KHDD\NEEGDLPEHKRPSAPVDFSKI DPSKPESILKMTKKGKTLMMFVTV SGSPTEKETEEITSLWQGS\LFNANY DVQRFIVGSDRAIFMLRDGSYAWEI KDFLVGQDRCADVTLEGQVYPGKG GGSKEKNKTKQDKGKKKKEGDLK SRSSKEENRAGNKREDL
832	6329	A	858	80	349	
833	6330	A	859	504	738	
834	6331	A	860	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFDFSFGNLSSA SAIMGNPKVK\AHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSRYH
835	6332	A	861	38	608	APSPDA\MGHFTEEDKATITSLWGK\ VNVE\ DAGGETLGRLLVVYPWTQR FFD\SFGNLSSASA\IMGNPKVK\AH GKKVLTSLGDAIKHLDDLKGTFAQ L\SELH\CDK\LVHDPENFKLLGEML LVTVLAIPFRAKEFTPEGCRASWQ KQKMAEDGDLQWPSGPVPPDTEA SWPMNSEAFKDKAFILASNYK
836	6333	A	863	727	1089	
837	6334	A	864	432	742	
838	6335	A	865	184	352	
839	6336	A	866	204	394	
840	6337	A	867	1	2286	MDLLGRVGS\WALQSSCLTDPELW GWEGTPRFLAAAAQFGGPVLKAQ ACSLGAGIAPTELPRPVRWSLLFLA VRSNYQALWPQSPAGLPLVPQPETP RGANIPSPVVHAGDDRGWHMTV EQKFG\LSAEIKEADPLAASEASQP KPCPPEVTPHYIWIDVRACSPTKAV GCSTWGARTVPGVGVAEPKAFGKL GQSAQNPSA\VSAGPRFLVQRFEIA KYCSDQVEIFSSLLQRSMSLNIGRA KGS\NRHVAAIGPRFKLLTLGLSLL

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						HADVVPNATIRNVLRKIYSTAFDY FSCPPKFPTQGEKRLREDISIMIKFW TAMFSDKKYLTASQLVPPADIGDLL EQLVEENTGSLSGPAKDFYQREFDF FNKITNVSIIKPYPKGDERKKACLS ALSEVTVQPGCSLPSNPEAIVLDVD YKSGTPMQSAKAPYLAKFKVKRC GVSELEKEGLRCRSDSEDECSTQEA DGQKISWQAAIFKLGDDCRQDMLA LQIIDLFKNIFQLVGLDLFVFPYRVV ATAPGCGVIECIPDCTSRDQLGRQT DFGMYDYFTRQYGDESTLAFQQAR YNFIRSMAYSLLLFLLQIKDRHNG NIMLDKKGHIIHIDFGFMFESSPGGN LGWEPDIKLTDEMVMIMGGKMEA TPFKWFMEMCVRGYLAVRPCLGST GDRVQQIESCLGDVQDVAGEAYM DVVVS LVTIMLDTGLPCFRG/QIKFL KHRFSPNMTEREAANFIMKVIQSCF LSNRSRTYNMIQYYQNDIPY
841	6338	A	868	3	164	
842	6339	A	869	1	5340	
843	6340	A	870	649	1028	
844	6341	B	871	1	5823	MCPVDFHGIFQLDERRRDAVIALGI FLIESDLQHKDCVVPYLLRLKGLP KVYWVEESTARKGRGALPVAESFS FCLVTLSDVA YRDP SLRDEILEVLL QVLHVLLGMCQALEIQDKEYLCKY AIPCLIGISRAFGRYSNMEESLSKL FPKIPPHSLRVLEELGVRRRSFNDF RSILPSNLLTVCQEGTLKRKTSSVSS ISQVSPERGMPPPSPGGS AFHYFEA SCLPDGTALEPEYYFSTISSFSVSPL FNGVTYKEFNIPLEMLRELLNLVKK IVEEAVLKSLDAIVASVMEANPSAD LYYTSFSDPLYLTMFKMLRDTLYY MKDLPTS FVKEIHD FVLEQFNTSQG ELQKILHDADRIHNELSPLKLRCQA SAACVDLMVWAVKDEQGAENLCI KLSEKLQSKTSSKVIAHLPLLICCL QGLGRLCERFPVVHVS VTPSLRDFL VIPSPVLVKLYKYHSQYHTVAGNDI KISVTNEHSESTLNVMSGKKSQPSM YEQLRDIAIDNICRCLKAGLTVPVI VEAFLASLNRLYISQESDKDAHLIP DHTIRALGHIAVALRDT PKVM EPIL QILQQKFCQPPSPLDVLIIDQLGCLVI TGNQYIYQEVWNL FQQISVKASSV VYSATKDYKDHGYRHCSLA VINAL ANIAANIQDEHLVDELLMNLELFV QLGLEGKRASERASEKGPALKASSS AGNLGVLIPVIAVLTRRLPPIKEAKP RLQKLFRDFWLYSVLMGFAVEGSG LWPEEWYEGVCEIATKSPLLTFPSK EPLRSVLQYNSAMKNDTVTPAELSE LRSTIINLLDPPPEVSALINKLDFAM STYLLSVYRLEYMRVLRSTDPDRFQ VMFCYFEDKAIQKDKSGMMQCVIA

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						VADKVFD A FLNM MADKAKTKENE EELERHAQFLLVNFNHHKRIRRV DKYLSGLVDKFPHLLWSGTVLKT LDILQTL SLSL SADIHKDQPYDIP APYRITVPDYEARESIVKDFAARC GMILQEAMKWAPT VTKSHLQEYLN KHQNWVSGLSQHTGLAMATESILH FAGYNKQNTTLGATQLSERPACVK KDYSNFMASLNLNRNYAGEVYGM RFSGTTGQMSDLNKM MVQDLHSA LDRSH PQHYTQAMFKLTAMLISSK DCDPQLLHHL CWGLRMFNEHGM ETALACWEWLLAGKDGVEVPFMR EMAGAWHMTVEQKFLGSAEIKEA DPLAASEASQPKPCPEVTPHYIWD FLVQRFEIAKYCSSDQVEIFSSLLQR SMSL NIGGAKGSMNRHVAAIGPRF KLLTLGLSLLHADVVPNATIRNVLR EKIYSTAFDYFSCPPKFPTQGEKRLR EDISIMIKFWTAMFSDKKYLTASQL VPPDNQDTRSNLDITVGSRQQATQG WINTYPLSSGMSTISKKSGMSKKTN RGSQ LHKYMKRRTLLSLLATEIE RLITWYNPLSAPELELDQAGENSV NWRSKYISLSEKQWKDNVNLAWSI SPYLA VQLPARFKNTEAIGNEVTRL VRLDPGAVSDVPEAIKFLVTWHTID ADAPELSHVLCWAPTDPTGLSYFS SMYPHPLTAQYGVKVLRSFPDAI LFYIPQIVQALRYDKMGYVREYILW AASKSQLLAHQFIWNMKTNIYLDE EGHQKDPDIGDLLDQLVEEITGSL GPAKDFYQREFDFNKITNVSAIHKP YPKGDERKKACLSALSEVKVQPGC YLPSNPEAIVLDIDYKSGTPMQSAA KAPYLAKFKVKRCGVSELEKEGLR CRSDSEDECSTQEADGQKISWQAAI FKVGDDCRQDMLALQIIDLFKNIFQ LVGLDLFVFPYRVVATAPGCGAIEC IPDCTSRDQLGRQTDGMYDYFTR QYGDESTLA FQQARYNFIRSMAAY SLLLFLQSKDRHNGNIMLDKKGHI IHIDFGFMFESSPGGNLWEP RHQA DG*
845	6342	A	872	1	337	
846	6343	A	873	1	337	
847	6344	A	874	838	929	
848	6345	A	875	21	338	
849	6346	A	876	2	424	
850	6347	A	877	3	452	
851	6348	A	878	3	604	PTLLVPTDSERTHPWLLSPADK\TN VKA\AWGKVG AHAGEYGAEALER MFLSFPTTKTYFP HFDLSHG\SAQV KGHG\KKVADALTN AVAHVDDMP NALSALSDLHAHKL RVGPGSTFKL LK/HTCLAGEPWAAHLPAEFQPLA VATSSSLGTFPGLLVEAPLLTFQIPV KAGSLGWPLFFCPLGLPPSPSPFLH

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						PYPRGL
852	6349	A	879	2	416	EGKPRTSGAEHRSCRGKASMSPNF KLQCHFILIFLTALRGESRYLELREA ADYDPFLLFSANLKRELAGEQPYRR ALRCLDMLSLQGQFTFTDDRPQLH CAGFFISEPEESLPFHYDQ*SIDGK AGNFLKVLMMGRIL
853	6350	A	880	1	187	
854	6351	A	881	2	1099	PRVRGRVGEVGRKAQDLRSRQHS SCRGKASMSPNFKLQCHFILIFLTAL RGESRYLELREAADYDPFLLFSANL KRDVAGEQPYRRALRCLDMLSLQG QFTFTADRPQLHCAAFFISEPEEFITI HYDQVSIKSGGGDF/LWKVFDGWI LKGEKFPASSQDHPLPSAERYIDFC ESGLSRRSIRSSQNVAMIFFRVHEP GNGISHLTIKTDPNLFSAFISSEFQ MGKFNLG*FPHQHRNCSFSIYPVVI KISDLYPGGHVNGSFS*RKSSAGCE GIGDFVELLGGTGLDPSKMTPLADL CYPFHGPAQMKVGCNTVVRMVS SGKHVNRVDLRLVQLEAVTSWEN PNGNSIGEFCLSGL
855	6352	A	882	2	645	HGIQAHGQIPSYKTIGGRDDSFHTFF SETGAGKHVPRLL*NWKPTVMDE VRTGTYCQLFHLEQFITARKIAANN YARGHYTIGKEIIDLVLDRIKLAD QCTGLQGFLVFHSFGGGTGSFGTSL LMEKLSVDYGGKSKLEFSIYPAPQV STAVVEPYNSILTTHTTLEHSDCAF MEEGEFSEAREDMAALEKDYEEVG VDSVEGEGEEEGEEY
856	6353	A	883	90	1657	EATTSPLRLRHQLGSREAATMRECI SIHVGGAGVQIGNACWELYCLEHGI QPDGQMPK*PKPLGEGDDSFNTFFS ETGAGKHVPRAVFDLEPTVIDEVR TG\TYRQLFHPEQLITGKEDAANNY ARGN\YTIGKEIIDLVLDRIKLADQ CTG\LQGFLVFHSFSGGGTGSFGTS\ LLMERLSVDYWQESPSLEFSIYPAA PRFPQPVVEPYN\SILPTQHPPWEHS DCA\FM\VDNEAIYDICRRNLDIERP TYTNLNRLLSQIVSSITASLRFDGAL NVDLT\EFQTNLGPYPPIHFPL\ATY APCHLC*RKPTHEQLFCSQRSPKCF AFEPTNPDG*NGDPRVHG*IHWLAC LLL\RGDVPKRCQMLPIAHPSKP KRS\IQFVDWCP\TGFKVGINYQPA TVVPGGDLA\KVTREAVCMLSKHH SPFAEAWARPGPTSFDLMLCQACPF VHWYLG\EGMEEGEFSK\ARKDMA ALARKDYEEVG\VDVKG\EGEEEGK GILIHSLFGPCSMSCSQNFSFSLTDR R
857	6354	B	884	46	386	XIRHESGSRSHSHCSTLSSIGDVAKK LGEMWNNTAADDKQPYEKKAACL KEYEKDIAAYRAKGPDAAKKG VVKAEKSKKKKEEEDEEEDDEE

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						EEEDXEDDDEEDDDDE*
858	6355	A	885	263	484	
859	6356	A	886	146	826	TWKGKDPKKPRGKMSSYAFFVQTC RGG\HKKKHPDASVNFS/ESFSKKCS ERWKTMSA*R/EKGKFEDMAKAD KARYEREMKTYIPPQRGRQKRKFK DSQLHPRGPSS\AFFPLLALEYRPKI K\GEHP\GL\SIGDVAKKLGRDVGIN TAAD\DKQPYEKK\AAKLKEYEYKD IAAYRAKGKPDAAKKG\VVKAES KKKKEEEEDEEEG\DEEDEEEDE EDEEDEEEDER
860	6357	A	887	1	456	RPRRPQREPTMVLSPADKTNVKA WGKVGAGAHAGEYGAEALERMFL/SF PTTKTYFPHFDLSHGSSQVKGHGKK VADALTNAVGHVDDMPNALSALS DLHAHLRVDPVNFKLLSHCLLV LAAHLPAEFTPAVHAFLDKFLASVS TVLTSKYR
861	6358	A	888	2	435	QTQREPTMVLSPADKTNVKA KVGAGAHAGEYGAEALERMFLSPTT KTYFPHFDLSHGSAQVKGHGKKVA DALTNV/EHVDDMPNALSALS DLHAHLRVDPVNFQAPKATGLLVDP GPAHFPGRVSPRLQGFLGKFLGF C
862	6359	A	889	9	390	NSARATDSERTHHGARLLPDKTNV KA\AWGKVGAGAHAGEYGAEALERM FLSPTTK\TYFPHFDL\SHG\SAQV KGP TAKKVAERADQTPWRNVDDMP KRRCP*SDLH\AHKL\RVDPVQLSS S*SHLPCW
863	6360	A	890	2	413	
864	6361	A	891	2	6281	
865	6362	B	892	79	200	XGDYPLGDLTPPTMEEATSGVNESE MAVASGHLNSTGVLE*
866	6363	B	893	209	502	MLLMYNSSDHDVYHMAVEMQRD VLEQIQQFLATQLIMQTSESGISAKS LRGRDSTRKQDASEKDSVPMGSPA FFSLSLWDTSGFGWILNKIIPMTLS*
867	6364	A	894	283	340	
868	6365	B	895	1649	1741	MSFAMTLKKKLEEEAEVKKRATD AAYQARQAVKTPPRLPTVMVRSPI DSASPGDYPLGDLTPPTMEEATSG VTPGTLPTPTVTSFPGIPDTLP PGSAP LEAPMTPVTDDSPQKMLGQKATP PPSPILLSLLKKGSLPTSRLVNES EMAVASGHLNSTGVLEVGGLVPM IHGGEIQTPNTVAASPAASESVSQ ATIVMMPALPAPSSAPAVSTTESVA PVSQPDNCVPM EAVGDPHTVTVSM DSSEISMIINSIKEECFRSGVAEAPVG SKAPSIDGKEELDLAEKMDIAVS YT AVEAALSFC EENDDPQSLPGPWEHP IQQERDKPVPLPAPEMTVKQERLDF EETENKGIHELVDIREPSAEIKVEPA EPEPVISGAEIVAGVVPATSM EPPPEL

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						RSQDLDEELGSTAAGEILEADVAIG KGDETPLTNVKTEASPESMLSPSHG SNPIEDPLEAETQHKFEMSDSLKEES GTIFGSQIKDAPGEDEEEDGVSEAA SLEEPKEEDQGEGYLSEMDNEPPVS ESDDGFSIHNA TLQSHTLADSIPSSP ASSQFSVCSEDQEA IQAQKIWKKA I MLVWRAAANHRYANVFLQPGTR*
869	6366	A	896	3	2926	PGSTISSGTGKHKLLSTGPTPEWSIR EKLCLASSVMRSGDQNWVSVSRAI KPFAEPGRPPDWFSQKHCASQYSEL LETTETPK*VQSQRKRGEKGEVVE TVEDVIVRKLTAERVEELKKVIKET QERYR\RLKRDAELIQAGHMDSRL DELCN\DIATKKKLEEEAEVKRKA TDAAYQARQAVKTPPRLPTVMVR SPIDSASPGGDYPLGDLTPTTMEEA TSGVTPGTLPSTPVTSPFGIPDTLP SAPLEAPMTPTVTDSPQKMLGQK ATPPSPLLSELLKKGSLPTSPRLV NESEMAVASGHLNSTGVLLVGGV LPMIHGGEIQTPTNTVAASPAASGA PTLSRLLEAGPTQFTTPLASFTN\VA SKPPVKLVPPPVEFFSQATIVMMPA LPAPSSAPAVSTTESVAPESQPDNC VPMEAVGDPHTVTVMDSSEISMII NSIKEKCFRSGVTEAPVGSKAPSIDG KEELYLAEKMEIAVSYTGEELDFET VGDIHAIIEDKVDDHPEVLDVAAVE AALSFCEENDDPQSLPGPWEHPQQ ERDKPVPLPAE\MTVKQERLDFEE TENKGIHELVDIREPSAEIKVEPAEP EPVISGAEIVAGVVPATS\MEPPELR SQDLDEELGSTAAGEIVEADVAIGK GDETPLTNVKTEASPESMLSPSHGS NPIEDPLEAETQHKFEMSDSLKEES GTIFGSQIKDAPGEDEEEDGVSEAA SL*EPKEEDQGEGYLSEMDNEPPVS ESDDGFSIHNA TLQSHTLADSIPSSP ASSQFSVCSEDQEA IQAQKIWKKA I MLVWRAAANHRYANVFLQPVTD DIAPGYHSIVQRPMDLSTIKKNIENG LIRSTAEFQRDIMLMFQNAV MYNSS DHDVYHMAVEMQRDVLEQIQQL\A ATQLIMQTS\ESGINAKSLRGRDS\T RKQDASEKDSVP\MGSPAFLLSLFD GGTQGTPLCPLKPDMMKMKVKPQS YPL
870	6367	A	897	150	425	VYHFLVALKIPPSLMVFPCPSPFPS/ PPRLPPHPVLFPLPPSPSPSNP*VLGS PRGLSPPLL*GP\PPKPACFCSFP RDPGKLRWALRG
871	6368	A	898	65	259	
872	6369	A	899	273	962	KRERAVSLGQSGLPVAVRAGPQGGG CTWGADALGGTGACGACSLRSSTP HFLGQSERVPH*QGG\TGIFHHPEHG S*AKK/DPVRPPCA*QKGVAFLPA EA*VSGDQGGPGA VLS/GRDCPFPS



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						PGP/PGNPQPLAARQGPAPGNSGSL WPWQEPPVDWPSEGTP/GPLLRRQL QSQPKNATGRERHPPQT/AKPPFSCP NTVL*IPEIK*NPWGEQQSRPALGST QDQRICNNH
873	6370	A	900	1	253	KRKVSLCHPGWSAGAPSRLTATSSS LV\KRFSCLSFSSWDYRCAPHLAN L/CRG/RGFTMLARLVLNS*PQMIYQ SRPPKVLGLQV
874	6371	A	901	327	638	LGLQGSTIFHKTLLKDLLQLEKQLN VNRDPGESNNSHNSQIKSFPIYHFF FFGLLRN*PTNTLDRFVFGFENTHLS VL/QRKTISFNLVCWSHTPSINVCAI YQ
875	6372	A	902	834	1187	RKYETCLSALEIFT*SCSAVGII*FFC LFLGDEVLLCCPGLFTGCHHRWNY SLKLLGSKRSFCLSLSSWNYRHAP PSLGF*KNFKKNFE\KDLAML\PLV FNS\YP*VILLWASSNG
876	6373	C	903	150	364	MSILPLQSYINMNAGNLYGQMHN FPYIVKQKKQVCRTVCTVSLVYHK MCVYMCVCECLXXXXXXXXXXXXX X*
877	6374	A	904	29	372	SYENNHSYAGWSGRKRFTLFLQIY /CRYITPLYILLYVFEQ*VYYPFKVT* I*MQEIYMDRCITIF/LYIVKQKKQV CRNSVYSITCLPQNVCGICVYVSYYI HTYIYIYTHHH
878	6375	A	905	1	815	MGNLQVRRRLSLWDYLLGLTHPRG LTTSQPGRSGLSPPAPPQSFQCMCQ NVTGIMALGMSAVYFQVSGTKEQ PVPGHMQSILLELWGFVHHCV GNPRPDFMEHSKDLTSLLDHSC WHGRSHSSKEYLELHRENFLILRS AFPTGLLRAWPRDGISQYLLVELKN NMFRLVAGSAEGAAGPPCPGPRK VAKKKPHLKQAPKNAGPRRWDEG R*GFPSQKQKEEQKLGGA*KRKA RGGRGWPWTGGIK\KSGQSKLFPW CLRRW
879	6376	A	910	140	512	PARGESRLDPSQWGEPAECAKEPT AVPRGPGLRNRTALTGTQKPPQSRE GARCIIGGSAPSTPPSSARRRWPGG HS*AGRPGRSSRQEPGCCIDRAPGP GLPPPASQPPGAAPLCPTAVGPS
880	6377	A	911	68	675	RSTRTVHIPLLSAQLPGQTP*PLSP WWFFCTPSSQGPPEPREDQPGCAPG PQEAPKPAGNLPPTDSSARAASETG RVLPSP/PTLIFCNLPRRG/FVSV AHL WLMSPFIRL*EATPGPGGQSGDLGG LILHPGQPGHGGQQRGAAGALQR GP/DTSPTPCSRAAAAGMPTA*TLTP *RILPRTAPSPPTTGEQLPRPGNSGR DG
881	6378	A	912	3	3492	GGTVPQGLRTHGTGRGDTVGDDE PPPQDRTLHLPQPPHPLPAPGQGA V PAGRGGGAAQP/AGSPTAPCGPGTS

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						GFAEDSREERGHRLPGEPEVPQP*R LHPG/PPGC/MPDVDFS NFSGESSDF DGLAGTSRN/RQAPGNPRSHGDIQA DRVPGWGHRRQAGGAEPGKGAEG GAAAAVPAAAGAPGPRDPCRGA PAGG*PQPHEA*G*RTL*GAEAE RDAQPLAAL*QCAAGEGAGRLTLP QPAGGAVSTEAGAAASQHGFL* GIARAVPEDSQRPGVRG*GAEPPEG GE*ETALADFQPGGEGHSGAEPGRG AGEPTGAGGAHPLAAGAGRGCREA ARAGQTLRAAELHGCVPLCPVLG REGTDPAAVPEE*DGLPTLQGE AAGPGVRAAEGARPGVLRGQCSE GDFPEPGGGLPPQAGVRADGPGL RAAHTASPAAGRASGCAQAG/RPGP GSPVHGRSSGWC GCMPSAPETTAT A\PRQLHRVSALVGPECHVQPRAGG QLPLQQPRAPQPAVPVQAGGRGLR GRTL VFQQLPGDPGGRPGSPAGS*G RRPTPGL*APRHGRPSAAGKQPAAS LPWKA*CLGECTSRSSPGLQRRPHA AEASPQDPEPGHHAGVPGGCIAGA DQRHRREPHGHLHPPGHPGLGGGP DGLAPGHPDCDG*LRSLRALVQGS GGHDPGGGRGASQEGGRLLPVCE GQHGR*EATPGPGGQSGDLGGLIL HPGQPGHGGQGRGAAGALQGR AR/PPTPCSRAAAAGMPA*TLTP*R ILPRTAPSTTPGLSSSS*PSSRT*LSS AP*PASHL/PGGPQ/IAGPHRQYQGS QGQPSAFVL*QGPVGPQQDGGLOH VLLGRELPHPGALYPGAAPSTRPAP ACAPRAQGGWEDPERETVPPRV*E VPGRVLEPGGV*GLEPAGGDIIIPGR GVRGPLLGEPA/SCGVPHGKEHPCP PGRPAGQCLHPAQDGHLPHRHPRL CQREDGKEAQEGPTAVGHLRGAAP GGCEAGGGRPGPGALSIIQPGS*RL ERPGRPAQLCPPGHRRRAEEGATPT SSKN*PQARGRASPPSNASVTEELT QGRGWALPPSNASVTEELTQARGR ASPPSNASVTEELTQARGRASPLH LRRLSKKDKLLPRNTTGSKLITSGSL LPISWKPAWGTGT
882	6379	A	913	232	485	TRLRLTPKVCPIRWSHFDRKFLSRV LMRRSAQKSRDRILNVFHELNL/NS VLDMRPMEF*GLRAAS*PQGERRGS LAFIREFHHT
883	6380	A	914	2	1163	
884	6381	A	915	771	1597	GACHLRLTPKVCPIRWSHFDRKFP SARVL/MRRSAQKSS/RDRILNVFHE LNLKDAISYVAEVAEPLALPGRGC SRLGHWLIQFWT*GQWSFRVSGLLP D/TQGERRGSLAFIRSPSTDNVVNV DFTPRSSTVEASVSLLYVAMVMQ LPWGRAQPRELRVTDRAVVAPGLG VAWKRGVQKEGVGVSSHKPSYIR

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						PWPDSLSAGRKVKGRGSSGLGARP DVFA GPQPVMVMPPLLLLRPW APQLTASSHRRSTLPDVQMLGSPSL TARALERDQ
885	6382	A	916	3	471	DSWLWWLRQRLQQIGGISGSTSTSS MLSRVCGTSRQLAPVLGYLGSQRQ KHSPLDLPYDYGALPHINAQIMQL HHSKHHAAYVNNLNVTTEEKYQEA LAKGELLEAIKRDFGSFDKVKEL TAASVGGKGCWGGGLGFNKERGH LQIAAWPNQDP
886	6383	A	917	54	873	GPRAAQERHSLWWLRQRLQQIG GISGSTSTSSMLSRVCGTSRQLAP VLGYLGSQRQKHSPLDLPYDYGAL EPHINAADHASLHHSKHHA/APYVN NLNV/TEEKYQGGWLWPRGDVYSPR* ALQPCT*KFNGGGVHINHSIFWTN PQAPNGGGETQRGSLLGSHQNVDF GS\FDKFK\EKLTAA SVGCPKAPGW GWLGFQ*GNRGH/LYQIAACPKSGI PLQGTG/LLFLLGIDVWEHALLPS SIKNVRPDYLKAIWNVINWENVTE RYMACKK
887	6384	A	918	24	452	APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSSA SAIMGPNPKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLVTVLAIHFGKEFTP EVQASWQKMVTGVASALSSRYH
888	6385	A	919	41	601	APSPRRPWGHFTEEDQGLLSTSLWG KVKCGKNAGRKKPLGKAPLVVL/H PWDPKRSFEQALGNPVPPLSAIMG NPPKSRAHGK\KVLTSLGEMPIKHP G*SSKGTFAQA*SELH\CDK\HVDP ENFKLLG\NVLVTVL\AIPFSAKEFT PGGCRASWAERWVTWSWPVPCSS RIPLSSLAHDCRAFQG
889	6386	A	920	14682	14931	EIGPGPRPLPSLP*ATSTSVLAASGR PERTR\HAGIKIVLEDIFTLWRQVET KVRAKIRKMKVTTKVNHRDKINGK RKTAKEQSPLLQESLFATGDVSHNL LRALDVGLLANLSALAELDISNNKI STLEEGIFANLNLSEINLSGNPFEC DCGLAWLPRWAEQQVRVVPQPEA ATCAGPGSLAGQPLLGIPLLDSCGCG EYVACL PDNSSGTVA AVSFSA AHE GLLQPEACSAFCFSTGQGLAALSEQ GWCLCGSAQPSSASFACLSLCSGPP PPPAPTCRGPTLLQHVFAPSPGATLL AAFHIAAPLPTATRWDFGDGSPEV DAAGPAASHRYVLPGRYHVMAYL ALGAGSALLGTDVQVEAAPALEL VCPSSVQSDSLDLSIQNRVSGGLE AAYSIVALGEEPARAVHPLCPSDTEI FSGNGHCYRLVVEKAAWLQAQEQ CRAWAGATLAMVDSPAVQRFLVS RVTRSLDMWIGFSTVQGVVEGPAP QGEAFSLESCQNWLPGEHPATAEH

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						CVRLGPTGWCNTDLCALHSYVCE LRPGGPVQDAENLLVGAPSGDLQG PLMPLARQYGLSAPHEPVEVMVFP GLRLSREAFLLTAEFGTQELRRPAQ LRLQVYRLLSTAGTPENGSEPERSP DNRTQLAPACMPGGRWCPGANICL PLDASCHPRPAPMAARQGPGLLGA PYALWREFLFVSPAGPPAQYSVTLH GQDVLMLPGDLVGLQHDAGPGALP HCSPAPGHPGPQAPYLSANASSWLP HLPALQEGTWACPACALRLLAATE QLTVLLGLRPNPGLRLPGRYEVRAE VGNGVSRHNLSCSFDVVSPVAGLR VIYPAPRDGRLYVPTNGSASVLQVD SGASATATARWPGGSVSARFENAC PALVATFVPGCPWETNDTLFSVVAL PWLGEGEHVMDEVVENSASRANLS LRVTAEEPICGLRATPSPEARVLQG VPVRYSPVVEAGSDMVFRWTINDK QSLTFQNVVFNVIYQSAAVFKLSLT ASNHVSNVTNVTNITVERMNRMQ GLRVSTVPAVLSPNATLALTAGVLV DSAVEVAFLWTFGDGEQALHQFQP PYNESFPVPDPSVAQVLVEHNVTHT YAAPGEYVLTVLASNAFENRTQQV PVSVRASLPSEAVGVSDGVLVAGRP VTFYPHLLPSPGGVLYTWDFGDGSP VLTQSQPAANHNTYPSRGIYHVRLEV NNTVSGAAAQADVRVFEELRGLSV DMSLAVEQGAQVVSAAVQTGDNI TWTFDMGDGTVLSGPEATVEHVYL RAQNCTVTVGAASPAGHLARSLHV LVFVLEVLVVEPAACIPTQPDARLT AYVTGNPARYLFDWTFGDGSSNTT MRGCPTVTHNFTSRGTPLALVLSS RVNRARYFTSICVEPEVGNVTLQPE RQFVQLGDEARLVACAWPPFPYRY TWDFGTEEAVPARVGGPEVTFIYRD PGSYLVTASNNISAANDSALVEV QEPMLVTSIKVNGSLGLELHYLWD LGDGRLEGPEVTHAYNSTGDFTV RVAGCNEVSRSEAWLNVTVKRRVR GLIVNASCTVPLNGSMSFSTSLEA GSDVRYSWVLCRCTPISGAENEV GSAQDSIFVYVLQIEGLQVVGGR YFPTNHTVQLQAVVRDGTNIYSWT AWRDRGPALAGSGKGFSLTALAEAG TYHVQLRATNMLGSAWADCTVDF VEPVGWLMVAASPNAAVNTSVTL SAELAGGSGVVYTWLEGLSWET PEPFTTHSFPTPLHLVTMTAGNPL GSANATVEVDVQVPVSGLSIRASEP GGSFVAAGSSVFFWGQLATGTNVS WCWAVPGGSSKRGPVMTMVFDA GTFNIRLNASNAVSWVSATYNLTV EEPVGLVLWASSKVVPAGQLVHF QILLAAGSAVTFRRQVGGASPEVLP GPRFSHSFPRIGDHVVSQSKNHVS

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						WAQAQVRIVVLEAVSGLQVPNCCE PGIAMGTERNFTARVQRGSRVAYA WYFSLQKVRGDSLFILSGRDVITYP WPRGCWRSSNRTLVEVQDAVQ YVALRSGPCFTNRLAQFEAATSPSP RRVAYHWDGFGDGPQDQTDKPR EHSYLRPGDYRVQVNASNLVSFFV AQATVTVQVLACREPEVDVVLPLQ VLMRRSQRNCLDAYVDLRDCVTY QTEYRWEVYRTASCQRPGCPARVA LPGVDVSRPQLVLPRLALPVGHYCF VFVVSFGDTPLARSIQANVTVAPER LVPITEGGSYRVWSDTQDLVLDGSE SYDPNLEDGDQTPLSFQWACVAST QREAGGCALNFGPRGSSTVTIPRER LAAGVEYTFSLTVWKAGRKEEATN QTCWWRPRLPSLFLMQILCNTTA CFSFASFQCHSSTYSLQATYALVT KATQSPSNTNRSSWLQYTRHTPV SALCMPFRRPGWKVANRMSILGGG WHDAEDAGAPLVYALLQRCQCG HCKEFCVYKSSLSGYGAVLPPGFRP HFEVGLAVVVQDQLGAAVVALNR SLAITLPEPNGSAMGLTVWLHRLTA SVLPGLLRQADPQHVEYSLALVT LNEGPSRELVCRSCLKQTLHKLEA MMRILQAETTAGTVTPTAIGDSILNI TGDLIHLASSDVRAPQRSELGAESP LRMVASQAYNLTSALMRILTRSRV LNEEPAFSRAPANLSDVVQLVFLVD SNPFLFGYISNYTVSTKVASMAFQT QAGAPIERLASERAITVKVPNNSD WAARGHRSSANSVVVQPQASVGA VVTLDSSNPVAVLHLQLNYTLDDG RYLSEEPEPYLAVYLHSEPRPNERN CSASRRIRPESLQGADHRPYTFFISP GTRDPVGSYRLNLSSHFRWSALEVS VGLYTSLCQYFSEEDVWRTEGLL PLEETSPRQAVCLTRHLTAFGASLF MPPSHVRFVFPEPTADVNYIVMLTC AVCLVTYVMMAAILHKLDQLDASR GCAIPFCGQRGRFKEYILVKTGWGR GSGTTAHVGIMLYGVDSRSGRHL DGDRAFHRLSLDIFQIATPHSLGSV WKIRVWHDNKGLSPAFLQHIIVR DLQATARSTFFLVNDWLSVETEANG GLVEKEVLAASHAALLRFRLLVA ELQRGFDDKHIWLSIWDPRPRSCFT RIQRATCCVLLICLFLGANAVWYG AVGDSAYSTGHVSRLSPLSVDTVA VGLVSSVVVYPVYLAILFLFRMSRS KVLDIDSCLDSSVLDSSFLTFSGLHA EVRALLGVLGWAGGPAALALGL QTLCTSQQAFAGQVKSDLFLDDSK RSGPVVPVFPFPPCKPPPLSWLPQG ALKGPGHAGIKIVLEDIFTLWRQVE TKVRAKIRKMKVTTKVNHRDKING KRKTAKEQ

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890	6387	B	921	1	714	MVKLSIVLTPRFLSHDQGQLTKELQ QHVKSVTCPCEYLKRVINTLADHR HRGTDGFGGSPWLLIITVFLRSYKFAI SLCTSYLCVSFLKTIFFSQNGHDGST DVQQRARRSNRRRQEGIKIVLEDIF TLWRQVETKVRACKMKVTTKV NRHDKINGKRKTAKEHLRKLMSKE REHGEKERQVSEAEENGKLDMKEI HTYISPLLQESLFATGSEWRQRSIVI LQDCPTGPTSQKLK*
891	6388	B	922	1	387	MRVRWLLFWLLFWLLGFISHQST CVINTLADHRHRGTDGFGGSPWLLI TVFLRSYKFAISLCTSYLCVSFLKTI PSQNGHDGSTDVQQRARRSNRRRQ EGIKIVLEDIFTLWRQVETKVRACK KMK*
892	6389	A	923	277	489	
893	6390	A	924	465	634	
894	6391	A	925	1	4652	MGSTGVYKVTTPRSCHRFEQAFYTY DTSSPSILTLTAIRHHVLGTITTDKM MDVTVTIKSSIDSEPALVLGPKSV QELRREQQLAEIEARRQEREKNGNE EGEERMTKPPVQEMVDELQGPFSY DFSYWARVLCFVGTGPAKLKYINY FRSGEKITVTPSSKELLYPPSMEAV VSGESCPGKLEIHGKAGLFLEGQIH PELEGVEIVISEKGASSPLITVFTDDK GAYSVGPLHSDLEYTVTSQKEGYV LTAVEGTIGDFKAYALAGVTLHSQ DVLMLPGDLVGLQHDAGPGALLHC SPAPGHPGPQAPYLSANASSWLPHL PAQLEGTWACPACALRLLAATEQL TVLLGLRPNPGLRLPGRYEVRAEVG NGVSRHNLSCSFDVVPVAGLRVIY PAPRDGRLYVPTNGSASVLQVDSG ASATATARWPGGSVSARFENACPA LVATFVPSPCWETNDTLFSVVALP WLGEGEHVMDDVVENSASRANLS LRVTAEEPICGLRATPSPEARVLQG VPVLLAGSSGYLVGFKFLESHGSD SGSANSFHRLISRNEFKTPLDLTRV PRYSPVVEAGSDMVFRWTINDKQS LTFQNVFNVIIYQSAAVFKLSLTAS NHVSNVTVNYNITVERMNRMQGL RVSTVPAVLSPNATLALTAGVLVDS AVEVAFLWTFGDGEQALHQFPY NESFPVPDPSVAQVLVEHNVTHY AAPAALGGGAVLTRQPSVLLHCS VPHVAWEPGLKAGPQVSTVLTVL ASNAFENRTQQVPVSVCASLPSVSV CASLTGACWYPRVLIRSGRVPIVSL ECVSCKAQAVYEVSRSYVYLEGR CLNCSSGSKRGYTFTLTVLGRSGE EEGCASIPLSPNRPLGGSCRLFPLG AVHALTTKVHFECMGWHDADAG APLVYALLQRCRQGHCEEFVYK GSLSGYGAVLPPGFRPQFEVGLAVV VQDQLGAAVVALNRSLAITLPEPNG

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						SAMGLTVWLHGLTASVLPGLLRQA DPQLVIEYSLALVTVLNEYERALDV AAEPKHERQRRQAQIRKNITETLVSL RVHTVDDIQIAAALAQC MRKLPE QDIAQGSYIALPLTLLVLLAGYNHD KLIPLLLQLTSRLQGVGALGQAASD NSGPEDAKRQAKKQKTRRTLATSIN TSREPSTDDQLPAHNQTMPQRHAR RSAPPRAYDRKTRQEENPHQTRSH AAAKRRERPPHDLQKQATTRLIPAG PRRRDGTSPRRTQPPNTRRPAAAG HLARFRRAAPGARGARPTARRGR EELDPAHIYAAAPGLPTPPRAGRTPP TPERRDRNTRRRRTREEGEGEFRPV SFLKTIFPSQNGHDGSTDVQQRARR SNCRRQEGIKIVLEDIFTLWRQVET KVRAKIRKMKVTTKVNHRDKINGK RKTAKEHLRKLSMKEREHGEKERQ VSEAEENGKLDMA*IHFYMEMFQR AQALRRRAEDYYRCKITPSARKPLC NRVSLLVFLAFGHSLPGQMDTFFS LRLCASSPAEGDGREEGCLQAFTVP SLLVTVLRKNTFIPTQWGPLHIF
895	6392	A	926	3	156	EMFQRAQ/ALRRRAEDYYRCKITPS ARKLLCNRCTYNLVLPGSEKKYYS HA
896	6393	A	927	183	1518	ASTQSAVGLVSSVVVYPVYLAILFL FWMSRSKVAGSPSPAGQQVLDID SCLDSSVLDSSFLTFSGLHAEVINTL ADHQHRGTDGFGSPSVLIITVSLRSY KFAISLCTSYLVWINTLADHRHRT DFGGSPWLLIITVFLRSYKFAISLCT TYLCVVSFLKTIFPSQNGHDGSTDVQ QRARRSNCRRQEGIKIVLEDIFTLW RQVETKVRAKIRKMKVTTKATRLT KIKERRKTAQDHWKLSMKEREHG EKERQVSEAEENGKLDMKEIHTYM EMFQRAQALRRRAEDYYRCKITLF QRKPLCNVRMAAVEHRHSSGLPY WPYLPATLKNRMGHQPPPTQQH SHDNSLSLKTPECLLTPLPPSALPS ADDNLKTPAECLLYPLPPSADDNLK TPPECLLTPLPPSAPPSADDNLKTPP ECVCSLPFHPQRMISRN
897	6394	A	928	123	1040	WRWFTIGTFRILLMFCCGLGYEWLSG /GCTTWHSAWV*GSSCHPAICFLCF VAKSDP*RNPGKLRKERTPRSQQGQ SWFGEDQKSGLSILWADIVHRGTDA FGGSPWLLIITVFLRSYKFAISLCTSY LCVVSFLKTIFPSQNGHDGSTDVQQR ARRSNRRRQEGKLSICMHTKKRVS SFAGIKIVLEDIFTLWRQVETKVR KIRKMKVTTKVNHRDKINGKKKTA KEHLRKVLGMKEREHEEKERQVSE AEENGKLDMKEIHTYMEMFQRAQ ALRRRAEDY*QHDKITPSARKAFFA NRVQQWRQW
898	6395	A	929	39	525	TKFVLGTFQILFTASFHPSWWPLA

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						LENPHDSNLSGLFPLIDLDFSP*VLS CWASHTMENCS*LRSKRQITLWCS RMAEVLVYCLSWKCSHLKRHDFPM GKYQTPTCIDKGNMLYLSKLLGIES QCLGAEMGIPIKAMQSFTTSGRPKN EHSRNFVIIWKVLI
899	6396	A	930	1030	1384	LIALRKMGRNAQAQICITSDG*NPS PLKTESTLKTQFSLYPWGEKFERT PSLMGQKNFRTVCQLSQMGAIGFQ/ HIQEWDERKSTITKKN*KDGEISW LECVMMNNVTCTPDMSMKK
900	6397	A	931	1	225	
901	6398	A	932	2	167	
902	6399	A	933	1	3339	PASVHPSVRPTVQRKGLQAGRTSTR GTEARRGAKSAADPCGPGQGTVA AMQSCARAWGLRLGRGVGGRRRL AGGSGPCWAPRSRDSGSGGDSAA AGASRLLELLPRHDDFARRHIGPG DKDQREMLQTLGLASIDELIEKTVP ANIRLKRPLKMEDPVCENEILATLH AISSKNQIWRSYIGMGYYNCSVPQT ILRNLLNSGWITQYTPYQPEVSQG RLESLLNYQTMVCDITGLDMANAS LLDEGTAAAEALQLCYRHNKRRKF LVDPR\CHPQTIAVVQTRAKYTGV TELKLPCEMDFSGKDVSGVLFQYP DTEGKVEDFTELVERAHQSGSLAC CATDLLALCILRPPGEFGVDIALGSS QRFVPLGYGGPHAAFFAVRESLV RMMPGRMVGVTTRDATGK\EVYRL AP*KPREQHRRDKATSNICTAQUAL LANMAA\MAFYHGSHGLGHIA\R RVHNATLILSEGLKRAGHQLQHDLF FDTLKIQCSCSVKEVLGRAAQRQIN FRLFEDGTLGISLDETVEKDLDDL LWIFGCESSAELVAESMGEECRGIP GSVFKRTSPFLTHQVFNSYHSETNIV RYMKKLENKDISLVHSMPLGSCM KLNSSSELAPITWKEFANIHPFVPLD QAQGYQQLFRELEKDLCELTGHDQ VCFQPNSSGAQGEYAGLATIRAYLN QKGEHRTVCLIPKSAHGTPASAH MAGMKIQPVEVDKYGNIDAVHLK AMVDKHKENLAIMITYPSTNGVF EENISDVCDLIHQHGGQVYLDGAN MNAQVGICRPGDFGSDVSHLNLHK TFCIPHGGGGPGMGPIGVKKHLAPF LPNHPVISLKRNEACPVGTVSAAP WGSSILPISWAYIKMMGGKGLKQ ATETAILNANYMAKRLETHYRILFR GARGYVGHEFILDTRPFKKSANIEA VDVAKRLQDYGFHAPTMSWPVAG TLMVEPTESEDKAELDRFCDAMISI RQEVADIEEG\RIDP\RVNPLKNVLH TPLTCVTSSHWDPRYSREVAAPLP FVKPENKFWPTIA\RIDDYGDQHL\ VCTCPMAEVYESPFSEQKRAVFLV LCSLSFKGIDFDGLSPEAFDKQERFH



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						LPTPSLK
903	6400	A	934	2	287	
904	6401	A	935	36	427	
905	6402	A	936	247	1183	CCWESPVDPQPLRQISGIALFCSFKE PPLLGLVHPNTKLRQGRKGCLKIN LLGPESMAHIGGCDVYWGQMQGR VVKLENG*NRRLPGFGSGPLAKPE DDEPCVWGDPLGIRGRGPKWGLLF VGRHLTRGLF*R*NPWETVKVLLLL SSETPI*GGRNMSFVNDLTVTPGW KEDLISPMPKQNGQRRKLPAFWV MGGHKMTGRLLV*YCDPGK*KFY WTQLRFPNGVQPV*QKTLSLVAET SMARIRRVYVSGPDERRADLFVEN MPGFDPNIRPSSSGGYWVGMSTIRP *PVGSSMLDFLSERPWD
906	6403	A	937	179	516	VFSVLRAEDKICELLFCLKIKLFAIS FLVFRNQLPRKNDFYSEPPSENPPP ETGESVCLQLKSGAHLRCVCGCLG PKTCSRCHKAYYCSKEHQTLDWRL GHKQACAQPGG
907	6404	A	938	41	274	KRGTERKTHFGGCSIQFSDIASGKNI LPGLCFLTHKR\WFCSL*RQGWVSR WSHE*GCTRCWRLGKFLWVADRFL GSG
908	6405	A	939	3	1111	CAPRQPAPRMAAAGARPVELGFAE SAPAWRLRSE\QFPSKVGGPAWLG AAGLPGPQALACELCGRPLSFLQV YAPL\PGR\PDA\FHRCIFLCCREQP \CCAGLARFLGIRLPRKNDFYSEYEP PSENPPPETGESVCLQLKSGAHLCR VCG\C*GPKTCSRCHKAILLAAREH QTLADWEIGDIRQACAQPDHLADHI NFQDHNFPFFQEF\EIVIETEDIMP* GVWKKEDYSRDY*GALG*STLKGR TWISMAKHE\SRED\KFFQKF*NFR ALGTEQDS*YAGRG\IPIWISGENIP QEKDIPDCPCGAKK\LEFQVMPQLL NYLKADRLGKSIDWGILAAFTCAES CSLGTGYTEEFVWKQDVTDT
909	6406	A	941	3458	4042	AGMIRRPSPWPSIRPPPAVFTNSCTS LQEPSGGTGRVQVPSIYQAS\STQIC VKGPD*GRNGKGNLSFGKAGIFHFP WCPKCPRPSSSPISMGLLSPEVDSVE R\PTFRFPLAPIYKECV*NGAG/AQ APDPRQKRGWPCWNLGMVGRMP RVSPHLPEAWGPKHPDDRYTKGTA ICPRNHLPCDPRISAIGQPQG
910	6407	A	942	226	401	TSGDHWNIIVAPHENSLLLLVQGH DYKYRYFGLIVCVL*QAIVTPEEPQS IVPRLRTR
911	6408	C	943	211	282	MFYPFFNPRYFSVGFIAAMNRHTD*
912	6409	A	944	1390	1698	HLFPHIKAGR*YGRPCREGILQ*KE* ETTGRHTCVLQGLAQEVVVQVRN VFLHEALQLVKFAMQIFEVLLKFP EPIVKHDLQDQNTCLFFRHMEKEHS SKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
913	6410	A	945	27	412	IAEGNWCVYMPDIIWVFPQAEAE DCHSDTVRADDDEENESPAETDLQ AQLQMF\RAQWMFELAPGVSSSNL ENRPCRAARGSLQKTSADTKGKQ EQAKEEKLIIIDIVTNYIFFFWHMEIF TGHSK
914	6411	A	946	24	1489	GGSSAAASGVSSRADAPVLAQSPAS AGNGRPSTPRVPGSRRHPSAPRSGP LPREDGCRTPGPQLPLHGALLRPR TLLSSAAEDKARSRH\PDTPHPSSG GRCKGGTESPSSAAGRPASMAEAE\ EDCHSDTVRADDDEENESPAETDV QALIP\MIQAQWKLEPAPRVSSSNLE NRPCRAARGSLQKTSADTKGKQEQ AKEEKARELFLQAVEEEQNGALYE AIKFYRRAMQLVPDI\EFKITF\TRSP DGDGVGNSYIEDNDDDSKMA DLLS YFQQQLTFQESVLKLCQPELESSQI HISVLPMEVLMYIFRWVGSSDLDT SL\EQSLSLVCQIPNLCPETPENMPV LALL*KFWGR\SC\IKLVSVTSPGRE DVF*ERP\RVRF\DG\YISKTTYIRQG EQSLDGFYRA\WH\QVEYYRYIRFFP DGHVMMLTTPEEPQSIVPRLRVTRE YQGLDAIPTGV\TIRLS\PRHRTIRTQSI WLLITKEKRKEKPL
915	6412	A	947	17	499	DRVLLCN/PRLECNGMITAHCSKP GSK*SSCFLPSSWDYKHEPPYRAN LKNFFVETGSLYVAQAGFELLDSSN PPCFLPKCWDRPP*ATPS/FKND SHFNFLNRF/SHFVVF*VLRLNLC NNIP*GLKVGELQSPKAETKLGVER GGKNYIRFSK
916	6413	A	948	9	296	RPSHQCRLLPPRASLGLSELCPEDQ QSYIP*LGHHSAECR*S/TSGGSCPLS SVSSQASRAS/GPTSLTTAAPTSPRT GASALTEQYWSNRLNHFAE
917	6414	C	949	114	383	MQMVGVWGGGLGGIKQDKVLLSSE GPRSRDGGGTWRPTLKSTVRXXXXX XXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXX
918	6415	A	950	1896	2251	IGTPLCRMEIDPFLEEAVPWSSVSSQ ASRASWPTSLTTAAPTSPRTGASAL TEVGRPKT*DHKISSVSTK/TSSHCP GPEHTTSAVPVSRASSCPVTVTTLK SKHPLQLARRVGFTLLY
919	6416	A	951	141	439	
920	6417	A	952	278	1177	RHPLAFFKASRAGPQRPLDGTGLGPE DSRASSPMIQNSRPSLLQPDVGDT VETLMLHPVIKAFLCGSISGTCSTLL LQPLDLLKTHLQTLQPSDHGSRRV GMLAVLFKGVRTERLLDLWKMS PSIVR\VSLGVGIYFGHSLLF*SSISW RRPIPQTALEV\NHAGGSGSRVAG VCMSPITVIKTRYESGKYGYKSIYA ALRSIYHSEHGRGLFCGLTATILRD APLSGIYLMFYNQTKNIVPHDQVDA TLIPITNFSCGDICWYSGPHVWTSTC

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921	6418	A	953	109	376	GMFIQNSYGRLLFHLKVSMDWPST SLTRAKSHLGQQFPTSRTSQEENWS P*RGSRTPPTPHLPCQNL RPSMPT/F *QVNFKQFRGAFLSG*KSSVAIRTIQ QSNMALMGTYAL
922	6419	C	955	123	329	MISRAPLPQLSELHCDKLHVDPENX KLLGNVLVTVLAIHFGKEFTPEVQA SWQKMVTAVASALSSRYH*
923	6420	A	956	41	565	APSPRRPWGHFTEEDKATITSLWG K\VNVE\DAGG/EKTPGKGPLVVLPP WTPEVPLTSFGNLS\SASAHHGQTP KVQGTMAKKVLTSLG\DA\TKHL\D DSQGAPFAQA*SELALVDK PAMWD PE\NFKASWGN\VLVTRFGQSHFRA KNFTPEGCRVSLGRKMGDLELASA LVPSRYH
924	6421	A	957	1	1000	STRAPSPGPFSSKLAGAYKSWCRR DPRTHSAGAAQAARSVPIRC PAPT ASATMSHHWGYGKHNGPEHWHK DFPIAKGERQSPVDIDHTAKYDPS LKPLSVSYDQATSLRILNN\GHAFN VEFDD\QDKAVLKGGPL\DG\TYRL ISVFTFWGSF*WDKVSEAYCGIKK KYAAE\TLGHWNTKYGDFGKAVQ EPDGLAVLGIFLKVGSAKPG LQKV DVLD\SIKTKGKSADFTNFDP RGLLP ESLADYWTYPGSLTTPP LLEC VTWI VLNF\PFVS\EQVFEIP*TLTFNGG GVNPEELMVDNWRPA\QPLKNR\QI KASFQIRWSHSLYSK
925	6422	A	958	3	402	EELTMAGIFV*PTIPIVSL/SLFCH*V LTLNSGISPAGSPVLIFSTPEPKR*TS QGSRFHTFYLLKKLGLNR*I*HPSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSQ NRFLKPLQHS LPPPLKPLTYAPNL
926	6423	A	959	1666	2187	NFPSSASPPPTDSFL\GLSSEAPSEHR SPSCALDPIFFQ TWL**SFSFSSLNFI NMLKFVPPLNKT KPLTL\FPYLKQL ASLPIQSCFF*DKILLCHLGWSAVA QL*LTATSTSWAQVMFPRSWAYRH APPHT/LASCFYFCRDR/SLTIFPRLV SNSWAQVILPPRPPKMLGIQA
927	6424	A	960	3	695	TQLLRRPAVFVGSAA SGIRRLWSA SSGHWCAPAAGRAHAPV PRLVRGL GAASTAAPQDAQTGPQMPRADCI MRHLPYFCRGQVVRGFGRLQASL GIP/TANFPEQVVDNL PADISTGIYY GWASVGS\GDVHKMVM SIGWNPY YKNTKKSMETHIMHTFKEDFYGEIL NGAIGDYLRPDDNFDSLQSLISAIQG DFEEAKK*LDLPEHLKLKEDNFFQ VSKSKIMNGH
928	6425	A	961	60	569	STDLEELPTLGWF*KQELIILSCPFVS LTYRERLPANFFKFQFRNVEYSSGR NKTFLCYVVEAQGGQVQASRG YLEDEHAAAHAEEAFFNTILPAFDP ALRYNVTWYVSSSPCAACADRIKT LSKTKNLRLLILVG\RLFMWEEPEIQ

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						AALKKLKEAGCKLRIMNLV
929	6426	A	962	62	858	QLRWDSGARAWPRPACLSPLPQRL LSHSPSMAQKEEAAVATEAASQNG EDLEN\DDPQKLKELIELPPFEIVTG ERLPANFFKFQFRNVEYSS\GRKTL \LCYVV*STGARGGKVQASWGYLE DEHAACPLQKESFSNTILPAFRPK PLAVTNVT/WGYVSSSPCAACADR\ IVKTLSTKTNLRLLILVGRLFMWEE PEIQAAALKKLKEAGCKLRIMKPQD FRILSWE\NFVEQ\EEGESKAFQPWE DIQENFLYEEKLADILK
930	6427	A	963	409	747	VILQAQGSMPGP*SLRAFAESERC QKQERLEPEEGRTCAAGLRGGPRR WWPLSSWTGDLRPSARN*ILPAA PMMEERKDPAPAQPWTS\TLPQFV SPEVLCSPPIENSHT
931	6428	A	964	1092	2338	RCYCSI*PCFHLFQLSFQILDPPVLGT TFL
932	6429	A	965	146	180	
933	6430	A	966	2	921	
934	6431	A	967	1	621	
935	6432	A	968	2	152	
936	6433	A	969	157	1203	NNSGVMPEMPEDMEQEEVNIP**G GFWVTGCHWGFLGRAVHKEFQQN NL/WHAVGCGFRRARPKFEQVNL\ DSNAVHHIHDQPHVIVHCAAERR PDV\VENQPDAAASQLNVDAAGNLG KGKAAAVWEHFSILHLGSGFCILM GT\NPPYREEDIPASLNLYGQTKL DGRKGCPWRNHLGAAVLRIPILYG EVEK\LEKKCCCELLMFE*KCQFQQQ SQAQQWIHWQARGSPPHMSKDVA PLCARQ\LAEKRLDP\SIKGTFWWS GNEQMTKYEKGMCQLPDA\FNLPS SHL/RDPITDSPVLGAQRPRNAQLD CSKLETLGIGQRTPFRIKESLWPF LIDKRWRQTVFH
937	6434	A	970	1	508	NSNRQNGPPKKGERERASN/C/YPG APAAQAE/APLVPLSRQNKSTVETS NLKMLISFPKTLRGPQEGWWHQG INPGGAATLGPGS/SPQRPS/IAAS CSMARRTFFAVSSNSFFLL/CFLCM GSSSGSQSSSLKQKKHWAKSGSFS VGQWMKPASAIRSGVQRSPRRAS S
938	6435	A	971	21	351	VVSITKAPAYREVSVHNSCLRSNEG GKQPSHTKCLCNSNLLTQFKTKPI E/CWPEKTYMGSSSGSQSSSLKQK KHWAKSGSFSVGQWMKPASAIRSG VQ\RSPPRRASS
939	6436	A	972	1	1011	
940	6437	A	973	2	94	
941	6438	A	974	661	2244	QYFKNPVGSTAVFEMDRLFISSGTA EMTSRGF\QRS\CNNPP\CSMTGRR ANQIHHLTPDFS\LRELL\PPK\KAGT WADCVSPPCGERDRCEGWADRHR

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						A\CSSPAKSPTASSQVI*KGFKATAF FSRGRSGQHVAPRLHLGLSNHTAV GKREYLARRFLSLYSVSSSTRSFTPF PQ*LRMAFVLSF*IVVCAIL*INNSN KIRKPCC*TVIEPGTSLSPFSHHTQV MHLPPKKKTKKHNNKKTVL*GGT GVTDKPEAAQIQQAPGKVPQDCD SLNNMRSRHHHCGRLC\HANKAVSS SKRDTAFLPHFSPGKPGNQNSKNE PPKKRERERSHC/YPAAPAAQAEA PLVPLSRQNRSTVETSNLKMILISFPK TLLRGPQEGWWHQGINPGSGAATL GPGSSGQRPQSM\AASCSMARRTFF AVSSNSFFLLLVSFAILFLALS\SSF KKFNQRVNSS\NCFLD\TERKAQPG RNCFLCSSMGSSSGSQSSSLKQKK HWAKSGSFSVGQWMKPASAIRLRG CRRSPRRASS
942	6439	C	975	597	683	MWFHVCLLVIFFYFLVHMKYLKC KFLG*
943	6440	A	976	224	290	MPIPIPMPIAPVFPFGPGFPP/VYFPV PLPLP/LLFPF*PLFPF*PEVSAKPVTL WSRKRQRSKGEKEGRGRGTGK
944	6441	A	977	3	1815	HFVPVSPEAAAAESTACGVTAKML SVRVA\VVVRALPRRAGLVSRNA LGSSFIAARNFHASNTHLQKTGTAE MSSILE\ERILG\ADTSVDLE*NLGVS *SIGDGIAPRTWG*RN\QAEEMV\EF SSRLKGYVL*TL\PDNVGVVVFNG DKLIKEGDIVK\RTGAIVDVPVGE LLGRVVDALG\NAIDGKGPIGFQRR VGEVGL\KAPGIIPR\ISVREPMQTGI KA\VD\SLVPIGRGQRELIIGDRQTGK TSIAIDTINQKR\NDGSDEKKKLYC IYVAIGQKRSTVAQL\VKRLTRCKM PWKYTIVVS\ATASDAAPLQYLAPY SGCSMGEYFR\DNGKHA\LIYDDLI QNKAVA*PVKMSLLLRPPGREAY PGDVFYLHSRLLERA\AKMND\AFGG GSLTALQV\IET\QAGDV\SATIQTDV NSI\TLPEQIFLET\EFNKG\IRPAIN VG\LSVSRAGSPPTNPGAMKPGSQV PWKLELASSIREVACFLPPVSVSDL DAATSTNLLESVA\VP*\LEFAESQG PVFSPWLIEGTSCLLSYAGCKGDIFD KLEPSKITKLRNAFLSHVVSQHQL VGALCRADGKISEQS\DAKLKEIVT NFLAGFEA
945	6442	A	978	532	878	SYHFGRPRQADHLRSGVQDQPGQH EETPSLLKRQK\LAGHGGIYL*PQLL GWLRLQENCLNLGGGGCSELGLHHC IPAWATEQDCLKKQNETKKESYS** GTSCLIAFLILKSDQK
946	6443	C	979	36	236	MGPTIPDXS\XFFWRKPITWMPWE GTSNVGPQPLSSSKSLHSXRGHPAPI PTGQAGPRDSGPGASP*
947	6444	C	980	26	160	MRFQSTGLGAPHCALNKC\VSCLNX XXXXXXFLLRGPKLNPFKGG*

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948	6445	A	981	1	523	FFPKGFFLGYPRVFPPFPLNPGPGQ I*FSP*K/RKLRAP*KKASSSSSVK TGNTFIESTVGCAPCALEPHHSAP/ PQQPAPSGPGPPGEPG*ERLCASHK AFISHKQSH*SPQ*PCQAGVTL SRLQ TTNSRPVPVRRGCGGLEPRP*VS/PS QPTACSENSQGSQSPSKRTLS
949	6446	A	982	145	1315	CLPPPGLGPAPSLSSSCWGPPMPRT IRGIPPGSICRLCFCPAAGLLSLVAL QRPASSPTRHSALLCLRWA*PTSPS LPQSLGSRAQLHSPLP*QAGSPCHA HTCGHLGPPVV*VPLPCPRSHSHSS CLFPAGSQCP*QAPAGVSISCQASSS ASSCGPGPGGYGQTPGPIPETPRDR\ PCHPTPPKSKLQARGPWRAWVG*R TADGSCGKKP*/CGPTIPDPKSSPLA GLSSPPFWFWAETHHPGMP*RGKR DPRKCGNPQPPSPKLRKSPPTAHGD HPAP*FPTGKGWTPKDSWTPGPPP* SRRPRPLN*WTAA*PWGQNPWAWT PAHPRKKP*RPRGSCLSLVSACGK WAPSPTSQGCCEGRCDV PKQQGL AHPTVLLNKCVSCLN
950	6447	A	983	1	682	PPLFFQAAGKMADIQTERAYQKIQP TIFQNQGRGSCCGETGK/EKLPRY YKEHSGLGQRHPKEAY*GPPTLT KCPFTGKCVHFEGGILSG/VVTKM KMQRTIVIRRDYLYIRKYNRLP RKRHKNSVHLSPCFQGTSRFGDI VTGGAKCRPSEARQWRFNVLKGH QGLARHQRSSFQKFLRLGHRGRSPT MEIRLVPASPGKKKKKSFVPTGGAV DSIGGRGV
951	6448	A	984	1	465	
952	6449	A	985	1585	2239	
953	6450	A	986	9	2580	SLPPKKCELRLHNCWGLFSPPARQ SGSVA AVVAASAVSGVSGPQSPPLT CASSLRSPRPARTRPVAVCVSPTTP RLPPRSSLRADMSGDHLHND SQIEA DFRLMDSLKHKD\KQKDENARAR GHKEEKDRVEESKHSNSEHKDSEKK HKEKEKTKHKDGSSEKHKDKHKD RDKEKRKEEKVRASGDAKIKKEKE NGFSSPPQIKDET*DDG\YFVPPKEDI KPLKRPRDEDDADNK/PHKKIKTED TKKEKKRKEEEEEDGKLKKPKNKD KDKKVPEPDNKKKKPKKEEQKW KWWEERYPEGIKWKFLEHKGPFV APPYEPLPENVKFYDYGKVMKLSP KAEVATTFAKMLDHEYTTKEIFRK NFFKDWREKMTNEEKNIITNLSKCD FTQMSQYFKAQTEARKQMSKEEKL KIKEENEKLLKEYGFCIMDNHKERI ANFKIEPPGLFRGRGNHPKMGMLK RRIMPEDIIINCSKDAKVPSPPGHK WKEVRHDNKVTWLVSWTENIQGSI KYIMLNPSSRIKGEKDWQKYETAR RLKKCVDKIRNQYREDWKS KEMK

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						VRQRAVALYFIDKLALRAGNEKEE GETADTVGCCSLRVEHINLHPELDG QEYVVEFDLFGKDSIRYYNKVPVE KRVFKNLQLFMENKQPEDDLFDRL NTGILNKHLDLMEGLTAKVFR/T YNASITLQQQLKELTAPDENIPAKIL SYNRANRAVAILCNHQRAPPKTFEK SMMNLQT/KIDAKKEQLADARRDL KSAKADAKVMKDAKT/KKVVESK KKA VQRLEEQLMKLEVQATDREEN KQIALGTSLNLYLDPRITVAWCKK WGVPIEKIYNKTQREKFAWGHLT WLDEYEF
954	6451	C	987	65	235	MQFRVKYHICSTLLSLKTKICITCIP SHLFPASTIPSWGCFHLYIHIAQKHV ING*
955	6452	A	988	16	148	SPAEQGCVCVCVCVCVCVCVCVCV CVCVCVCVCVCVCVCVCVCVCVQV ACVCN/CVCVCVCVCVCVCVCVCV CVCVCVCVCRCRWLACATCVL
956	6453	A	989	287	504	LPRNFKTIYLDSEMVLESSKRGVCV SVCVCVCVCVCVCVCVCVCVCVCV /C*YLDLNHGKCTHPVSFSVRIFLA
957	6454	C	991	201	488	MGSRPRFCLFTNTLCPDVTSSVC SPKTTXRRLLKXTFMPRCRKPQAVL TSSEMALAACSXFSRSPDDFTQYQV AELVWDSLQPLGQXRSHCSLR*
958	6455	B	992	53	302	MTSALTQGLERIPDQLGYLVLSEGA GLASSGDLENDEHAASAMSELVST ACGLRLHRGMNVHFKRLSVVFGEH TLLETRVLTEX*
959	6456	B	993	277	573	TSALTQGLERIPDQLGYLSSGDLEN DEQAASAISELVSTACGRLHRGMN VPFKRLSVVFGEHTLLVTVSGQRF V*
960	6457	A	994	134	1271	NPGPVQVGVEGGQEEGPSSKKQAK TRQVCLASITEAPGPKIRFSEPLRPP AGCRHQMGSPSTSGSASSPQTPFCPG/ PPSPA VCV/PPKTTGGETHQ TGA*RA HSMPRCSRKTAGCAEQLQRWHWL PAHHSPGPQMTPALHLHSPVGSRA GLGFAPAPGSAQKSSG*RCKS*EAC *RDGRPDTLHLQTQVSGLT/WPQVF SFPSQVPSRPPPPYMLVNTDLPEPPS APTLAPRLPWPSTSHLCYPKGPVLP LWPLPSDPASSPPFVSARPA/ALPAAP EHPPTDPSPAFSSPSLPFPSPLPPRAD RR*GWSAGPPGG/EPHRLGSRDAEP PAGPLAHASSLTIAVFGAGGAPYQI GSFRLQAPVTCLQPLRSSFCLRHWP LAPLA
961	6458	A	995	1	422	
962	6459	A	996	3	760	TSRGRVGTQAGEPRDLRPPPCPSSPL RVAAVVCLEQPERGAWAHNIPQ NGDSAVRSFGTGTGVKLPGPAPD/ NPNVYDFKTTYDQMYNDLLRKDK VELFTQNGILHIAG/RNKRIKPGPERF

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						QNCKDLFDLILTCEERVYDRVGWK I*ISR\EQGDLSPVHVVN\LDIQDNH EEATLG/ARFLICE\VCQCIQHTEDM ENEIDELLQEFEEKSGRTFLHTV\CF ILFSFLDICF
963	6460	A	997	425	591	EYLKQWNVVFVDIKNHL/MHLHA HIHTQV*THTQTHTHRHTHTHTPT CHCLVHTA
964	6461	C	998	120	368	MGTAHKPGYPQISTTVCIYVPDFAIL SPVLSFCRLIYLHTRMLQATELLQ ALQNSTTKGNRRERARDNSKMRH DGRAWRC*
965	6462	A	999	2	393	ARGKKPNLRAFLPLPRAWPEPQTL QQPRWP*TVQLPVAIGDKALALGR RKSGPGPGFVVLRTVPHALSHVRS FRSLLLPLSLTLCVSFSFCLSVFSP PCSDGANPWQSQSWKQEDGSSSPW EVSA
966	6463	C	1000	1247	1716	MLRPRLRCFFSSSQACSSDLNRSV GSSQARPOGSPSSFSASCRKCSSVLH KEGPQLLVVGQVPSFYGPSTCPFHT AAADSAWPCRSRASFKVLSHDFHR PLVLLAAQRLPPARFPLGRLGARSH TAGGAERAGVGAAQQLQRRPRWP GRRARAPR*
967	6464	A	1001	3	630	FCPRGQEFGEENKLLSPRRPWGHFT EEDQGLLSTSLGQG*ILEDAGRKK PLGKAPLV\YPMGPQGFL*TGFGQ PCPSCPLPIMGQPPKVQGHMAKKV LTSLGEMPIKH\DDPQGHLCPSLSE LHCDK\LVDPENFKLLGKCAGDV FGNPFRQRIHPWRLQASWQKMAED GDCKWPVPCPPDTTEASWPMNSEA FKDKAFILASNYK
968	6465	A	1002	41	625	APSPDAHGVISQRRTKATITSLGQ G*ILEDAGGRKPLGKAPLVVLPKW DPKRSFEQALGNPVPLPSA\IMGQPP KVQGHMAKEGA*PSLGEMPIKH\LD DPQRAFFAPA*SELH\CDK\HVDPE NFKLLG\NVLVTVLAHFGKEFTP/E RLQASWAEDGD*SGQCPVLQIPLK PLGP*IQKLSKDKAFILASNYK
969	6466	A	1003	106	1315	KQSGRAPGKVVSRAFPGLNPCGW K\LLTQ\VGAVLGRGDGLGAALG PGNRTHIWLFRGLHGKSGTWWE HLSEENVF\IKQLVSDDKAQLASK LWPLKDEWP\HPWETGSFKV\GL FDLKAGHVGLLWTKDGQKHVVTL LQVQD\CHVLKYTSKENCNGKIGNP VC*EGKTVSRFRKATSILEFY\REL LPPK\QTVK\IFNITDNAAIKPGTPLY AASLFVQGGYVDVTAKT\GKGF\Q SCSLKRWG\FKGQPAYRIGQTENPT GRPGA\WAT\GDIGRVWPGTKMPGK MGKHIHGQNMGLK\WVR\INTKPPH YVNGSVTDIKNCLVKV\KSLP AYKDLGKNLPPFYIIFLMGDGRGNL PERFCID*KPCCQPRWRPPINICPNIL



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						WDVGRTLTIFL
970	6467	A	1004	218	530	KFEGCLPPRDETRIPWARRCAYVV *SKEVSL*HCNTVTPGVGKPNKTRVI WGK\VTTRAHGKPVAMVRAQIPEG NLSCLRPFGRHVRSDGCYPSRILNLT EKS
971	6468	A	1005	2	269	FESEDEGEFFDDWEDDYDYPEEEQ LSGAGYRADKMFRLRTREPALDGGF QMHYEKTPFDQLAFIEELFSLMVVN RLTEELGCDEIIDRE
972	6469	A	1006	1	456	AELSELYEESDLQMDVMPGEGDL PKWEEATGTRAAIPWVPPATGAQQ LEEEGPMEEVEEAQPMMAPEGKRS ANGPNAGEQPGQSPGRRTSRAEDE AIEFDDWEDDYDFPREEPVKGAR LRFLPPS*KTPPSFWENRNTPLWGG LKIFY
973	6470	A	1007	563	771	WSMVSLCSTAAVAPVCSRIPERTR ATASVTHFCGDLG*SPVKPLSLGYR SNLGGPEEGREGGRKARRK
974	6471	A	1008	300	391	AVCTMSEMAELSELYEESDLQMD VMPGEGDLQMEVSGSRELSLRPS RSGAQQLLEEGPMEEEAQPMMAAP EGKRS LANGPNAGEQPGQ\ VAGAD FIESEDEGEFFDD\WEDDY\DYPRRR SQLQWCPVTRVSAALEEA\DKMFL\ RTREPALDGRVSRCHYEKTPFGSV SLLSEELFFT*LVCQSV*PEEL\GCDA WRG
975	6472	A	1011	100	270	LRSSAVTVLVSLIHSPSSFAHHPVSD T*PHCLESPPGFKAIFIRGLFTEACF CRIA
976	6473	A	1012	13	670	RQRPKARASIPHLHQPPQEACQPPAA ALTRPQPRP/PSALSHPAKPHSVSSA GSSYKNNPFASSISKHGVSSGSSSSG GTPVQSSVSGSLVPGIQPPSVGQATS RPVPSSAGKKMPGFPEVDSGSPSRR SK\GDSSGGTQGVAKLLTSPSLKPSA VSSVTRLPPCQKERVGLCCWPAPL *WLHPTNPAQSCCLGP*ARTPRGLG AAGVSLAQRKSLSTYRA
977	6474	A	1013	3	578	GIPWWTHASEAVQTEIPVVGPREW QSC*PRR/RLKPSAVSSVTSSTLSK GASGTVLLAGSSLMASPYKSSSPKL SGAMSSNSLGIITPVPIPVQCSAL TPLPKQGSMPSSQALPPGPSTRP WPQSSGWLALQPAPCSASPTRCGA HPYPAESAR*SPDGQCAHAHRVPLP SPPLGALPLPRVLVSLP
978	6475	C	1014	426	653	MVTWGGGSHQRRERKEGPGTRVFM GREALESPCSASHCRPLLGFELSNT NLLWLFCYYLRLLCKQTGNPSCK KYI*
979	6476	A	1015	1286	2318	RTVPFYPMLMVMMKTEPKIGVCK NPIIIVESTKVFLKELHCHVPREKL APTIVST/PLGVLSISQGCSPSCGS/ GPEFCPL*AHSLGMGRHWDHPGSL

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						LQPEGAPEQWGALRYSDQMPGDQ ADSPTGVPTALPPEPVNTVPPTTAQ RKPQPRAAPLTTV*RQSCKAQSTGQ SAPPEQQGPGSLHGRHIRSAEKRSA ENSRSSRRTPSSRKGA VSVHPGRPA RSDS\PRPKWQALPLKRSQFPWYSR PFPVKLRSTWKRVRKIRTQVFHAL* FP*GSSNQTSRETPK*QKSPNAECRS AQTSHETPASSYSCTLLLATACKHTI TVKVGGHSAQCFQNSNSAVQL
980	6477	A	1016	315	480	
981	6478	A	1017	1	1845	
982	6479	A	1018	1	447	
983	6480	A	1019	218	544	SGFSLSLRGSISFSL/CFKVGMCVTY PRCYC*S\VPV*KPLIKPGWVSELPKP MNWASCSRTLASFLLQAARSHPW PMKMETMEQSKLRSQPCKPAAGAV DPRAVVHGT
984	6481	A	1020	198	562	LKCGKQWSDPITSPQTESQLLGSSQ QQLHQQRHLQGP*K*NRDSPLCFSL SSCPIPKTYTNRHILLP/SSSKSLCKF L*PA*ISPQKMGFSFLSQSVCKFSKL LCSASLIKLFKAFNSIQVTS
985	6482	A	1021	72	270	
986	6483	A	1022	545	812	
987	6484	A	1023	477	750	
988	6485	B	1024	537	867	XEQAAPCSALSPLMASCLRGHGEA RADPWSSTRPIDLKFKGPFDDVVT NLKLRNPSDRKVCFKVKTTVPHRY CVRPQQWNLLTPGSTVTVSVMLQP FDYDPNEKSKHKFM*
989	6486	A	1025	822	1750	SSAEPSPSPAPSQQTAAGAPPLC AVSPMASASGAMAKHEQILVLDPP TDLKFKGDG*VFIRPEQYTV*KWC KRSKRHGPFRP\FTDVVTNLKLRN PSDRKVCFKVKTTAPRRYCVRPNS GIIDPGSTVTVSVMLQPFDDYDPNEK SKHKFMVQTIFAPNTSDMEAVV/W KEAKPDELMDSKLRC\VFEMPEN DKLNDMEPSKAVPLNASKQD\GPM PKPHSVSL\NDTETRKLMECKRLQ G\EMMKLSEENRHLRDEGLRLRKV AHSDKPGSTSTASFRDNVTSPLPSLL VVIAAIFIGFFLGKFI
990	6487	A	1026	184	282	VIAQNIFVLSSVTGPKDRSGRQPLV FLKSPG*THPS*SVSRNLFS\FA*PGD FRKTKGCRPDLSFGPVTLLRTKIFW LAIT*D*CFLG YIKMGHIVEHCQQ
991	6488	A	1027	445	992	HCCGRNCLQRRWG WKRVRSLLAGI VFVSPFFKLELQKPLPSEQITIGML LPFFPHFFCCFVFCFLFVCLFF*DRV MLCHPGWSAVVRSQTLVTSASRVQ AIIICSLPSSWDYRHPPCLAFSR/DR GFTILARLVLELMTS*ATTPSLFCCFI ADSVQQYAPSLYILRNTNPRLLAK IFVA
992	6489	A	1028	33	476	HEDHAGPEPPRSYIPPYNATVVQKL

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						LDQGALLMGKTNLDEFAMGSGSTD GVFGPVKNPWSYSKQYREKRKQNP HSENEEDSDWLITGGSSRGSA AVSA FTCYAALGSDTGGSTRNPAAHCGCL V/GFKPSYGLVSRHGLIPLVNSMDV PG
993	6490	A	1031	187	1611	RAWERQERQRSGCSWLTRGVRRG GEGRTTRRKMASKEMFEDTVEERV INEEYKIWKKNTPFLYDLVMTHAL QWPSLTVQW/LSLKVTKPEGK\DMP LHWLGLGHTSD*SRILVVARVHI PNDDSQFDA\SHCDSKGEFGGFGS VTGKIECEIKIN\HEGEVINRAR\YM PQNPSHPLLTKTPSCLMVLVFDYTK HPAKPDPSGECNPDRLRGRHHKEG YGLSWNSNLSGHLLSASDDHTVCL WDINAGPKGKIVDAKAIFTGHS AV VEDVAW\HLLHESLFG\SVADDQKL MDM\WDTRSQYHLPRPSSLGWDA\ HTA\EVNCLSFNPYSEFILATGSA\ KTVALWDLRNLRLNLHTFESHKD\ EIFQ\VHWSPHNETIFGFKCTCRRNLN VWDLKIGKEQSPEDAENGPPENLL IHEGHQVKISDFSWDPPMKPWVICS \VSEDNIMQIWQNGLKIFYNDERVR CHDHPKLEGKGS
994	6491	A	1032	3	551	FLAPVEVSEGSFAEIWGQITGVGLF LCLGESPACWERGLSKRDLMSVKA CGPKAHFCLGYKAGGLPGTQRGAT QALL*KFEGVYARRMKPDSNLG\RR CAYVV*SKEVSL*HCNTVTPG\GKP NKT\RVIWGKSKLGAHGKQAWWF VPKFPKAIIPA*RPFGHR\IRSDGCYP SRILNLTEKSN
995	6492	A	1034	20	867	ALERRVRKSGDCCTDSGMTNIFDR K\ITFDALLKFSHITPSTQQA/HMKK VYASFA\LCYFGAA\AGAYVNMVT HFVQAGL\LSALG\SLILMIWLMATP HS\HETEQRKRLGTSLLGFCIPYRKL LGPALGSFVIAVKRQASLPTAFMGH SNGSFPAFTLSALLC\RRPRS\YFLG\ GILMSALS\VAFCPLG\NVFFWIPF WVFQA\NLYVGLVVMCG\FVLFD QLINEKAEQGDQDYNL\WHC\IDLFL DF\ITVFQKNSMKDPGP*MKKDKKK RRRNEVTIQPFPI
996	6493	A	1035	153	546	PAQETGRPRSKAHVASTWRAFPPE DQVLLAGAP/LWEDEAHFWAKCG VEAL\TTLEVTRPACLEGK\VHGSL ARAWKSDEGQTPK\VAKQGERKK KTGSG*/RRPDSSYNRRFCQTLLPTF GKKEGPQWPTS
997	6494	A	1038	1	433	
998	6495	A	1039	101	1898	SAAMIGGLFIYNHKGEVLISRVYRD DIGRNA\DAFRVNVIHARQQVRSP VHQHLLRTSFFHV\IRRSNIWLGSSS PRQN/VSTVAMVFEFLYKMCVMA AYFGKIS\EENAKNNFVVHYMELLD

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						EILEFGYPQEFRD/SGALKTFITQQG IQGVQAS/AQKEGSSQFTSQVTGQIG WRREGIKYRRNELFLDVLESVNLL MSPQGGVLSAHVSGP/VWVMKKNYL SGMPECKFGMNDKIVIEKQGKGTA/ G*NQARAGKQSIADDLHLSTQCVR LS\KFDSESRISIFIPPDGEFELMRYRT TKDIILPFRVIPLVREVGRKLEVKV VIKSNFKPSL\G\QKIEVRIQPPLNT\ SGVQVICMKGKAKYK\AGENSFVW KIK\RMAGM\KNTHIIEIGFLPNKEK KKGCCPPLFPRNFGFKFAPSGLKVG \YLK\VLNPKLNYSDDHVIKWVR* GR\SGIYENSACKATRQLAQLPQPPF LQQVQVPLLPQTTHQVSPSPPCFAC PSPLQPSPEVLGLGQSNITKWDWRWK QPLGSPGQGSSEGSCSPHPVCSWP NAQALSSVTQSPGGFPFLPHPCGHS SGVGGLVAPHLRAPPKASEWIPGLS PYSALG
999	6496	A	1040	255	662	TGEGYAGTEATDITHPQLRNQQWV PRCKPFPICDLKIQPERNYLFFLR/QR VSLCHPGWSAVV*SRLTATSAPFGS SYSPAFLSPSSWDYRCAPPRPANFCI FSRD/RGFTMLARMVLIS*PVIHPP WPKVKVLGLQA
1000	6497	A	1041	2	297	TLILPQHVNCPPGINAWNTITSYIDN QICQGGQKNCNNTGDPENCPENG CVPDGPGL/VLRDSGSHSIRLHSA/ LGDPAPKSQDFMNYIGLTIDLRIS
1001	6498	B	1042	1	786	MAPHPGSLTTLVPWAAALLLALG VERALALPEICTQCPGVSQNLKVA FYCKTTRELMLHARCCLNQKGTIL GILPQHVNCPPGINAWNTITSYIDN QICQGGQKNCNNTGDPENCPENG CVPDGPGLLQCVCADGFHGYKCM RQGCLSAAPQALAGKWPPKNCHL PSFVDGQPOGQKEPCNNYPSIYTFV PVCQGICGIKMLKTELLHLKYWDIG PGNRNSYKFAAGNVKFAVTLNSL LIPQKAKRNYHMTQQFRS*
1002	6499	A	1043	137	1021	GRAEAGSLASQCVALASGSPVLLG GPAVLISLTLDPAQPDMPMSRE RAKFVKSGL\YCKTDTKS*CLHARC CLNQKGT/ILWGLDLQNCSLAEDPG QNFSIRHITTVIIDLQANPLTGDLAN TFRGFTQLQTLILPQHVNCPPGINA WNTITSYIDNQICQG\QKNCNNT GDPRKCVPEKGILCYLNGPKVFWQ C\VCADGF\HGIQSVLPGLVPHCL MFLREFWEPTHSIRL\HSAFAGGSA* KAKDFHGTIYIGSLPFDLKLINLELSLA PVRGALLPRKGIFRPVGFRLKG
1003	6500	B	1044	203	308	XRPLFAPVRARAVEAAGPGSGRAA EHSPTGTAGCA*
1004	6501	A	1045	78	308	
1005	6502	C	1046	35	259	MQFSTHRGQKYERTPDTSGARVIER PYLTVIIHHNNLEGLRLEKESGKPYKF

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						AFYVILRCHFTDNFTTAALFVTR*
1006	6503	A	1047	162	1341	PPFQLIMGEIKVSPDYNWFRGTVPL KKIIVDDDDSKIWSLYDAGPRSIRCP LIFLPPVKWNCKMSFSRQILALTWM GLTGLIAFAVIPVYCDHLEFCDFGR KLLDHLQLADKVHLFGRFFGKGLWP MRFTGIPLQIS*SPIPLILCNLSMDTS IFNQTWDCKQLLA*CPAFMLQKNSS LG\IFHPGPGGPYGWAGCHLDFHG* DRA*ESFGVQELNLAQGLTLELSK FLCGNLH*NSGTYL*TIYGMCLDPG GGAFLKLLKKKWKLYPNPCKKL HLKTGGNFPYLCSAEGNLMVQIH LLQFHGTKYAAIDPSMVRPRSLRC RKAALASARRSSSVSSPVNDELTP VCSLYSQWAFSTRSDRPFQVPSG LTRGPHWGLGKVGLDGHL
1007	6504	A	1048	321	888	VELSVHPPIPADPRSLLAGAMPWKL PISLPAE\PPCSLSCCLLPATQHPLH PALPAVDGAKKNPVFSGRLPPPP/PT QRTSASGISALYA*DREV*AQISELW AMRG*VQKVGTVQISRAGQLAAV TSVGNMSVYPLALMTPPPPSPPLPP PPPPVGRWSVGLRDLSPAVPSSEV CLWRSVLCLIPGY
1008	6505	C	1049	137	320	MLKSSFTCFPTEKGPKFLEDNLKTK XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXLV*
1009	6506	A	1050	231	477	GVYFIFFIGLVVFCFVLFDDGRFTVA QAGVQWCDLGSLLQPP/PPGSNDSP WPQLPE*LGITGACHHARLIFILLE TGFRPC
1010	6507	C	1052	60	523	MAEAGFIHCPTENEPDLAQCFCK ELEGWEPDDDPMPQKPTIRRNLR KLRRKCAVPSSSWLHGLRPLRLXLP PRVAAPLPGFIPWCHQPSGPLSNV LGKEINIFKLDVSTVLLFCLESGTRG VLPVQVRVLLVQLLALSLSPPFGGPF WRFE*
1011	6508	A	1053	61	208	IFETGQRKSQEQNWSYSVTQA/GVQ WCDLGSPPRPPGLK*FSHLSYMG
1012	6509	A	1054	198	1011	QTHGLQQPSQHLP/TSTLRTVTAST/ SMRSRHHHCGRCHANKAVSSSKR DTAFLPHFSPGKPGNQNSKNEPPK KRERERSSHCPAAPAAQAEAPLVP LSRQNKSTVETSNLKMILISFPKTLR GPQEGWWHQINPGSGAATLPGGS SERPQSIEASCSMARRTFFAVSSNSF FLLLVSFALLFLALSLSFFKNSPRVNS SNCFLTERKAQPDECFLCSSMGSSS GSQPSSSLKQKKHWAKSGSFSVGQ WMKPASAIRSGVQRSPRRASS
1013	6510	A	1055	1077	1457	ARRPEPPHPAHRRGGGTPAQGGAG SPGASDTSRLRLEAPPQSIACWRSCC NAASWWTRSRGTCSRQTQR*GWP* CWRAQRGCAPALAAPQFLAAHHG QRSAAASTTPGLHAGLRRSRPPRP PRP

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1014	6511	A	1056	2583	3580	DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS\DSPT LASQSAGITGVNHHAWLFFCS/RD TVSLCYPGWSRVA*SRJTATSA\PG K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLR\YPPA SASQSAEIIIGVSHHTWPQEVFLNLN FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYLFYFHRDEGSLCCPGWS* TPELK
1015	6512	A	1057	166	409	WSDVVGTRHLSAASFNSHAFWNLE EELTLVKGQALPSRGLDCPGRPAPP AACPGPKWRACLWV*FPNQNPISPG RNFNLKT
1016	6513	A	1058	10	604	ARPPKKPTSPTATTTTR*GARPATPP PRRPTAPIRWPCTPSTAPPRACI*AT AP*QPQAPHQQTAAFWASPPPSH QAPWIPFPLQPPS/LPPPPHSPRGP PGAQQGGAPAEKPWRPWTAR*D WTPPGAGLELGGSPGLWGHRRARE GGAGEGRGFPEDRGTGRFYKRIFVGR GDSKLPGPRGSFRSFSGKFFLCF
1017	6514	B	1059	167	355	MASGSNWLSGVNVVLVMAYGSLV FVLLFIFVKRQIMRFAMKSRRGPHV PVGHNAPKRSHFILK*
1018	6515	A	1060	67	458	
1019	6516	A	1061	164	528	
1020	6517	A	1062	203	364	
1021	6518	A	1063	103	1019	GNGRGAPGDPCAVASAEPLTSQD SGVNPNNARGREAMASGSNWLSG VNVPLVMAYGSL/DVCTAIYFCEEA NHALCNEISKGTSCPCGTQCPQGT* K*EIDIRLSRVQDIKYEPQLL\ADDD A\RLTTGKPRGNQSC\YNLVIGM KALGLPFRTS\EIFHSEGRHSFP* WGKNFRSYLL\DLRNTSTAFQGCTA KHLIDTLFGMAMET\ARYGDKGVF WPRMKYLR\YQELSELATAVKARI GELFSDIH/HVQAAKDLTQSPEVSPT TIQVTYLPSSQSKRAKHFL\ELKSF K\DNYNLT\AESTL
1022	6519	A	1064	1027	1365	PEVNRLYCLFKNKI*KALLSFQTYIC IYVLDVLIRESKMFVKMCQVVVCVC IYMCVCVCIH*CVCVCYIHTHTHT C/VCDW*AIQ**TCPHYFFLILDQCC PNCTFPLMVTML
1023	6520	A	1065	675	819	HRLDRAHP*RAEGNCLLPVYLSY/G PLIA*TGQGTSSPCLCSL/*PRSAIHT PSQPGDPRQPQTVHSGELNPRVYTK
1024	6521	A	1066	3	603	VDDFVQPARRRWEMLGVLPVSFLG LRRFVHPAKGMKQTRGDSFAFQSG

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						SPGVCFEGQEAEGSLSYGVGLIAAG FVLLSPPSQC/HDSLATQVLVCGVA LLWPSSGRAGTVQP*PAPENRSASP FCLPGHIQVPVFTVPRSAITHTPSS NLGTPRQPQTVPLRGAESPGQPCPM SLRKLPQARPLVLYTCSCHPAVDEC FR
1025	6522	B	1067	46	1983	MRPRKAFLLLLLGLVQLLAVAGA EGPDEDSSNRENAIEDEEEEEEDD DEEEDDLEVKEENGVLVNDANFD NFVADKDTVLEFYAPWCGHCKQF APEYEKIANILKDKDPPIPVAKIDAT SASVLASRFDVSGYPTIKILKKGQA VDYEGSRTQEEIVAKVREVSQPDW TPPPEVTLVLTKEFDEVVNDADIIL VEFYAPWCGHCKKLAPEYEKAAKE LSKRSPPIPLAKVDATAETDLAKRF DVSGYPTLKIFRKGRPYDNGPREK YGIVDYMIEQSGPPSKEILTLKQVQE FLKDGDDVIIIIGVFKGESDPAYQQY QDAANNLREDYKFHHTFSTEIAKFL KVSQQLVVMQPEKFQSKYEPRSH MMDVQGSTQDSAICKDFVLKYALPL VGHKVSNDKRYTRRPLVVVYYS VDFSFDYRAATQFWRSKVLEVAKD FPEYTFIAIEDEEYAGEVKDLGLSE SGEDVNAAILDESCKKFAMEPEEFD SDTLREFVTAFFKKGKLKPKVKSQPV PKNNKGPVKVVVGKTFDSIVMDPK KDVLIIFYAPWCGHCKQLEPVYNS LAKKYKGQKGLVIKMDATANDV PSDRYKVEGFPTIYFAPSGDKKNPV KFEGGDRDLEHLSKFIEEHATKLSR TKEEL*
1026	6523	A	1068	1	849	
1027	6524	A	1069	74	2705	KKLDFFRSLPVFQADFSHWQLFRVL FLLHPPLVISMDSWFILVLLGSLIC VSANNATTVAPSVGITRLINSSTAEP VKEEAKTSNPTSSLTSLVAPTFSN ITLGPTYLTTVNSSDSNDGTTRTAIS TNSIGITISPNGTWLPDNQFTDARTE PWPGNSSTAATTPETFPSPGNSDSK DRRDETHIAVMVALSSLLVIVFIIIV LYML/RGFKKYKQAGSHSNFRLS NGPH*GMWEPQSVPLAARSPSTNR KYPTPGPWDKLEEEINRRMADDNK LFREEDALPACPIQATCEAASKEE NKEK\NRYVNILPYDHSRVHLTPVE GVPDSDYINASFISGYQEKNFIAA QGPKKETVNDVFRMIWEQNTATIV MVTTLKERKECKCAQYWPDQGCW TYGNIRVSVEDVTVLVDYTVRKFCI QQVGDMTNRKPQRLITQFHFTSWP DFGVPTPIGMLKFLKKVKACNPQY AGAIVVHCSAGVGRTSTFVVIDAM LDMMHTERKVDVYGFESRIRTOR* QMVQTDMMQYVFIYQALLEHYLYG DTELEVTSLETHLQKMYNTIPRTNT

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						NGL*EEFKKLTSIKI\QNDKMRTGNL PANMKKNRVLQIIP*EFTRVIIPVKR GEENTDYVNASFIDGYRQKDSYIAS QGPFS\HTMRDFWRMIWSGKSCSIV MLTELEERGQEKCAQYWPSDGLVS YGDITVELKKEEECESFT\VRDLLVT NTRENKSRQIRQFHFGWPEVGIPS DGKGMISIIAAVQKQQQSGNHPI TVH\CSPPGGKERTGTFCALSNVLAE RVKA\EGILDVF\QTVKSLR*\QRPQI GSRQLEQY*VLAYKVVPGVILDAIP QINAQLQSKAANKGPVDPGGLPFNI LVIFLFC
1028	6525	A	1075	734	1151	YRRGPGGLRWAEMSGDFPPIPLPVR GIHPIPLRASQ/PVL*GGQQGMGTGP ISQ/PGETEFQTGLSACPKPHRVPGP SSCTTEKPSQRLHEQMVRGG*SSMG GAGNGVGMESGTVQGTSPSGSWR PAGTGVGARNCWYLPL
1029	6526	A	1076	118	399	
1030	6527	A	1077	1	214	LLMRVSLPSEVFFCVVFETESRFVT QAGVQWHDGF*LOPPPPRFK*FSCL SPPSSWDYRHVPPCLANFCIF
1031	6528	A	1078	2	152	ETESLYVTQAGV\QWHDGLGSLQPPP PRFK*FSCLSLPSLTTFDTSLSME
1032	6529	A	1079	2	426	
1033	6530	A	1080	1	1716	
1034	6531	A	1081	2	886	VGGRGEALDGGGSGAPPSVSQTES RAGTMSAYPEKSYNPFDDDDGED\EG ARPAPWRDARDL\PDGPDAPADRQ QYLRQEVLRRAAATAASTSRSLAL MYESEKVGVDSSSEELARQGR\VLEA HREDGGTRLDQDLKISQKHINSI*ER VLGGLVN/YTFKSKPVE\PPPE\QNG TLTSQPNNRLKEAISTSKEQEAQYQ ASHPNLRKLDDTDPGPPEAWASAP GVLMLTPKNPHLRA\YHQIDS\NL DE\LSMGLG\RLKDIALGMQTEIEEQ DDILDRLTTKVDKLDVNIKSTERK VRQL
1035	6532	A	1082	1549	1712	SNL*FFFEMESRSVARL\ECSGVIS A\HCNLC\PGSSNSPT\SAS*VAGITG A\THHSRLLFVFLG\ETGFHHVVGQA GL\DSLTLMIQPALASPKCLGLQAVS PPMPSPYSSSFFCPLNLT\PHVLYPG LNPPSSFCSDL
1036	6533	A	1083	2	336	
1037	6534	A	1084	218	1080	PSSRMNHLPEDMENALTGSQSSIAS LRNIHSINPTQLMARIESYEGREKK GIS\DVREDFCLFVTFDLLFVTLW D**EFKC*MGGHLRNTFRRRR*LQY *LTISSIFLILFLPGQFFRF*KCLILAY A\VCRLRHWWGQ*RLTTAMTSALL LAKVILLKLSSQGAFGYVLPFISFIL A\WIETWFL\DFKVLPQEAEEENR/L SLIVQDASERAAL\PGWSFWMGQF YSPPGIRRQDLEGLKEKQGLRKP



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						LFRNYEYYFLFKCGKLTESHGKK RQAVESPCRQ
1038	6535	A	1085	3	400	
1039	6536	B	1086	333	436	XTPVFSYGDEIGLDAAALPGQPHEG LLLRFPYAA*
1040	6537	A	1087	127	2041	RGVWGGHVPGGSREEWSGEDQGG KRRGDAVAENCAEAREAGESVLGP RVQVGVEPPSDRKLRRVAGSAGTM SQDTEVDMKEVELNELEPEKQPMN AASGAAMSLAGAENGLVKEIFPQ KKKGGGSAEDEAEAAAAAKFTG\L SKEELLKVAGSPGWVRTRWALLLL FWLG\WL\GMLA\GAVVIIVRAPR\C RKL\PAQKWWHTGAL\YRIGEPLRP FQGQRRGANLAGSLKGRLDYLSSL KVKGLVLGPIHKNQKDDVAQTDLL Q\DPNFGSKEDFRSLLAHSVTKNL RGILD\LTPNYRG*ELRWFTQVDT\ VATKVKDALEFWLQAGVDGFQVR DIENLKDASSILGLSWQN\SPKGFSE \DRLLIAGTNSSDLQILSLESNKD LLLTSSYLSDSGSTGEHTKSLVTQY LNATGNRWCSWSLSQAR\LLTSFL PAQL\RLRYQ\LMLFTLPGTPVFQAT GNE\IGLCSCPLLQPMGGSQFML WDEVPAFP\DIPGGC*VANMDCGR GQSE\DPGSL\LSLFRRLNDQRSKE APPYCHG\DF\HAFPLPGPWTLSPIR QLGTQNETFSG*CLNLGDVGLSAG\ LQASDLP\ASAKPWPADLLSTQ PG\REEG\SPLELERLKLEPHE\GL\LL RFPYAA
1041	6538	A	1088	652	905	HLLPPLTPTTTQWGRDLLSPISQM RKLHRKVKKKTRT/WPGVVDHPL\ NLSTLGGGAWRIA*GQEFETSLGNI ARPCLYKKKFK
1042	6539	A	1089	3	591	
1043	6540	A	1090	266	1905	LGGHTWGTAAAGVWSDWPGRSW AELTSENSAGLSPSWGSPQDEVPGA WPMLOGAVEPMQIDVDPQEDPQN APDVNYVVENPSLDLEEFAASYGL MIERLQFIADHCPTLRVEALKMA LSFVQRTFNVDMEYEEIHRKLSEAT RSSLRELQNAP\DAIPESGVEPPAL\D TAWV*\VTRKKALLKLEKLDTDLK NYKGNSIKESIRRGHDDLGDHYL\D CGDLSNALK\CYF\RPREDYWTS AKH VINMCLN\VIKQGRFTLQNW SHVLS YVSKAESTPEIAEQGERDSQTQAIL TKLKCAAGLAELAARKYKQAAC LLLASFHDHCDPELLSPSNVAIYGG FCALVTF\DRQELQRNV\SSSSFQV VLGSWEPQVRDIIFKFYESKYAS\C LRRLDEMKNLLLDMYLAPHVRTL YTQICN\RALIQYFSPYVSPDMHRM AAFTNTGGPPWKNELIKFIL\EGLI SARVD\SHSKIL\YARD\VDQRR TTF* ESLCLMG\KEFQRRAKA\MMLRAA

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						VLRNQIHVSYPTQRKDARGELTPA NSQSRMSTNM
1044	6541	A	1094	2	397	SQDHVRGFLEKESAI\SRPLNPFTA KALSGTSPGSDDDVQPGPSVGPPSK DKDKVLPFSWIPSLTPEAKATKLEK PS/RLECVEKLIRKDMVDPVTGDKL TDRDIIVLQRRGTGFAGSGVKLQAE KSRPVMQA
1045	6542	B	1095	30	310	MTRHGKNCTAGAVYTYHEKKKDT AASGYGTQNI\RLSRDAVKDFDCCSL PRSCCHAYEKQ\RGTRREEQKELQR AASQDHVRGFLEKESAI*
1046	6543	A	1096	29	449	
1047	6544	A	1097	2	1069	IETRCTPRCRNSARGESLVRMTRHG R\NCTAGAVYTYHEKKKDTAASGY GTQNI\RLSRDAVKDFDCCCLSLQP CHDPVVTDPGYLYERE\AILEYIL\H QKK\EIARQMKGLTRKAGGGTRPPK EQKELQR\AASQDHVRGFLEKESA IVSRPLNPFTAK\ALSGTSPGSDDDV VQPGPSVGPPSKDKDKVLPFSWIPFA TPRAKATKLE\KPSRTVTC\PHVKGS PLR\MSEPERPVHFHNR*NSS\VEPR GASITPQASAYVCA\VTR\DSLSKRQ PPVA\VLPSGAVVTLE\CEVKLIRKD MVDPVTGDKLTDRDIIVLASGAVT GFAGSGVKLQAEKSRP\VMQALRC AGGPNKPGLGP
1048	6545	A	1098	5	576	SRVVEFAKMAENSGRAGKIIRDDSG VKGAVSHEQVIAGLQTTFRNQRG LASQS\AAELGDWKLNEATALVIDT TGREVIDETRKCYRMVWKEFLVEA NLSKEVACPAFGRTTKEQIQKII*DT *HSSFQAKGKELK*ISGKKHNI\RVL MGEDEKPSQPKENS\EGGLGLKASIS AGVVWSPRDQGLCIFLP
1049	6546	A	1099	534	1004	RMSAGALFIWGTA\YFDRKKTEVT PNFQEPGFRERRKKQKLAQGEKLG FPK\LPD\LKDAEA\QKFFL*RN\TSL GEEL\LAQ\GEYEGV\DVHLTKPELP VCGQPTASLLQVL/QQANFFPPPV\F QMLLD*SSPTISQRIV\SAQSLAEDD VGMRNKCLH
1050	6547	A	1100	91	942	GLLVGVGAAAVMPGIVELPTLEEL KVDEVKISSAVLKAA\AHHYGA\QC DKP\NKE\FMLCRWEEKDP\RRCLE\ EGKLVNK\CALDFFKA**NRHCAE/P LFLQEYWGLCIDYTRPSKLPSTVR KQAGKSFDEC\VL\DKL\GWVRP*PG ENCQKVTKVKTDRLPENPYH\SRP RPDPSP\EIRGEILQP\ATHGSRFYFW TKLKMGPVAHTRSCAQTTTDENAH AGLHPTDSGVLSGIHQHLTKKLTID DLAVILYHFLSIKIFKGEAPPLQHYP QSHQTTLCSQNPNG
1051	6548	A	1101	140	812	GDFGDRAGAGRETEEIFHSSQQLKI RPWAGAGRAAEPKDWRIWGTGEW GSRQIPSPVPSPSRNP\HFLPQAGAG

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						HFVQNPCKYPTPSPLQRSLEELPLSP TVFKLLHPDPPPCAKPLTLQPVAPK *I*ESPPLPPMLDPRDFSPAPHPANE LKKRRGNPRQWFFLSEPRLSHLQN GTGWGWKGKDGRRRTGMELGLI PEAPVPISGPPFIHSHSQPPCYTGL
1052	6549	A	1102	228	860	STAQGNLLTVFIQPRASMSGGKYV DSEGLYTVPIREQGNIYKPNNKA MADELSE\KQVYDAHTKEIDLVP RPLNIFNG*PWSKIDFKDVIAPEGT HRF*RAF GKASFHLSL*RYWFLP LCWSALFGHPRWALIWHGFTSANS LLFLAHL/WAVVP/CIK/SFLI*GFQCI SR/VSYSILRSTTGLVTPLEAVG\KI FQQLSASN\QKEI
1053	6550	A	1103	825	920	
1054	6551	A	1104	222	1244	RWEKKMALLCYNRGCGQRFDPET NSDDACTYHPGVVFHDALKGWSC CKRRTTDFSDFLSIGGCTKGRHNSE KA\PEPVKPEVKT\TGKELCELKPK FQEHIISSPLSQ*KQLKRSPDEPMT NLGIKNIWPLKQALDKLKLSSGNE ENKKEEDNDEIKIGTSCNKGCSKT YQGLSLEEV CVYHSGVP\FHEGMK YWSCRRKTSDFNTFLAQEGCTKG KHMWTKKDAGKKV VPCRHD LHQT GGEVTISVYAKNSLP ELSRVEANST LLNVHIVFEGEKEFDQNVKLWGVI DVKRSYVTMTATKIEITMRKA EPM QWASLELPAAKKQEKQKDDTTD
1055	6552	A	1105	87	313	ISQERG*RRDKERLAQREIK/RRRER EK/ER*EERIDKKREAKREKR/ERER KIPEREERKKGIFVFIWFNPMSVP H
1056	6553	A	1106	37	404	PQLSRCRSECMYVNPTVMTSMGQ ATWSDPHKAKTMLNRIPLGKFAGE SGGSPASVVPAPVCALGRGGRER WAAASFLYAPDPRPAHEVEHVVN AILFLLSDRSGMTTGSTLPVEGGFW AC
1057	6554	A	1107	19	919	AVWWNSEFLAGRRVLVTGAGK/G WAAGKGGQRPAAGRGGQGTPSLSP LPAGIGRGTVQALHATGARVVA\VS RTQADLDSL VRECPGIEPVCVDLGD WEATERALGSVGPV DILLVNNAAV ALL\QPFL\EVTK EAFDRVCPSASRS FE\NLRAVIQVSQIVARGF/I*ARGV PGAIR/VNVSSQCSQRAVITNHSVYL LPTKGVP LDM LDQG*WALAE LGPH KL SRCRSELNASKP/TTVGD*RSMG PGPPWSDPHK\AKIMLNRIPLGKFA EVEHV VNA\ILFLLSDRSGMTTGS\T LPVEGGFWAC
1058	6555	B	1111	28	384	MKAAVLT LAVLFTGSQARHFWQ QDEPPQSPWDRVKDLATVYVDVLK DSGKDSVTSTFSKLREQLGPVTQEF WDNLEKETEGLRQEMSKDLEEVKA KVQPYLDDFQKKWQEEMELYRQK

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						*
1059	6556	A	1112	44	1009	GGIREGGPPRPFMRKAAVLTAVLF LTGSQARHFWQGG*SPRAAWDR VK\DLATRVPTVLKEQRTETYVS QFEGRLGENS*TLKLLDNWGQR* PSTFQPSCAKQLGP\LTQEFWYNLE KETEGFRQEMSKDL\EEVKAKVQP/ YTLDDFQERSWQEE\MELYRQKVVE PLARKNFQEG\ARPESLHELARRSL PLGEAVSRPRARPMWDALRTHLAP YSDEMMPALGRAPLALRENGGAR MGQYHA\QATEHLSTLSEKAKPALE D\LRQGLLPVLESFKVSFLSALEEYT KKLNTQLRRPPPPYPVLRINVSKV EKKKKK
1060	6557	A	1113	62	393	IPAKQPTPTSLKTPTEECDQHENTAS SPSPMTTPCT/PSTNQSPKLPVSHSP NP*KPPAPKLLREMDLTFPPHFPPSV APTMKPLSSATTPMPRRISLGSHSR RWDPFVG
1061	6558	A	1114	3	450	QTQREPTMVLSPADKTNVKAAWG KVGAHAGEYGAEALER\MFLSFPTT KTYFPHFDLSHGSAQVKGHGKKVA DALTNAVAHVDDMPNALSALSDLH AHKLRVDPVNFKLLSHCLLVTLAA HLPAEFTPAVHASLDKFLASVSTVL TSKYR
1062	6559	A	1115	9	675	NSARATDSERTHHGARLLPDKTNV KA\AWGKVGAHAGEYGAEALERM FLSFPT\TKTYFPHFDLSHG\SAQG* RAHGK\KVA\DALTNAVAHVDDMD PQTALSALSGPATAHKL\RVDPVQL SSS*SHLPCWWTLGRPTSPSEFNW RLHAFPGTKFPGLLVEAPLLEPSKLP LKLGLSLRVGHAFAPLGLPPRALLP FPGTRNPVGLLNKILNWGGKKKKK KKIF
1063	6560	B	1116	61	348	ESALTQLLKAGGSLKKFLFHPGDTV PSTARIGYEQLALGVIAAGAGAIHV EKHPGKLAGYISSLLTLAGFATAMA AVVLCVNSFIWQTEPFLYIDT*
1064	6561	A	1117	2	256	CLSCAFWAGSVVIAAGAGAIHVEK HPGKLAGYISSLLTLTGAFATAMAAV VLCVNSFIWQTEPFLYIDTVCDRSD PVFPTTAIVL
1065	6562	A	1118	3	270	AVVLCVNSFIWQT/EPFLYIDTVCDR S/DALFLAVCVLKVIVSLVSLGVGL RNLCGQSSQPLNEEGSEKRLGENS VPPSPSREQTSTAIVL
1066	6563	A	1119	1	642	
1067	6564	A	1120	46	998	AIVPSWDLDDKDTISLLSPVLCIFSPS SQTSLLYVFSLAGRMTQNTVIVNGV AMASRPTQPTHVNVHIIHQESALTQL LKAG\GSLKKFLFHPGDTVPSSTARIG YEQLAL\GVTQIFAGALRGVIL\GVC *SWGPGTVLRASGCAFWAGSVVIA AGAGAIHVEKHPGKLAG\YISSLLTL

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						A\GFATAMAAVVLCSNFIWQTEPFLYIDTVCDRSDPVFPTTGYRWDAAKSRRNQWQKEECRAYM\QMLRKLFTAIRALFLAVCVLKVIVSLVSLGVGLRNLCGQSSQPLNE/EKGSEKRLLENS\VPSPSREQTSTAIVL
1068	6565	A	1121	504	1026	KIKRKKKRPHIPVLEIPGLLNIPCLWLEWVTLSPSKRFAFAVGGNGGESGWLGGTRP/PSPRGMHLPSSSSESEPHRNCPCPGSAQPCGHQAGSEDPQNTGPVAS/EL*PPACWRLCGQPGPL\GAPAAPLAGHPRPPWRQVGP GTSGSSQSWVSSCDHGGQHSQGHSQSWQ
1069	6566	A	1122	461	548	KNLEQKNAMIHSAGEHHQGAERRSTWEELEGPRVTSLLV*RAWSSGPAAPSPT*PPSCTPPRRSS*APAGPSDASPSRRPRA/SPASRQAAPKDKLPETPRRIEKEP\PGPFAPGIFE/GGFTVSGGREQETPFAGTSGCY/RPTPHFCWLGSPPRSTSSKAGGPSSSPSPPTAEASTARPAKSRTMPTSGWHIGSTRPPRRPSPR*RTSCTAHRRTSCSFGTMPARSRGLHSEIRRLQHQCTDLTYELTVKCSEQTGDGTSSSELKKRCEELEAQLKVKENENAELLKELGAEKRDDSQCWRTPSRSREKKYLGA
1070	6567	A	1123	148	197	DPLGFL*QKRNNQEDD
1071	6568	A	1124	1333	2383	RMKKEHVLHCQFSAWYFFRGVTKSVILPLPQNVKDYLLDDGTLVVSGRDDPPTHSQPDSDEAEIQWSDDENATATLTAEFP*SLPLKVQGSYQIPLGGQVSFPKV*FGSAPRDAYWIAMNSSLKCKTLDIFLLFKSSDFITRDTQPFHCTDDSPDPCIEYELVLEKWCEMIPGGAEFRCFVKENKLIGISQRDYTYYYDHISKQK\EEIRRCIQDFFK\KHIPVQIL*MKDLVFDIYR\DSRGKVWLIDF\NPFGEVTDLLFTWHEELISENNFKRRFLVKVDAQEQDSPSFVAQTSEVTVPQPPLICSYRL\PKDFVDLS\TGEDAHKLIDFLKLKRNQPEGR
1072	6569	A	1125	162	413	GADGQINQQTLLDRSGDECLDECPGPPRRGKGPQREVQPASPPGT HQ*GSDGSSCTPSPV\SIGSPGLGPPIWRPHKPG
1073	6570	A	1126	2	228	GGPRNKEYPYQGPKNRAQSPKNLVHSLTSM*SSP/LPFKPSKSTIIDNCPLTHQ*NPLKP*PLFPPSPNIPPGFKKP
1074	6571	A	1127	302	488	SPICLTPKSSLTHSSDDYKYSVWQRAVAHTCNPSTLGAEAG/WVT*AEFKTSLHNIVRPCLY
1075	6572	A	1128	66	703	RRRRLPSVAIMILPGPSSSHDEMFSDIYK\IRGDRGRGLCLEGGRGWVSRTE\GTID\DSLIGG\NA\SAESPRGAKGTERHK*STGV\DIVMNHHLPGNKF SQKEASKKVHQRTMKSIKGGP*KNRRPRKSKTFL*QGAAEQIKHILAN

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						FKKLQF/YFIGENMNPRAWVLLLDY*RDGVPP\YMIFFK\DG\LEMEKMLTNVAIILDLSCHP
1076	6573	A	1129	1	1006	LLLLGHASTSTGGGGKRAKSMATTKRVLYVGGLAEEVDDKVLHAAFIWGDITDI\QIPLDYETGEK\HRGFAFVEFELAEDAAAAIDNMNESELFGRIRVNLAKPMR\NIKEGSLRPACSDNDWLKKF\SGKTL*ED*RGRVRASQSRDPG/TGRAHLLKRRRSNPQVY\WDIKIGNKPAG\RIQMLLRSDVVPMTAE NFRCLCTHEKGFGFKGSSFHRIIPQFMCQG\GDFTNHNG/TLGGKSIYGEEVSM MENFILKAYGDQGLLS/MLACGDPNTNGSQF\FLTC*KTDWLGWASHVVFGEVHRKALGCLCGQIEAQQSKDGKPKQKVIIAGLWGSTC
1077	6574	A	1130	1	574	DTRFLERLRLSISFLVQTPIGHSTEEDQGLLSTSLWGK\VKCGKNAGRKKPLGKAPLVVLPPWDPKRFL*KSGFGQTLSLCPLPHPWGP KPKSQRHHGKERC LTFPWGDAHKA PLDDPQRA PFAQA *VNLH\CDKPAMWDPENFQAPGEMLLVTVL\AIPFSGKEFHPWRLQGFLGRKMGDLELASALVPSRYH
1078	6575	A	1131	200	740	HGSMRLLIPLALWLGA VGVGVVSQI*ENPSPGGLQVALEEFHKHP\VPQWAFQH/TAVLES AVDTPFPAGIFVRL E\FKLQQ\TSCPEEGTWKKPRVQKSRPQWDG NRKLPWPCIQTWAL EDKSSWARLVPPPIKTQVL AGGWRSTQEDPSCLRVQRAC*RTPPSFYFPQGFAF SK\ALPRS
1079	6576	A	1132	79	933	EWPSIDL VNELQVGISEKVSFLNRKIKPQVPLWYRLDGKVILTA AAQGIGQAAALAFAREGAKVIATDINESKLQELEKYPGYSK/PRVLDVTKKKQI*SSLPMKLRDFDVL FNVAGFCPS\RELVLGL*GRKDWGLLR*ISMWRSTYLMDSR AFLPKML/RFRNLGNIINMSCGLPSVKGVVEQDVCTA QPKASRGLASTKSVGCRFHSRQGHSGANLCVARGTVDTPISYKKEYNATRKS*TTARE*FP*RDKKPGKIPQLPEEISHALRRISASD\ESAYVTW
1080	6577	A	1133	1601	1778	MEQIRASGKLYKSLYQKREIYIMCSTTYIYT*Y/HSTAYIYICLYVHIYIYMYRQYVVF
1081	6578	C	1134	58	394	MAEKPKLHYSNIRGRMESIRWLLAAGVEFEKFIKSAEDLDKLRNDGYLMXQQVPMVEIDGMKLVQTRAILNYIASKYNLYGKXLKGESPFNLREQDAKXCLDPRGNPKIX*
1082	6579	A	1135	133	985	RNLRGIAILAGKPQVQFFHSRG\RMESTRWLLAAAGVEFEKFMK/SLAEDLDKFR\NDGYFDVSSKCPMV*DL MGLKL\VQTRAILNLHLPANYNL/HYGGKDIKGREPLI*YCILGRY*PDFG

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						VEIV/LLSCLPYCSTLREQDCQALPW IKEKN*KNRPTFFPCPLEKVLKRAHG TKTYLVGKKS*ARAGPFHLVELSS TTVEELDFQSLSPSFPLPERPLETPES RQPCPHSERKFPYSPGQPQGGKPSW DEE/SL*EGRQKDFSGFLINGSPWE GPRNLAINPMVS
1083	6580	B	1140	866	942	MDRHCPKLSGAPFGPPAPILGLTDP EFSHEPKLHHARILHRAPPPTRDHP VGVISRLPRAGRGRAEGSPPGDLF*
1084	6581	A	1141	405	536	KSAPRPGVVAHTCNPSTLAGRG/G WIT*GQEFENSLANIVKCCFY
1085	6582	A	1142	49	365	TPDKPIRSHETLPIHEK*PRGKTGPPP DSDDPPPGSPSQHVGNSSQKINSKLP ISSGDHSPNPHYHW*CPLPSVLGIP/PV RRDPLCGPESPQEEGGQQRNESFDIF
1086	6583	A	1143	3	452	
1087	6584	A	1144	9	486	NSARATDSERTHHGACLLPDKTNV KA\AWGKVGGAHAGEYGAEALERM FLSFPTTK\TYFPHFDL\SHG\SAQG* RAHGK\KVA\DALTKRRGATWDDM /PQTALSALSDLHAHKLARVGPSTF KLL\SQLPCLGEPWAAHLPA\EFQPL AVARLPWNKVSWGFC
1088	6585	A	1145	1890	2027	KCLCPPR/RCPQPLTPYPC*GVKCPP SEIKYKP*MCPIGCPKPSIQC
1089	6586	A	1146	1	903	
1090	6587	A	1147	1	1131	
1091	6588	A	1148	1	1376	WALPAGFDGVMShrkFSAPRHGSL GFLPRKRSSRHGKVSFPKDDPSK PVHLTAFLGYTPCL\AHIVREVDRPG SKVnkKEVVEAVTIVETPPMVVVGI VGYVETPRGLRTFKTVFAEHISDEC KRRFYKNWHKSKKKSFTKYCKKW QDEDGKKQLEKDFSSMKKYCQVIR VIAHTQMRLPLRQKK\AHLMEIQ VN\GGTCARESWDWPREGKQQ VPV\NQVF\GQDENDRTSSGVTQGP KGLQRGSPSR\WHTQESCRKDPPE GLRK\VACIGAMAIPARVALPLWQR AGQEKATHH\RTINKKIL*DLAQQ Y\LIKGGKL/VSKNNASH*PMTLSDK S\NPLGGFVH\YGK*TNDFVTFKSL VWLGPKKRVLTLRK\SLLVQTKAA GLWRRITLKF\IDTTSKFGHGRFQTM EEKKAFMGPLKKDRIAKEERSLMP GTDFASWWGLNKSYPFLKKKKK
1092	6589	A	1149	3	497	PTLLVPTDSERTHPWLLSPADK\TN VKA\AWGKVGGAHAGEYGAEALER MFLSFPTTKTYFPHFDL\SHG\SAQV *GPRARKVADAL\TNAVAQRGT DIA QRACPLSDLHAHKLARVGPSTFK LLKATC/HCLGEPWAAHLPA\EFQPL AVARLPWGQSFLGFLKQRC
1093	6590	A	1150	26	508	NSTDERTHPWLLSPADKDQRRQGP AWG\KVGGAHAVRSMCAEALERMF LSFPTTKTYFPHFDL\SHG\SAQV*GP

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						RARKVADAL\TNAVAQRGTIDIAQR AVPPLSDLHAHKL\RVGPGSTSKLL KPLACLVDPGPPTSPAEFHPLRLQG FPGDKFPGLSVGKFKI
1094	6591	A	1151	3	520	AKKHGHRGSSLTVFGGPHRLRENPP WCSSPADKTNV\KAAWGVKVGHA VRSMCAEALER\MFLSFPTTKTYFP HFDLSHGFCPG*RATAKKVA\DAL KRRGATWDDMPQTALSGPEATLH\ AHKAFGVEPGSTLKL\SHLPCW*P LARPPSPAEDPWRVERLPWDKFP WVSC
1095	6592	A	1152	232	783	TCNPQTSSNGSQNSKLGRISRKWR MRRFCFCSITRWLECTSPRSRGRW KTDDVLLKLENMGVSELGQRI*LER FTKDTARFKDELDIMKFICKDFWTT VFKKQIDNLRTNHQGIYVLAQGNKF RLLTQMSAGKQYLEHAS*V/Y*HLP CGLIRGGLSNLGNKSIVTAEVSSMP ACKFQVMIQKL
1096	6593	B	1153	28	249	MFLSFPTTKTYFPHFDLSHGSA ATARRWRRADQRRGHVDDMPNAL SALSDDLHAHKLRLVDPVNFLLSHCL L*
1097	6594	A	1154	3	511	DKTNVKAAWGVKVGHAHPGEVWCGP LERMFLSFPTTKTYFPHFDLSHGSA QVKGHGKVNADALTNAV\AHVDD MPNALSALSDDLHAHKLRLVDPVNF LLSHCLLVTLAAHLPAEFTPAVARP SLGQVSWAFL*SNRCWTFQISLPAE FTPAVHASLDKFLASVSTVLTSKYG
1098	6595	A	1155	2	247	PADKTNVKAAWGVKVGHA\AGEYG AE\ALERMFLSFPTTKTYFPHFDLSH GSAQVKGHGKKNVADALTQGELGG EVGGQGHQQA
1099	6596	B	1156	74	195	MFLSFPTTKTYFPHFDLSHGSAQVK GHGKKNVADALTNAVXT*
1100	6597	A	1157	3	224	
1101	6598	A	1158	3	136	
1102	6599	A	1159	1	371	TQREPTMVLSPADKTNVKAA/WGM FLSFPTTKTYFPHFDLSHGSAQVKG HGKKNVADALTNAVASVDDMPNAL SALSDDLHAHKLRLVDPVNFLLSHCL LVTLAAHLPAEFTLAVHAFLGQFP GFF
1103	6600	C	1160	1	156	MVRRPWRCSCSPPGXPPRRVHP CGAXLPGQVSXFCEQRAELQIXLRL EL*
1104	6601	A	1161	1	577	AAWGVKVGHAHAGEYGAEALERMFL SFPTTKTYFPHFDLSHGSAQVKGHG KKNVADALTNAV\AHVDDMPNALS LSDLHAHKLRLVDPVNFKPPRPTSRT ST*ATALPRLRATARRWPTR*PTPW PRGRHAQRAVRPERPARAQASGGP GQLQLLSHCLLVTLAAHLPAEFTP AVHASLDKFLASVSTVLTSKYR
1105	6602	A	1162	1	680	ERTTMVLSPADKTNVKAAWGVKVG



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						AHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHG/GRMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADALTNVAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR
1106	6603	A	1163	2	1758	TMVLSP/ADKT/NVKA AWGKVGAAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADALTNVAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLT SKYR
1107	6604	A	1164	121	521	SFNKFFKKAKAVSQKKIPATKLRDKGLQTKYSCLYYYFYLRHGLALSPRLACSGTITAHCILKHRGSSDPPAT*ASHVLKLQYFCTS**LGITGACHHASLLLKFFVETDLTVLPRLVSNFWPSSCPSL LKCD
1108	6605	A	1165	407	548	VPFTKWHQKIEAGQAWWLMPIPAVWEAEAGGSLEIRSS*PAWATW
1109	6606	A	1166	25	628	EFHRLRENPPWCLSPADKTNVK/APAWGKVGAAHAGEYG\SEALER\MVLFPPPTPKPYFPHF\DLSHG\SAQV*GP RARKVADAL\TNVAQRGT DIAQR AVPPLSDLH\AHKL\RVGPGSTFKLL KATC/HCLGEPWAAHLPAEFQPLA VATSSLGTFKPGFLVEAPLLTFQITF KGWKLWLAIVFLPFGLPPSPSPFLH PYPRGL
1110	6607	A	1167	2	121	TFVRLGTLSTPLWGSYDFFFPS*FSLFLFYSVHFMPPLAF
1111	6608	A	1168	3	582	AKRELRFLLVYLHGDDHQDSDEFCRISQALRENTYPFLAMIMLKDRRMTVVGRLGLIQPDDLINQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLASLRADQEKERKKREERERKRRKEEVQQQKLAERRRQNLQEEKERKLECLPPEPSPDDPESVKIIFKL PND SR VERRFHFSQSLTVRTT
1112	6609	A	1169	30	130	QILLSPCLPPP*YLNKRWPEDNTCLL KTKLKRT
1113	6610	A	1170	2	1412	GIAGPTISCRGGGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQHNWNIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVS RPQPRGLLGWGYLIMLPFRFTYYTILDIFRFAPRFIR\PEP\RSR\VT*PRLGTIVSIYGT PFEEKYGRAHPVIFYQGTYSQALND AKRELRFLLVYLHGDDHQDSDEFCRNTLCAPEVIS\INTRMLFWACSTNKPEGYRV SQALRENTYFL\AMIMLKDRRE*PV\VGRLGLIQPDDLINQLTFIMDANQTYLGV/SERLEREERNQTQVLRQQQDEAYLASLR

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						ADQEKERKKREERERKRRKEEEVQ\
						QQKLAEERRRQ\NLQEEKERKLEC
						LPPAEPSPDDP*KVSKIIFKLPNDSRV
						ERRIPLFHRSLTVIHDFLFSLKESPEK
						FQIEANFPRRVLPICIPSEEWPNPPTL
						QE\AGLSHTEVLFVQDLTDE
1114	6611	A	1171	232	427	STKISHTKKTKARINKTKGGRGQAW
						WLSPIIPTLWEIKVGGLFEPRRSRLQ
						*AVFMP\CTPSWATQ
1115	6612	A	1172	232	427	STKISHTKKTKARINKTKGGRGQAW
						WLSPIIPTLWEIKVGGLFEPRRSRLQ
						*AVFMP\CTPSWATQ
1116	6613	A	1173	77	1775	GRKVVMIDLIPNLAVETWLLAVSL\
						VLLYLYGTRTHGLFKKLGAGGTPL
						PFLVNALYFRKGYWTFDMECYKK
						YRKVWGIYDC*QPMLAITDPDM\K
						TVLVKECYSVFTNR\RPFGP\VGFMK
						NAISIAEDEEWKRIRSLSPFTTSGK
						LQGDGPLSLPQYGDV\LRNLRREA
						\ETGKPVTLKDVFGAYSMDVITSSSF
						GVSIDSLNNPQDPFVGKHQGSF*GF
						NPLDPFVLLQLKVFPFLTPILEGIKY
						SLCFPRKSY*VFLNKIC*NRLKEGRL
						KETQKHRVDFLQLMIDSHKNSKDS
						ETHKALSDLELMAQSIIFAGYETT
						SSVLSFIYELATHPDVQKEQNEID
						TALPNK\APPTYDTVLQLEYLDMVV
						NETLKLFPVAMRLERVCKKDVEIN
						GMFIPKGVGVMIPSYVLHHPKYW
						REPEKFLPERFSKKNKDNIDPYIYTP
						FGSGPRNCIGMRFALNMNKLALIR
						VLQNFSPKPKETQIPLEI\DAVGGL
						LLTEKPIVLKAESRDETMSGSLNFPK
						DILVCSLRKLVQKHQRPSNYFTNR
						PLKRRRGFIPNVAAIK
1117	6614	A	1174	3	403	
1118	6615	A	1175	2	465	
1119	6616	A	1176	1	1112	AGEFFGQLHSRASFCARSASAAAL
						RMRPVRLMKVFVTRKIPRRCRVA
						LARAADCEVEQWDSDEPIPAKELER
						\GVAGAHGL\CLLSDHVDKRLDA
						AGANLK\ISTMSVIGIDHLALDEIK\
						KRGIRVGYPRLSLTDTTAE\AVS\
						LFLPT\CGRWPEAF\REVKNNGWTS
						WKPLWLCGYGLTQSTVGIIGLGP*
						AQAIARRLKPFQVQRFYLTGRQPR
						PEEAA\EF\QAEFVSTPEAGWPNLIL
						VVACSLTPAT\EGLCCKDFFQKMKE
						TAVFINISRGD\VVNQGRPCTRALAS
						GKIAAAGTGM*TSPEPLPYKPPFSL
						TLERIVVILPHIG\SATPQEPGNTMFL
						VWAVNNLLDGLRGEP\MPSELKL
1120	6617	A	1177	518	780	EVLPSGPGLLALVLRGSEFKLPHH
						EVSVGT/HPCQTSGAPARHRSTRDP
						VFPLSRGHNNPVPSWKHRAALTRH
						QTFLYCERGLPACIH
1121	6618	A	1178	117	1166	ITMATGQKLMRAVRVFKFGGPEVL
						KLRSDIAVPIPKDHQVLKVHACGV

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						NPVETYIRSGTYSRKPLLPYTPG\SD VA\GVI*AVGDNASAFKKGDRVFT RQARSSGG/YMAEYGFAGRTTLFY KLPGKTGTFKQGSPLSDFPYFCFIR GL\IHS\ACV\KAGESVLVHGASGGV GLAACQIA\RAYGLEVLGTAGTEEG \QKICFCKNGAHEV\FNHREVNYIDK IKKYVGE\KGIDINIEMLANVNLSK DL\SLLSHG\GRVIVV\GSRGTIEINPR DTMGQRSPSIIGVTLFSSAKEFEQQ YAAAL\QAGMGIGWGGPVIRSQYPL ERVAEAHEDIIHG\SGATGKMDSSL MDD
1122	6619	A	1179	264	647	NLGTCPFPVPALQCLLLVETVSRGS LLPVSPLLFQLLYPSPPA\PSYSINSL LPP*PCPASLPFYDSLVI*RPAPF*SH PSPSTPRTEGGV\PSQSHPPCCPQAP APPPSLPASLSQRHLLPPLSHHSC
1123	6620	A	1180	1	575	NFALEAKNSARAISVVQTPIGHSTE EDQGLLSTSLWGK\VKCGKNAGRK KPLGKAPLV\VL/HPWDPKGSFEQAL GNPVPPALCPSWGNPPKSRAGK\K VLT\SLGEMPIKHPG*SSKGTFAQPD VNCTCDK\LVHDPENFKLLG\NVLV TVLGNPIFGKEFTPEGCRASWAERW VTWSWPVPCSSRIPLKPLGP
1124	6621	A	1182	265	714	HFTYKYTAGTTIKSKNICITPKSYSC TFLVINTLTPLSNHYSGFSLRLVLI VLEFFLFWRWLALSPRLECSGMIS AHCNLCLLD*SDSPASASQVAGITG TRHQA CLIFVFLVETGYPHVG*ARL ELLTSGDPSPWPVKVLGLQT
1125	6622	A	1183	84	1009	HSMMM KIPWGSIPVLM LLL LGLID ISQAQLSCTGPPAIPGIPGTPGP\D GQPGDPRG*KERKGFQGLAGDHGE FGEKGRPRGFLGNPGKKFGPKGP MGPKVPGAPGTPQAPKGDSDYK ATQKIAFSATRTINVP/LLRSQTIRF GPR*FTNMNT\NYE\PRSGKFTLQGC PGLY*FNLSTPVSRG\NLCV\LMRG RERAQ\KV\VTFC\DYCLTNTFPGPPP VGMGPQLKKAPKGGGGGEKKT\VF LQA\TDKN\SLTGA WEGA\NSIFSRV PGFFPDMMGGPDLWAGFTSTPGSPCP ATLTIPPTTTI
1126	6623	A	1184	115	361	GWRGLPHCVPGRNCCSVLLMGS/C CL*GPHAL*KPSCSVRCWPEAPLH SKTDPRLSAA*PPFC*VR*MRYGLR TVCAQILSV
1127	6624	A	1185	3	734	GGSRERARSPESRRLPSRRSAPHRP PPQPCEQDNSPRKIQFTVPLLEPHLD PEAAEQ\RRRRRPH\ATLVLTSD\QS SP\ETAEDRIPNPHLKSTL\AMSPRQR KKMTRITPTMKELQMMVEHSPGGN RQQGEEP*RGPLESTG\LQESRPPGI PDTEVECKCWAPFGTAKKTAECIP\ KTHEGRSGEPSTKEPSTH\IPPL\DSK GANCGERGGGILGSRLQFGNAWT

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						PDLFLIPSLLGKISCF
1128	6625	A	1186	1	1359	GGPRDVNCRRCRRRLRAAETPPAWHL CMRSGAPTPPAAAMESETEPEPVTL LVKSPNHRHRDLELSGDRGWSVG HLKAHLSRVVYPERPHPEDQRLIYSG KLLLDHQCLRDLLPKQEKRHVLHL VCNVKSP/SQKLPEINAKVA*IPQRE PVGSN\RGQY\PEDSSSDGFKGKGKF FR\NLSFPWGWENIFKGLEACPSRH FQGLG\PGFLPVYTPYGV/WLQLSW FQQIYARQYYMQYLAATAASGAFV PPPSAQEIPVVSAPAPAPI\HNQFPA\ ENQPANSGMLAPSSGLFNP\G\ANQN FAG*IAQGGPIVEEDDEINRDWLD WTYSAATFSVFLSILYFYSSLSRFLM VMGATVVMYLHHVG\WFPFRPRPV PNFPND\CPPDVVNSDPHNNLRE GTD\PELKDP\NHLPP\DRDVTRMGE AGPGPFLYGGTAWVCSFKDFSLASS FFPEGPPSPSAN
1129	6626	A	1187	314	1614	
1130	6627	A	1188	128	1910	RVVDRGRRWDSPSPLLGGGTWPGR SSLRFASASSDSDSGLYRASLHPS PGRAALGLCLYLTKTSCCAAIGTLY WGNIA\YKQEA\YSLSGENFFMSETE NSCSPFMSSLLLQTEDTKKLQSKNL FILLIKPTNPKM\SVNVNPQRCTQ FYRLQDAPRLIAQG*GAKGNGNPR PVI\MSNMVDVGK\SLIGPPNVSPN IPIELGAQTQFDVKNDRIYVNGASH GGELSCQDML\DGFH*KNFVLC\PEC GGFLETDLH\VNPK\KQTIGNS/CGK ACG\YRGMLDTHHKLCTFILKNPPE NSDSGTGKKEKEKKNRKGKDKEN GSVSSSETPPPPPPNEINPPHTMEE EEDDDWGEDTTEEAQRRRMDEISD HAKVLTLSDDLERTIEERVNTLFFLF LNKIKEEGVIDSSDKEIVAEERLDV KAMGPLVLTEVLFNEKIREQ\KKY RRHFLRFCHNNKKAQRYLLHGLEC VVAMHQA\QLISK\PHILKEMYDAD LLEEGFFISWSEKASKKYVSKELAK EIRVKAEPFIKWLKEAEEESSGEEEE DEDENIEVVYSKAASVPNVIEFVKS DNKDDDD\NIDAH\LGK\GWMQPSLTV
1131	6628	A	1189	132	362	RRVDWKIQKISIGSSE*KLFNESHGI FLGLQRIDEELTGKSRKSQLVRVSK NYRSVIRACMEEMHQVAIAAKDPA NGRQFSSQVSILSAMELIWNLCILF IEVAPAGPL
1132	6629	A	1190	97	355	AFSYNCPSKISCQRKSQHFHLGGGLY VILFLFQKGQGVCCQSHPERPEGNP RRHQGQKERSCVGKTLL*LPEQDFV PEKVSAFPWWSLCHHPVSVPKGA RRLSAESSRKTGGQSETSSRTEGEK LRRQNASPRTYGGTRDTFPGMSVG H
1133	6630	A	1191	137	474	

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1134	6631	A	1192	307	583	
1135	6632	B	1193	1	969	MRPYSQTVFSTQYRWVEQHLGPQF VERIILTRDKTVVLGDLIDDKDTV RGVHKSMCPGVTAASWGAKDAM SICGCWLRELWDTSSRENSAAVKT GREADKPEVTKQTQFSTRKDEQAC SGYPYSDCWLAIELLHSAEPQAPRS RSDANASRSGPLRAGCETRLRLGV SCSACKPKPSVLRCLLSARPPLCGP LHASFLPGVDSKSGKTAPRTDCTQS TALTGSGGAGDTLRIDEELTGKSRK SHTQVFICTSPLLKYHHCVGEKYR WVEQHLGPQFVERIILTRDKTVVLG DLIDDKDTVIRGWTRYWPQSSLA CPD*
1136	6633	A	1194	834	1834	PSWCCRAGWMKPKDMLSKEADAS PASAGICRDHGGPDEDNAHS*SWE HPDTRAGAASGSTGTRNVERYLQ DSTFATSPHL\ESLLKIMLGDEAALL EQKELLSNWyHFLVTRLLYSNPTV KPIDLHYAQSLLDLFLG/E*EQPSN PWTTSCWQPLSLTSI/NVIKECSIALS NWWFVAHLTDLLDHCKLLQSHNL YFGSNMREFLLEYASGLFAHPSLW Q\VGVDYFDYCPGLGRVSLGAAHLS GYL*TPRQKARKVLRICEAAADD* TSSQHL*DLSESPTSATIAWVLASF WSIRVKGCRCLPRSCQTGSSGITVSE AAFLIWISLATWGQP
1137	6634	A	1195	32	393	
1138	6635	A	1196	102	888	RNLQETAIMEKPKLHYFNARRRM ESTRWLLAAAG\VEFEKFIKIWQ KIWDKFKEMMGYFDVSSQVVP/VV *D*WGWKLVTQRAISQLTFASKLQP SYGGKDIKGRALDLI/DVF*EGFSQ ILGLKLFPPFLPVMSPHEEKRCPSLA LGSKRKIKKIGYLPPEKSLKEPMG QDYPCWANKLEPLGLDIHLVGTFFY YVE\ELGLGLISSFPLEGPWKTRI QLTCPTVEEVSLQRAAPREAPPRD EKPLEEAKEDFPGF
1139	6636	A	1199	46	399	PGSKYDKTAILVSHLNFNLNLIKQP NPTQISPOGMFKRGGAR/PLLKTGPF LPTWKGDSFCYKGHSNSGWFEAKG FRRLPSFKNERKRNIGSPPLRVVIS SESPHAPFGTKSIPED
1140	6637	A	1200	37	454	PGSKYDKTVILVSHLNFNLNLIKQP NPTQISPOGRPPPPQCRVTEWTTTAS TQTQAGLKLKDSDDFQVSRMKEKE T**GAHHQDL*LFPQKAPMPHL*QN PFLKTDSSRNQVRSRTFPTSITFQNV GRSLPNTIYSGKK
1141	6638	A	1201	298	523	LLKVQSRQKHVAVGLRTLVRGA VLIRVPPLREPLAPPILVGASSRENI SR*VTGCSPTHSSSTPLATSPRORA
1142	6639	A	1202	80	589	IFLNLLIKQPNPTQISPOGRPPPHVQ GD*VYNYGPTPASQPERRALKRGI* RKGEGGPRERVWAGAPPGLPTPF

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						PENQGEKACG/GGRCLSPISSLQGPR FPADWWEIPIL\*SPDLHRDWGPAPP PPTSSNRPTPTVLRQERSGLG\PPSP GHLGKLVFFQLAWDSFL
1143	6640	A	1203	2	661	FVEADRGGLAVGSLRPLNLRGARA AFRFAAGRESRGKGTGERRTRVA VAGKVTSVPFVVSQGREHSHAPTR LPTIPPAAMSAAGVARGLRAAIYHRL LDKVELMLPEKLRPLYNQSRQVPR TVFFWAPIMKWGV\VCAGLA\DMA QTLPEKP*AQLQSACFGWLTRGLIW \SRILHL*IIPNTNWSLFGW*FPFVG AAGASQLFRTWRYNPRTKLKAH K
1144	6641	A	1204	20	400	
1145	6642	A	1205	457	1011	SRRPWGHFTEEDQGLLSQSLWGQ/V *NVEKMLGRKKPLGKAPLVLPWP TPRGSEKALGNLVLLPSCPSMGNP QKSRAPWARRVLTFFWGDHAKSTP G*SSKGTFCPA*SEPA/HCDKLH/VL DPENF\KLLG\NVLVTRFGQSIFGKE FHPLRCKAS\WQKMGEQVGHFPV LQIPLSSL\PMMQSFQG
1146	6643	A	1206	3	452	
1147	6644	A	1207	9	485	NSARATDSERTHHGARLLPDKTNV KAAVWGKVGAGHAGEYGAEALERM FLSFPT\TKTYFPHFDL\SHGFCPRK GPRQRRWPDALT\KAAV\HVDGHA QTALSGPEATLHGAQSFVDPVQLS SS*SHLPCWLT\GRPPSPAEPNPCR V ARLPWNKFPWVSC
1148	6645	A	1208	37	298	RQGLPLSPRLECHDRIIAHCNLEVLG SSSPPTPASPIA*\TTGVGHHTQLPFK LPYFFHSGLFFFLKKILYQFCDTYRA RISSDFCR
1149	6646	A	1209	49	564	SQTPMGHFTEEDKATITSLWGKIV NVEK\SWKEKTPGKGSLLVLPWP TPRGSF\DSFGQTCPSALCPSMGKPPKS RAPWPRRVLTSLGRCQSTWDDPQ GAPFAQA*SELHC\DKPAMWDPEIN FKAPGEMLLVTRFGQFHFRANKFT EGCRASWAERWVTGV\ASALVPSR YH
1150	6647	A	1210	134	673	QRRTKATITSLWGKGEMWKDAGG E\TPGKGSLLVYP\WTQ\RFDD\SFG NLSSAFCPSMGKPPKSRLHGK\KVL TSLGRCP*KHL\DDLNGHLLPKPDV NLHC\DKPAMWDPGGTFKLPGENV AGLTRFWAIPFSGKEF\TPLEVARLP WQKMAEDGDWQWASCPVPPRIPL EAHWPMISELFKG
1151	6648	C	1211	50	373	MGTVGSAWAAAPVQTHMFCSSSSC ISSSLTLPDSAAPLSPLASSWPVPPRP LLHWPFQDQSSLLFSLSPSFXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX RALHTSLA*
1152	6649	C	1212	45	424	MNGDXGLCLAAAPDQTHMLGSSSS

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						CISLSTLPDSPAAPLSPLASSWPVPP RPLLHWPFDQSSLLFSLSPSFXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXLTHFTLSLRRGGVLSISIRMW VRLS*
1153	6650	A	1213	97	1382	SACAWRLPSPGPSAMWPLWRLVSL LALSQALPFEQRGFWDFTLDDGPF MMNDEEASGADTSGVLDPDSVTPT YSAMCPFGCHCHLRVVQ/CAPTL GLKSVKPEISPDITLLDLQNNISEL RKDDFKGLQHLIALVLNNKISKI HEKAFSPRLKQLYISQNLVEIPP NLPSSLVIELRIHDNRIRKVPKGVFS GLRNMNCIEVMGGNPLENSGFEPG AFDGLKLN/YT*RHLQRSKLTGHSP KYLPELNLHLDHNKIQGHRTGR DLLRYSKLYRLGLGHNMIRMIENG SLSFLPTLREVHL/DNNKLARVPSPG FPDLKLLQVV/YILHSNNIHQSGVF NEFLFPWGFGEAGPYNGHSAFS TTPLPYW/ERLQPATFR/VVTDRLAI QFGQLQKVEAAAATLVSQWGLG NRARHPDGEAEPGS
1154	6651	A	1214	938	1501	AGVGPDGFLFQGIVANDSHPTALL KRMFASGGRRSWCQPFQGTAMG GPWAKGCLGPASCAAKVGGPHPKT NPGPKPTGGQGFPATGLRGVGISPP K*PCQ*AVQPGSHCPATCAEPSPPW G/PGVPRFEAPPPQTPP*PRLWPETG EPPLGVQKPP/QMPGPGAPLEN*S ASGGPRSPRGWESVWF
1155	6652	A	1215	883	1216	YISNSQLVQHFFFFFFFLFFFETESC PVAQAGTQWCDLGSQPPPPG*SN SPASASRVAGITGVHHHAGANFLYL *QRWGFTMLAQAGLELLTS*STRLG LPKCWGLQT
1156	6653	A	1216	197	821	RLFHSNQTVDHSQKNVDITLKG RPNRVRAPKGTLRIRDFNPHQM*NSA LLGKEQQRGFRVDKWWGYQKGN WPTRSGLFGSHVQDMIKGWLPLGL PVTKMRISVYAHFPHTLLSRENGV SLLKSRNFLGEKYIPQGRMKTRVL LCQYLKAQKR*N*SLEGNDIGLVS NFSRLIPASPTRLKTKGIRK/FLDGI FCLLEKGLFRQA
1157	6654	A	1217	241	514	DGQRLGKPHFVLLVLQ*LQTGLWS WWGKLGVE/MLGVGEILGSFISP VLERVEGSGSGNQAGPREEGWLG KPLRPEAPPSTFIQHHTLG
1158	6655	A	1218	3	496	SSGLFTQQSPEAWFCVSKCSYP AWQNVKIVDLSHKLQEIQRSLIPFAQF PAMVTVCAPGRFCHPCWHV*P/HP HSHDTEHGHHKCLVLCYPFTASA PPSCAPLRICIYGCILSCLVDVPWRT DRLNKQRVCKEAQSRREGSPA WLI GQSHRLALPLLAALS
1159	6656	A	1219	1326	2014	QLMIYTFRTELAWPGDQKH YFHT CVMILFFLRQSLALLPRLGVQ WHD

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						GSLQPA\PPPPGFRLFSCLSLPSS*DY RHHVPPQQLIFFFVLLVETGF/TPMLG RMVVIS*/PSDDPPTSASQSARITGVS HSWVNSCDLPLKNFFFFLEESHVS QAGVQWHDLSLQPLPGFKLFCL CLLSWDYRHAPPCPANFCIFSRDG VSPCWAWSPSLHLVIRPPWPPEVL GLQA
1160	6657	A	1222	1	459	IEIHIKCGGIPAVLAAPAMGLELFLD LVSQPSRAVYIFAKKNGIPELRTV DLVKGQHKSKFEFLQINSLGKLPTLK DGDFFLTS/SANRSVYLQGGCWHIT EMRFSKCKAEGPAKRSAILIYLS KYQTPDHWYPSDLQARARVHEYL GWHAD
1161	6658	A	1223	2	310	
1162	6659	A	1224	205	454	
1163	6660	A	1225	2	384	
1164	6661	A	1226	1	1276	MPGLGFREKKGGSRTPVPSRGCGL PAPILCTKWELPLSGSSRCLAAAAAL QGTVWTAESSSLTPAFQSRGWGLIP YFPARRDPATAAAHTALSAFTAIPA VLAAPAMGLELFLDLVSQPSRAVY IFAKKNGIPELRTVDLVKGQHKSK EFLQINSLGKLPTLKDGDFFLTS LIYLSCKYQTADHWYPSDLQGGF ARVHEVPWAWHADLHPVGTFWY YPWGVQGVWGHSLGVQVPEEKVG TQTRTAMDQALQWLEDKFLGDRPF LAGQQVTADLMALEGS*CKPVAL GYELFEGRPRLAAWRRRVEAFGL AELCQEAHNIILSILEQAA\KKTLP PSPAEAYQAMLLRNRPSPGSGM GAKEISNKDSFCYLLAPFYLSLLPQS LLSKLQCEALHRQRHSSVLWQVLL LLRCKHT
1165	6662	A	1227	151	278	G*KYDSDIYHEAVVPHQNQMSARS DKEKKRFIFYSSYIPFC
1166	6663	B	1228	1	690	MASWDEKDLTVQPQDTRKGSVLR GLSSRALRWAGRGHVAAGWRPLA PESAGGWGMAAAMVPGRSSEWER GEPGRPALYFCGSIRGGREDRTLYE RIVSRLRRFGTVLTHVAAAELGAR GEEAAGGDRLIHEQDLEWLQQADV VVAEVTQPSLGVGYELGRAVAFNK RILCLFRPQSGRVLSAMIRGAADGS RFQVWDYEEGEVEALLDRYFEADP PGQVAASPDPTT*
1167	6664	B	1229	1	975	MSPPGREQGLLLNLLRPSGLDNAG KTTILKKFNGEDIDTISPTLGFNIKTL EHRGFKLNIWDVGGQKSLRSYWRN YFESTDGLIWVVDADRQRMQDCQ RELQSLLVEEVGSSYPLCTWRFFSY LRIEQMYNLVLYRDIQFPDFCFNSN TDWSKGLKTHARFGNTSLHVAHTD STNTTNFVDVWRGRTKSLACLLQL SSLTCIYTAGKMRLQDRIATFFFPKG MMLTTAALMLFHLGLGIFIRDVHNF



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						CITYHYDHMSFHYTVVLMFSQVISI CWAAMGSLYAEMTENKYVCF SALTILMLNGAMFFNRLSLEFLAIEYREE HH*
1168	6665	A	1230	1	211	
1169	6666	A	1231	950	1326	RPESQRANGVDSGPNLKTVPQPDTR KGSVLK WISKRGKPLAVEIEESHCL CLPLRTECLGKPAIVHLFSCTRPVIV PSLELNYDVDSIAHMFVADLLLMIT LPSYDIPFYCLVFQNLVLVEFYQL
1170	6667	A	1232	271	927	NQGLRHVRLCRMCLVNQMFASSIL GKSHHSLVPINQGHNAWKAAG PLPLKAGYCAQGFSPCHSLKYG\SW DEKDLTVPQRDTHKRSVLKVELVQ RGKNLPVEDGGKAHCLPELPPGELE CPG/ILKHGLYHWSSEMGEKPAPM VGGARHVACSNAALVIPLPLRCLGG EKHKSGLAHARPVI\PSLELNHDT D SFAHMFADLLLIITLPS\YYIPFC
1171	6668	A	1233	62	1158	GHLCARPETSLLQVRPGPLPSSFSG MDVGPSSLPHLGLKLLLLLLPLR GQANTGCYGIPGMPGLPGAPG\KDG YDGLPGPKGEPG\PAISWIRGPKGQ KGEPGLPGHSWGKMGPMPGPGDC QGLPGPLGDFPG\EPG*G\GRYKQKF QFSFSLIRQTHQPPRTNSLIRFNAV L\TNPT*Y\NTCTG*FTSKVPGLY\YF VYHASHATANWCVVLYRSG\AKVV TFCGPHVPKPISSNSGGCACLRQV GRGRCGWLS\MTYYGHGWGIQGL* KSVFSGLPWLLPRTKGGARCGSRPT GPSPPQLPAWTPQYWPVCILALDH SPHQMDFSPPGSPPLTHPHCTPLPM GSLLPLNFFRSHCLCGSWDT
1172	6669	A	1234	2	907	AVAFGAKGTDPAEARSSRGIEEAGP RAHGRAGREPERRRSRQRRGGLQ ARRSTLLKTCARARATAPGAMKM VAPWTRFYNSCCLCHVRTGTILL GVWYLIINAVVLVDFIECPG*SGSSI TFQVLELGGDFEFMDAN/NGAFAI AISLLMILICAMATYGAYQRAAWI IPFFCYQIFDFAL\TC*VAISGLIYANS IQENIRELPPKFPYRDDAMSVNP\TC LVFIILLFISISLTFKGYLISCVWNCY RYINGRNSA*CPWFMLPAMTLRCC YPPYDDATVNGAAKEPPPPYRVCLS L
1173	6670	A	1235	966	1564	NDFFKTNKSSIIRNSCLTAILVFLCC YDLTLTGTLF*ILTFRWL*LGLIIRLN MASRSTIYVYGSQPSLFTFENTDF YQLWILFLVICLPFLFKLFTIFLWP KLLTLENQILHQICFSVFLMSAPI TTVRGIHVLPVIVILQTDLAWINQLL HLLFSKLGVDSDSVQDWVSLMWN GTHGRKCRSQFYMPIKGHL
1174	6671	A	1236	155	303	AFQEGDPMFKPSRCPCPYLPKPCPS TCLP/SFAFRAVVTQVP*CCVCKCPG
1175	6672	A	1237	739	1629	GTSQMPTSAVPSLLSPSKFARKGFS

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						KVLQLCLYRRIGLCPAPPPPVPTQC PRPQELIGP/WRE*CPPGSFRNSPRNL FSFLQELPEESV
1176	6673	A	1238	1	554	NFALEAKNSARAISLVPDA\MGHF TEED\KAT\TSLWGKGEMWKDAGG ET\GRL\LVVYP\WTQRFFD\SFGN LSSASHPWATPKVKAHG\KKVLT\ SLGDA\TKHLADDLKG\TFCPSLK*TC TC*QACNVGS*GTFKLPGEILLVTRF WQSHFRQKNFTPEGCRLSWAERW VTWSWPVPLFLPDYH
1177	6674	A	1239	29	454	
1178	6675	A	1240	1	1368	
1179	6676	A	1241	1	1266	LSRVAEFEHLGWSPKPPTTCTPACQ GLSGAAMKSLVLLLCLAQLWGCHS APHGPGLIYRQPNCDDETEEAALV AIDYINQNLPGWKHTLNQID\EVK VWPQQPSGRAVLRFEIRTPWGTTL CCWDPTLVGQDASLEGSLKEHAVE GDCDFQLLKLDGKF\SVVYAKCDAS SQDSAEDVARKVCQH\CPLAPL\ND TRVVHAAKSCPGPPFNAQNGFQF FSLEEISRAQLVPLPPSY\VEFTVS G\TDLLFA*KKATEAAKCNLSGQKS NMGFCK\ATLSEKLGSGQRLQLTCT VF\QTQPVTSQPNPEGANEAVPTPV\ VDP\ADAPPSPPLGAPGLLPSWLT PKT TMVLLAAPPQHQLHR\AHYDLCHT FMGVVSLGSPFRRKCSHPRKNT/RT VVEA*WLGAAAGATGFLPLFRGGI RHFVKV
1180	6677	A	1242	1134	1247	
1181	6678	A	1243	1330	1517	KLNMVFKKISHGMQLRKSYNLFYQ KSGKIMT*IWEIFFPEFFIFPPTY\LF LKREFLLNEPS
1182	6679	A	1244	213	287	
1183	6680	C	1245	249	323	MYKLRRKLEDNRNKIENENIVKSFR*
1184	6681	A	1246	1021	1985	IAWAFKINWLPPIIFLFSVLFYPIFGFI FFYLLYFSNTCLS/FVFPFSYLKLLTI FSFSILFLSSNFLSLYLPLAFCFLAC LFFFCFLFRFKFIFFLPKSMFLSSNF PIF/CIFFFFAFPYSCLPVFHCQTFYLL QIVVIL/IHSQIFPFSSAFSKCG*QGF *MTQFSLRHGFQGLLITFGLISF*KIA FKLF*SPTTFKLNFKLFK\YLHFNLK ALPSLLGLNSGLL*/FLSHQFSFKYIF YSMKKLHLNLRHVLETVLSFPSSCY SSKFVHFALSFLFPSLSFFFCFLFRF KFIFFL/RKSMFLSSNFPIFSILFYLP IF
1185	6682	A	1248	147	460	PFYKNCVSIVVVVFETGSCSVTQAG VQWHDFFSLRPRPPG\SSDPPTSASR VAGTTG\MCHHIQLIF*SFFIETGTHY VVQAGLKLGGSSHPPTFSLPKWLGL QA
1186	6683	A	1249	168	407	ISHTREHSLDFFSFLFFETESH/STR RLEYNGGLSAHCNLHLLGSSDLPTS

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						AC*VAGTTSIWQHVQLTFVFFFLIIIF
1187	6684	A	1250	163	396	TRFPILGSIA*IFFLFFFETESH/STRLEYNGGFSAHCNLHLLGSSDLPTSAC*VAGTTSIWQHVQLTFVFFFC
1188	6685	A	1251	37	698	RSSSPALEGGRKVDMECLGSTIGPGPGSGQPACPLIWLHC*NPVEQAGPKP/PARPARSGP/QPPPTAGPA/PVGP KPPPTAGPA/PVGP KPLPTAGPARSWRP*PSGARGIKETHTEI*VP/PQGFFACLIPTAPTGPTD**WLHLDLPTTP\QPHPEAVQHTGGSCLTYPDGP PPPQPISSKHPLPSYPTSPKLPLEHPSQILGETDFS NHQILVSHSLVSV
1189	6686	C	1252	150	308	MALQORTHXLLLLLLTLLGLGLVQXPMARMXCTSDSCGNTCTLRQVASDRY*
1190	6687	A	1253	2	470	
1191	6688	A	1254	92	1047	RAAWQGGAEASGPPSALRGGSALA AAARWGPAEEGARIPGSFFAWAAP AAPGAGAAAAPAPRADPGGRGLLG EAGRGP NYAEAGTPTLHTLPRPHLR PCTHTHTRTPTPPRCKAGFKRTSLR FLPAPHHRTREEEAGEKQNFPLSC PFLRTCSEAE E P V L E E M V M G L G V L L LVFVLGLGLTPPTL\AQDNSR\YTHF LTQHHIA\KTRGR\ D P L S C K T F M R S R GLTSPCKD\NTFIH\G\NKRTLKGQS CENKNGKPLTEKNLKE*SKSFLSQV T\TCK\ LHGGSP\WPP\CQYRATAGF RNVVVACENGLPVHLDQSFRRP
1192	6689	A	1255	199	792	PGSTAAADQRSRNWNPGRVRKKPD LEGGCGTVLSGRWRSRRNRRTSGQ SLVPVYIYSPEYVSMCDLAKIPKR ASMVHSLIEAYALHKQMRIVKPKV ASMEE MATFHTGCFICISRRSAKR AMMIIRTSLEYGVRFINFPATEGIFT LCSS\*GGATITAAQCLIAGMCKVAI NWFGGWHHAKKKTCVYVALYKAF
1193	6690	A	1256	1368	2229	WHPRQVLTGNDEVIGQVLSTLKS DVPYTAALTAVRPSRVARD\VSVEA GGLGRQLLQKQPVSPVIHPPESYND TAPRILFWAQNFSA\YKDQWEDLT PLTFGVQELNLTGSFWNDSFARLSL TYERIFATTA\TFSFIPAHQRYPPSAR HWFTMERLEVHNSGSA\YFNASQV TGPSIYSFHC\ E Y V S S L S Q E G * S P R W ARTQPSSWQMML\QGFDPGFASTL MGEQFSYA\SDCGQASSPGIWMGL LTSLFMLFIFTYGLHMLSLKTMDRF \DEHKGPTISLTQIV
1194	6691	A	1257	2	630	PDSSGPHRLRENPPWCLSPA\DKTN VK/APAWGKVGHAHVRSMCAEAL ER\MVLFPPPTPKPYFPHF\DL SHGS AQV*GPRARKVADALD/TNAV AHR GTD/DCPNGVVPPLSDLHAHKL RV GPGSTFKLLKATC/HCLGEPWAAHL PAEFQPLAVATSSLGTKFPGFLVEA

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						PLLTFTQITFKGWKPRVGHAFALW ASPQPLLFPAPVPPWSFE
1195	6692	A	1258	207	591	
1196	6693	A	1259	1	541	WNLSASPARQHPLLPHPVSCILLKPS SKKCLPNLTGYRFSQKNMEDYL QALSSPH\DISLAVRKIALLLKPDKEI EH\QGNHMTVRTLSTFRNYTVQF*/ HVGVEFEEDLRSVADGRKCQGPCW HCNFSSQSHLLSSRAMFSTAYKIQL ALHIHGFCIHSFSKLQMEKYLGIKI KNNNTK
1197	6694	A	1260	214	491	ESHGAQIYIPHFCVPWSRWGNVRR CEALAVIYVTNNKIYVLSDEISCLQ PTSIN*QSNLLACK*GKN/RKTGQAR CHACNPSTLEGRSRIN
1198	6695	C	1261	48	173	MVRKRMEMKMRKLSQLRASGQLK MMRMXMSIPRSRRPRGIX*
1199	6696	A	1262	59	306	FGTDRTAVQTSSSQRLCLPWVAQK TYWLLVPSSLLKDLKEKKEVVEEA* NGRDAPANGNAVSVCFAPWPQLP PHKIFPVLL
1200	6697	A	1263	279	889	TLAVFLIPCIGSPACPTMSDAA\VD SSEITTKDLKEKKEVVEEA\ENGRD APANGNAVEEEDGDEDEEAESATG KAGQPED\DEDDVDYQKQKTDE D*IRQQRKKLNLKKRPAHRGQC HPADDTRSPPPNPNHENLQQGREKR NQNFQGPFFLSTLKRKFVCIFYL HFIFLYILLRVSHFLMISDDQTSLEP SLSYF
1201	6698	A	1264	358	508	DDVDVTKKQKTDDEDD*TAKKRKV KLKKKKAAVTYSPSTSLRYLYVFT FE
1202	6699	B	1265	46	386	XIRHESGSRSHSHCSTLSSIGDVAKK LGEMWNNTAADDKQPYEKKAACL KEYEKDIAAYRAKGKPDAAKKG VVKAEKSKKKKEEEDEEEDDEE EEEDXEDDDEEEDDDDE*
1203	6700	A	1266	263	484	
1204	6701	A	1267	157	886	TWKGGLKKPRANMSSYAFFVQTC RGG\HKKKHPDASVNFS/ESFSKKCS ERWKTMSA*/R/EKGKFEDMAKAD KARYER\EMKTYIPPQGRGRKRFK DSQLHPRGPPSGLSSSCSEYRPKIK\ GEHP\GL\SIGDVAKKLGRDVGINTA AD\DKQPY\ERRAAKLKEYEKDIA AYRAKGKPDAAKGVVVKAEKSKK KKEEEEGEEDEEEDDEEIEEED EEDEEEDDGLMKNLGS GAVFFFSCL
1205	6702	A	1270	2	343	
1206	6703	A	1271	3	647	
1207	6704	A	1272	59	1297	NHASVQVKLWILSRSYLQLTMEAN GL*PQGLPDLKNDTFL*AAWGEETD YTPVWCMRQAGRYLPEFRETRAQ DFFSTCRSPEACCELTLQPLRRFLD AAIIFSDILVVPQMFSPPGTGQWKV TMVPGKGPSFPEPLREEQDLERLARD

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						P\EVVASE\LG YGFQAIT\LTRQ\RLA GTCAG*LAFAGAPMEP*MTYM\VE G\GGSS\TMAQA\KRWLYQRPQ\ASH \QLLRILTD\ALWLPYL\VGQVVAGA \QALQLFES\HAGHFWPHSSFNKFCT ALTSRDVAQAK*RPRLPGSQALATR CPCIIFA\RDGHFAPGRSLAQAG\YE\ VVGLDWTVPK\KARECVGKT\VT\ LQGNL\DP\ALYA\SEEEIGQ\L VKQ MLDDFGPHRY\ITPHLGHL YPDM D PEHVGA FVDAVHKHSRLLRQN
1208	6705	A	1273	7	1047	
1209	6706	A	1274	7	960	
1210	6707	A	1275	3	53	
1211	6708	A	1276	237	441	AHFLHIVLVLLSCWYSVRSRCTSQ QGVQSDILAQLLPLRQRLEGEALV ALGAGVERRHVRPGRNST
1212	6709	A	1277	94	1003	VRVSLSLRLECNGAILPHCNLHLP SSDSPASASQVAGITGVCHHAPIFV LLVETGFHHVGGAGLELLTSSDLPA WASQSAGITGGSH/LCLANVKYFKS HFKIFVIDETWFQHT*LLSLSSCD*V *TSI*/PQVLD*NVLCPDV/SQ*LLPW LIKIFLKYTLDCW*KRQAWLYWY* FGTELF GCP*GRQTL CFFFLRRSL/DS VAQAGVQ*CDL GSLQPLPRFK*FS CLSFPNSWDYRCAPPLPANFCIFSRD /MGFAMLVRLVSELLTSGDPPASAS QSAGITGMSYRAWPKPYAFEVECR PCDN
1213	6710	A	1278	4077	5102	KEASPAKRASGEGSRRLRVEAGGR CGKVCSGRGGGSPELRLRRQKMLR ASSQRNAAGHRGWASGSRGSPTA AAERP KKG GGSRAAQTASSSGTR RRRRRLRESRRPRSRSGCRPPAFQ AAPDPPLPLPAGSHFRQATAELA/G RAPRRKWPKPAFAS/VGRGRGRAL ATFPTASED/SPRPPAAPR*HPGQGR GAGRRGLWEARGGAPAAFGAPQL ASCKGRR/HTPSTINLFLNDPPPLP KH/PH*ASPPTLGIEFQHEIWRGQTS KLSQHPSFSLRTLTYSSQTAAFEFL FCRCLPTGHVPSSLLHSAADTAVSG DYATEGWECHCCWGCWEAKVGV LLH
1214	6711	A	1279	316	1180	KEASPAKRASGEGSRRLRVEAGGR CGKVCSGRGGGSPELRLRRQKMLR ASSQRNAAGHRGWASGSRGSPTA AAERP KKG GGSRAAQTASSSGTR RRRRRLRESRRPRSRSGCRPPAFQ AAPDPPLPLPAGSHFRQATAELA/G RAPRRKWPKPAFAS/VGRGRGRAL ATFPTASED/SPRPPAAPR*HPGQGR GAGRRGLWEARGGAPAAFGAPQL ASTQAAFEFLFCRCLPTGHVPSS/TP PFSSRYSSFRRLCLIFRCWTEVLNE GGANSDSWSLTKLESGSSECSS
1215	6712	A	1280	2	315	

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1216	6713	A	1281	195	739	KFSSRITVCHWKDVLLSGFQEPDRG SAMDYVRK\YAAIFL\VTLSVFL\HV LHSAPDVQDCP\EFTLARENPFSPAR VPPIQLQCMGLPASPR\YPTPTKGPR KDGCVVPKEPSPSPCLW*PKIHI NRGPQ*MGGFPKVGEPTACPLGS YLFYYPQIFKMFLPQVLSWMDWLDL LGIGKI
1217	6714	B	1282	29	200	MSRTRLVCPSLIPFCIYVVDVGFSPG PQSCTSHEPKDIAKCELAFLHHQR FYKNEG*
1218	6715	A	1283	138	1908	ASRTAVARWECVLQNVRRPSPSR AWPSQLRPIASTATKCRE\CGPGYST PLEAMKGPREE\VYL\PCILPETQGT EGPRLSWATVDVDPKSPQYCOVIH\ RLPMPN\KDELHHSWNTC\GSCF G*LAPSRGTK\LVLPFHLFGIYVG GTWGEPRAPKLAQGSLSPRDIAK CNWAF\HTSHCLASGEVMISLGD VKGNGKGGFVLLDGETFEVKGTWE RPGGAAPLGDFWYQPRHNMIST EWAAPNVLRDGFNPADVEAGLYGS HLYVWDWQRIE\VQTL\SLKDGLIPL EIRFLHNPDRCPKAFVG\CALQAPNI QRFLQRTTRGGTLFSGRR*FQV\PPRK LKGWLLPKMPGL\TTILASPWNDG FLYFS\NWLAWGP*GKYDISDPQRP ALTGQLFLGGSIVKEGP\QVLEDEE L/TSPSPEPLVVKGKRVGEGP\QMN\Q LSLDGKRLNNHHGRCT\ALGQSSF YP*SQSGERLLVNAGRVEW*DNSK KGGA*KLNPQLSWVDFGEGAPLPK PLPH*ARYP\GG\DCSS\DIWLN\SPPS HPHSLFWALHFPGGPGLSFCISLGR TLGKHVPTAKLRLWQCVES
1219	6716	A	1284	155	336	HFKIINRGWAPWFMPIPALWEAE GG\HLKL**AMIVPLHSSLGDTVRL KYL\CIYSLIF
1220	6717	B	1285	251	570	XELLVQLASLQTSFVTLDEAIKITNR RVNAIEHVIIPIERTLAYIITELDER EREFFYRLKKIQEKKKILKEKSEKD LEQRRAGEVLEPANLLAEKDED LLFE*
1221	6718	A	1286	83	977	HNQLTPVEEDTVESQFWSYCSLGC AGDPSRKVIVRMSGKDRIEIPSRM AQTIMKARLKGAQTGRNL/L*RKKS DALTSFDFRQILKKVIGDLKCLMG\E VMREAAFFTSWKPSFTAGDFQALT VIPKCSIKGGKLVSE/DEGKVIVRP VFTFASNFEHYH*RN*PVMELTGLA RGGE\QLAKLKRNYAKAVELLVEL ASLQTSFVTLDEAIKITQQAC*MPIE HVIIPIERTLAYYSSQSWRRERE EFYRLKKIQEKKKILKEKSEKDLEQ RRAAG\RCWS\LLIFLAEKDRGSFL F
1222	6719	A	1287	1	3249	
1223	6720	A	1288	504	932	RYRCGVGSVLQAGGLILHLRKEGIL

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						HNKGKIEGMGLLEYVQGSLLQGW VMFVSVTAFFSLLFLGMFLSGMV AQIDANWNFLDFA YHFTVFVFYFG AFFVMEAAATSLHDLH*NTTITGQPL LRDNQYNINVAASIFAFYDDS
1224	6721	A	1289	66	1363	RTAVMPREDRATWKSNYFLKHQLL DDYPKCFIVGADNVGSKQMQQIRM SLRGKAVVLMGKNTMHAQAPFEG TL*NNPSLWRKLLPHIRGEFGLLFH PGRTLTEIRDMFAGPIRLPTAARCW CQLPPCEVTVPA\QNTGLGPEKTSF FPGL*VSPTK\ISQGAPIENPEVNPA ESRTGDKSGKPSEATLL\NML\NIS FSLWGWSSSQVFD\NASIYK*KCLI SPEETLHSR\FLGGCPQMLPSVCLQ\I GYPTVASVPHSIINGYKRVLA\ASVE TDYTFPLAEKVKAFL\ADPSAFVAA APC/AVVAPPAAPAAAAAPAKVEA KEESESEDEDMGFAAAVLPGGTKP GALPLAPGLALPRGPRCDPEAFRK RFRSQPRQDGGGHAELQKFTLPSLY FFSPKPSGCEPRANAKSSLNFVFSKY SLSTYYEQGL
1225	6722	A	1290	3	231	CSSSTSPSSEYCPSWGTEFRSGEMGS K*SSL*GASSLSPTDGRGTGSSSSSS GGGGPGGVVLGPLGCGLGGLPLN
1226	6723	A	1291	221	984	ETGLMCSSPLDGQNSV*RLTPWTLA PGTTAEVNQEDQKKSQIL*KKWQA AANSSRLVKNS*MPAT*KIQNGRMD KNSPTKYLLSSRDSS\THKESHKLKD IALILPSSSEGSISELEQLSNSLPNKEL MTSICDLLATLANSESSYNCLLTC VRTMMFLAEHDYGLFHLKSSLRKN SSALHSLLRVVSTFSKDTGELASSF LEFMRQILNSDTIAPVCVAALSVSM CSHRSAPTWFPPKGLKGARTTSRNS SEA
1227	6724	A	1292	817	1826	SCYPFCTS*KSFHSFCHTNDTVQSFK SI*LKR\SDT*SANRSSNNPLITPACSS PVTP*APHSASEDTNLVPALSCRTFK AIGWRSATCKFKACMVQSTNWP SCFVFFNCK*LNPFIKLGISSKAVTH FAPLSSLYKSKSSVNFTEASIAPEFSL SGP*SFILLISISKVVLYGQLKYKSGT SSLSYGSYVIGGTEAKSSAVYSTSKF GYLNVSRSKSAIPSSSLEICS*PSSPSP SSSSSPSSSSSSSSSSGILSTVRRSSSS SSSSSTSTSSSSSPSSCCSSSTSPSS EYCPSWGTEFRSGEMGSK*SSL*GA SSSLSPDTGRGTGSSSSSSGGGGPGR SSWSPWLWSWRASIKLIFFLPISMF WDSFSNLGCGLGEGGWRWEGGGG GRVSVMTLSLYPLDPYIASVRQLYQ PLSTRPSVFTFELGLKMMEVFSSYS RLPNLSKTGALGLPYIVEE
1228	6725	A	1293	25	771	LDGPQGTSRPWGLPSLPPPRAGAGL SQGFGSSLRPARTPPSSGSKMSTEA QRVDDSPSTRA\QSSDGDQRESVQQ

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						EPEREQVQPKKKEGKISSKTAAKLS TSAKRIQKELAEITLDPNNL*VAGP KGDNIYWRSTILGPPGSVYEGGVF FLDITFSPDYPFKPPK\VTFRTRIYHC NINIQQVICLDILKDNWSPALTISKV LLSICSLTDCNPADPLVGSATQYM TNRAEHRM\ARQWTKRYAT
1229	6726	A	1294	449	826	QKSRRLIDDLFFFFFFCETGSCSVTQA GVQWHNHGSLQPPPGSNDPPTSA SQVAGVSVACHHSRVCARVCVCV CVCVCVCVESGLKLLGSSNSPLAS QNARIIGMS*IVPKKLYFKSKVKGRI
1230	6727	A	1295	1	727	NTEDQRNEEKAQREANKKIEKQLQ KDKQVYRATHRLLLLGAGESGKSTI VKQMRILHVNGFNGDEKATKVQDI KNNLKEAIETIVAAMSNLVPPVELA NPENQFRVDHILSVMNVPDFDFPPE FYEHAKALWEDEGVRACYERSNEY QLIDCAQYFLDKIDVIKQADYVPSD QDLLR\CRVLTSGIFETKFQVDK\V NFHIV*RGVGQRDERRKWIQCFND VTAIIFVVASSSYNMVIREDN
1231	6728	A	1296	2	1271	PVRSSAPRRGHSVASAPRSGLRQVA GRRGAALPCSLAPGCGAAAGASPC PGAGRRRAAGGRCLACECTSLTCA GESGKSTIVKQMRILHVNGFNGEGG EEDPQAARSNSDGEKATKVQDIKN NLKEAIETIVAAMSNLVPPVELANP ENQFRVDYILSVMNVPDFDFPPEFY EHAKALWEDEGVRACYERSNEYQL IDCAQYFLDKIDVIKQADYVPSDQD LLRCRVLTSGIFETKFQVDK\NFHM FDVGGQRDERRKWIQCFNDVTAIIF VVASSSYNMVIREDNQTNRLQEAL NLFKSIWNNRWLR\TISVILFNKQ\ DLLAEKVLAKGSKIE\DYFPEFAR\Y TTPE\DATPEP\GEDP\R*TRAK\YFIR\ DEFLRISTASGDGGHYCYPHFTCAV DTENIRRVFNDCRDIIQRMHLRQYE LL
1232	6729	A	1297	235	1571	GRPRPPPPQGRAPPPPPRPMGCLG NSKTEDQRNEEKAQREANKKIEKQ LQKDKQVYRATHRLLLLGAGESGK STIVKQMRILHVNGFNGEGGEEDPQ AARSNSDGSEKATKVQDIKNLKE AIETIVAAMSNLVPPVELANPENQF RVDYILSVMNVPDFDFPPEFYEHAK VLWEDEGVRACYERSNEYQLIDC AQYFL\DK\IDVIKQAD\YVPSDQDL LR\CARVLTSGIFETKFQVDK\NFH HMF\DVGGQRDERRKWIQCFNDV TAIIFVVGSSSYNMVIREDTGHNGL AGRL*TSPKGIWDNRWAAAPSLVIL FLTKQ/EILLA*ESPLAGNSK\IKDYF PEFAR\YTTPEGCYSRPGEHPHGV YRGQVTPFEDEFLRSSNCPVEDGRH YCYPHFTCAVDTEN\IRRVFNGLAV DIHFSGMHLSFSYGAGFKEGEPKPF



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						NLKA
1233	6730	A	1298	176	505	ILKFPWIDIFLYSFNLVFLIFETRPHFI LSPRLECSGMTSAHCNLCPCSSDP PTSAS*VAGTTGTQHAWLI*LFGE RELHHVTQAGLKLLS\VILSPQPPK VLGLQA
1234	6731	A	1299	310	326	SQHFGKLRRVHSLNSGVQDQPGQH EETSSLLKIQ\QLARHGCVCVLAQL LRRLGWEDHLNLGGRGCNEPRWC HCTPA*VTE*DSISKNNNNN*QAGV QWHHLGSLQPLPPRFK
1235	6732	B	1300	99	430	XVITQRELVSQRVSNDLTEQAATFG LILDDVSLTYLTFGKEFTEAVEAKQ VAQQEAERARFVKEKAEQQKKA QQKKVEQQKKA AVISAEGDSKATE LIANSLAHRGGPP*
1236	6733	A	1301	64	967	NFRVEAGVRGVQOKETCAFKVLESI GKLG\LA LSVAGGAENSALYNVDA GHRAVIFDPIPGQK*QDIVGEGTHF \LIP\WVQKPQLSNDCSRPRNCCQS ITGSKDLQNVNITLRHPSSGPVRQP SFPRIFTSIGED\YDERVLAVPSQLEN LKSVVAPFDAG\ELITQRELVSQV\ SDDL\TERA\ATFGLILDDVSLTHLTF GKL\LTEAVEAKQVAQQGKQRRAR FV/VLEKAEQQKKA IISAEGDSKA AELIANSLATAGDGLIELRKLEAAE DIAYQLSRSRNITYLPAGQSVLLQLP Q
1237	6734	A	1302	424	598	
1238	6735	A	1303	3	371	
1239	6736	A	1304	1	1596	
1240	6737	A	1305	2	556	WDMMYVTRFASFLRNVLPSFISDW LYVQKMNTWFKHENYGLMPLNGY LKMEIFFIQKRGALI* IYLSIKPSVK EFTETSAVFEDGTMFEAIDSVIFATG YDYSYPFLDETIMKSRNNEVTLFKG IFPPLMEKPTLA VIGLVQSLGAAIPT ADLQAWWA AKVFASRWAILSFIHFI NEHLLNTCY
1241	6738	A	1306	955	1187	IFFFFFFFKMESC PFAQAGVQWCDLG SLQALPPGFTPFSCLSLLSSWDYRRP PPHLANFLYF**TWVFTVLARMVSI S
1242	6739	A	1307	6345	9041	
1243	6740	A	1308	236	437	LLTLRWSHSSHVLLKTRGQPRRSG WCL*SH/HFGRPRRADHLRSGVQDQ PGQHSEIVSTKNTKIGWAWWQVPV IPAT*E
1244	6741	C	1309	182	433	MHLDLFLNKTLPQIRGVESEQSSRL HPLPDRGDRHRMADNLPMEIHGS SATSSGKPSDFNQAAVDGAGERGG KEVLGGTLDVL*
1245	6742	C	1310	72	254	MVSTQLRQASDPRTTIGRERFELL RRVDKLMSPRLPTGTNLPHHFWTL SIPQVGRCNAP*
1246	6743	A	1311	225	735	GELRVNSLHVSTHFQIPEETDIGWL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VSPGQGPAPFPEDIQWPPGSLMAA EPTDQSLEESH*DRWITTFTFAR\Q EGRK\D*PQRSNEFKE\VTQQLPHL\ LKDVGSLDRKN*GAWDVNQDFGG SRFN\EY\WRLIGGAWPKEIRKEEKT LKIQERSKAAWLEDGVGQGR
1247	6744	A	1312	165	629	TGEMLRKHCLYIVCKLSLLFIFRDM SCSVAQAGMQWHATNAVDGD*LT ASLKLGGSSNPPPCNPKRAGIIGMH QHIQLIFCWSFF*KQAFRLRITKALRN FKKI*FQNTLVTGKY*HCSLTFFFCH FNENRILHLLAQMAKQDSGLLRV AWEA
1248	6745	A	1313	76	523	ELGRNLWNASQGRGLEWVSNRKF WAVYAYITFLSHPERVVKHNCPL FE*KGECWEW*EARAQ\NDRVQKQ MWLLRIQTSFSSRKETQSLRVTFWR YPVSPSPISMR*MSPGNSYRTLYKR NVPLKAHFPTAVLAVVPPAVTNQG KEQG
1249	6746	A	1314	55	391	
1250	6747	A	1315	996	1334	WASVGLSGPRSPSSRPQ*ARPRPG APASLRQADLGRGWRDLGAPRPR PPRTGGWRSCCRGRGPGSRPRGAR AGLGPGAPGGWRRSRRSWTRARA ATRPRAAARGSRTPRG
1251	6748	A	1316	1	993	
1252	6749	A	1317	72	496	PPWARGSARRPPAWRTVRMPSCHP RMFGAPQKTFLRVSVWSRCRPWGI VMRMM*PMRGQVRRHNSCMAKPT EE*NPTVSATFCCCSFVCSWPPVTR YSSILFTAAM
1253	6750	C	1318	202	378	MTPYLTFLSPLPPKGEIWGLLLFLT PLGFLPSLPLLLPCPAPAGVRRQW DGPTEGA*
1254	6751	A	1319	1	1541	
1255	6752	A	1320	9	345	YLSEVGVSVGIVIRPRQWIRPEGDP FHGGRLKMDPLRAQQLAAELEVEM MA\DMYNRMTSACHRKCVPPPFKE AELSKGESVCLD\RCVSKYL\DIHGA *WGKKFDRVVLLQG
1256	6753	A	1321	199	985	VRGSGADPGGRLCSASVRRGGPLE GAFNSRTRQATMTENSTSAPAAK\P KRAK\ASK\KSTDHPQVFQT*IVACN SSPRRTGAGS\SRQSIQ\KIKSHYKV G*ERLTSQ\KLSIKRL\VTGVP SRQ TK\GVGASGSFRL\AKSDEPKKSVAF KKTKEIKKVATPKKASKP\KKAAS KAPNPRNPKSSPVKKA\KKKLAAPG PKKA\NPKPTVAKPGKAFKAHWR PYLV*PKCKCPVAKEGRARRKLTMI VFFLRDTPSWSPIFCK
1257	6754	A	1322	3	129	
1258	6755	A	1323	376	545	NILHRLFTFREKTSYAPFVVRRFHSHK GRHTPPFALKWEWVWRKKGPGEG DSDMALSYSPPPPPPPPMVMG*/SP PSH*PLLLCRRVKKEGF

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1259	6756	A	1324	14	262	FQTQTKYQAPLHPAPGHRPTPLPPP PPASHCHLFLWSVCKRSNKPQAPFI SPPPSNPLPEPGPCSSLCQPWGRTG EGLAPPD
1260	6757	A	1325	234	275	
1261	6758	A	1326	52	454	SQTQREPTMVLSPADKTNVKAA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGK\KVADALTNAVAHVDDMPN ALSALSDLHAHKL\RVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLKD FLASVSTVLTSKYR
1262	6759	A	1327	3	616	PTLLVPTDSERTHPWLLSPADKDQR QGPWAG*G*GSHPPSNVAKTLER\W VLFPPPTPKPYFPHFDLSHG\SAQV\ KGHGK\KVADALTNAVAHVDDMP NALSALSDLHAHKL\RVDPVNFKL L\SHCLLG*PWAAHLPRPSFTPCGCK ASL\DKFPGLFVEAPLLEPSKLPKL GSLRLAMLLCPFGPFPQPLLPFAPV PPWSLK
1263	6760	A	1333	732	1634	RRFWQVENHEILTEQAFVGQKPIFR/ MKSLKEKLTATKRKPKNIGDILT KRKNNRTGSEAGEPQRWKPRRCPI RRAQEKNSQRPRKRREGKVPIWRK KPLKTGRDRSW*P*KLLALCPSTVG IRSRAG
1264	6761	A	1334	1	531	FFFLHVVAHLIFTATQMGSNILITVL QMRSPRRRVEYLAQDHTPFATPHS KSHRQLRLSTSMVTYHLPLQTISS LVPYSQWGHLSQPGPKLGNRKPF LTPPSPPTPSKWNPSPGTMYFFRVL QSPLSSPRPRC*PIVRCPAAAPGSSLP STLFAGPSPFPAS\YTLRLRCAF
1265	6762	A	1335	130	361	GACCPSPGGESGT*C/SPRGRPKPS GPSPKAKCS*QSTGCGQCASSPPSPS PGRAPCDSPILACDLGQGGFLQLHT H
1266	6763	A	1336	144	224	
1267	6764	A	1337	1111	1200	PGVVTLGGGACSEPRCATALQPGR ESETLP*TLHSHNQSKPLPPICYPIS VNGNFILLVAQVKPKCAGCGGPR L*SQHFGRPRQADHLRPEVQDQTG QHGTKASL/LKNTKISQVS/WTLGG GACSEPRCATALQPGRESETLP
1268	6765	A	1338	344	512	ETLYTME*YTAIEKNEIMSFAGTWL ELEA\VIL\SNLV*EQTKMLPCSP MGWELK
1269	6766	A	1339	274	393	
1270	6767	A	1340	1	561	VRSAVGGTGMSSGASRKS\WDPGKP WPPDW\PI\TRK\MK\VL\WAALLVHI SCQNPMPKW*QAV*NKSRPELR\Q QTEWQ\SGQ\RWEL\ALGRFWDYL RWVQTLSEQVQEELASSQVTQ\ELR ALM\DETMKE\KAYKSELEEQLTP V\AEETRAR\LVK\EPQAAQARLGAD MEDVRDRLVHYMF\DV*AI
1271	6768	A	1341	1	746	MAAAGAFRLRRAASALLLRSPRLP

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						ARSCRPRPDSITRSPDVRLPLEKQL KNAINQRGKGPYIRYYPEVVDHY ENPRNVGSLDKTSKNVGTGLVGAP ACGDVMKLQIQVG*KRGRFVGC*G FKTFSAVGSAI\ASSSLSHLNGVKGK TVEEALTIKNTDIA\KELCLSPFWK LALAPMLGLKVAFKAALADYKIET RTQKKGEAEKKWSPPLGEASSRPTP AVQPAPVPTLDVSGSRLPSPTEGA L
1272	6769	A	1342	160	381	SWGLDSALGVSDTTHHPKVVGRAK HRGFLKWLP PPPG PPLGKRNCQYP NPQLPESGPPQYFYLKCCPFYEL
1273	6770	A	1343	653	814	WDSTPLSSFTDWMLWPEKRQVGA CSHPTPNFL/C*GKLNISPNSPCQPKV LDLT
1274	6771	A	1344	954	1245	DLSLTTSRQRKHEFKEVILPNYTHD KLYLINSNHPTKMCP*NQVLKCLI ITQQWTGAMIHAYNPSTLGGRWG WIT*SQELETTLPHIRGTLIHKI
1275	6772	C	1345	155	431	MRERGLGPLGVFRSDAGLKS LPEG RRESGALEECVIHTQRVCDWKVPE HPLAPLLLVSAVLRILAKPLPTQR DLFLLSRSSLFNQHFPLC*
1276	6773	A	1346	2	70	
1277	6774	A	1347	1	271	LFF*TESCSVTRLQCSGMISAHCNLH LPGSSNPASASRVAGTTGARHHAQ LIF/VVFLVETGFHHVGDGLDLL/N LVICPPRPPKVL*LQA
1278	6775	A	1348	117	229	KKTMFRQKLFYKRKQLQKGPRP*G SAKKKLCFGKSYFIRGSSFRKGQGH EERGLKYKKKTGEV
1279	6776	A	1349	255	381	IHFSINSQLFSPSSPPNKKG*FPKVT* KR/P*NGPRYIPQRF
1280	6777	A	1350	72	577	TTGVRGALQREGGSLPTQPQGERA LGRRRNQAPAGDPGFA/G*RG*WP TGCKQGRGGSPSPQLGSGGR\QNL ARLKPPRPPP/PQGEDKGRPRQOG PSWRSKSSPPPILPSTYPGGDKGVVP KHKLEAVNSVRARSSVSRNKCWSN RMDIALRCPVTVAHELTYSDAL
1281	6778	A	1351	160	336	
1282	6779	A	1352	1625	1920	LSFPAKKGNDCLPHVPGLSFKGRVP ESRQEFCEQESSLENPRLCIPV/CHP WAPWRWEPGETAEPVLRKEAF* PGPPCPPPNRVSETREAVLLQPRI
1283	6780	A	1353	9	249	KVHTKPRTSICRSHIGFCLFF*ETES CSVTPPGVQWCNLG\SLQTPPPG\SS DSPASAS*VAGTTGMHHAQLII*F YVFTGFFWQ*QLSDGILTH
1284	6781	A	1354	426	744	DNLLKSFHLIISINCLFFCFFFL*TESC SV\SLKCSGAILAHCNLCLLGSSDS HISASLVAYRCLPPCQANCFFSFLAE TGFHHVVQAGLELKIQLAECG MRQ
1285	6782	A	1355	184	422	GYIQGSPALVSTHGGHAV*PPTQSK PTEHAHPLQPRRWARTRVGEIGIP

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						AHPSPSCSPRPLATQKRFAQNRRGR LEGLC
1286	6783	A	1356	3	1221	HFIYLFIFIFLRQSLALPLRPECSGAIS AHY/RHLCLPGSSDPN\SASRVPGT TGMPRCTWLIFVFLVEMGFHHVQG AGLKLLTSGDPPALASQNGGITSVS HRVQPKNFFE*SRYYYLNFKGN*DS KRLKK*KIRQLEN/RRNMIQILLFF* L*NSCSRMKDNS*AREKYLOHILRG LRFLTCKDSTKLDLKATNRNTTLE* MENMMKQFTEEKIQMPNPKDLKRC* TSLGVREMQIEVIRYFYSRSS*QKFK RVV/IIPGQLQRKCQF/PCTW*KSKPL KRFSEEI*YNINQIHLFEAGSCCVVQ DRVQ*YHHSSL*PQPPRIKQSFHLSL PTSWDYWHMPP/HPS*FCVCLFCFF SRDEVSPGCSSWS*TPELKLSSHNLN PKCRDARPEPPCVAQYDINQNCKK HVLS
1287	6784	A	1357	703	918	TREVEVAVSRDHATALQPGQQQRQD SVSKKKKKGRVQWLAPVIPSTLGD QGGWIT*GQEFETSLTNKVKPHLY
1288	6785	A	1358	273	561	DRQAEKKRNIL**NEIVLDLPR*PHT AS*ISSTT**FENTALRPGVVAHACN PSTLGGGA/GQIT*GQEFETSLANV VKPISTKNIKINWEWWCRL
1289	6786	A	1359	375	663	LITKQLGLGVVAHVCIQHFGRPRW ADHLSPIGVQDQPGQIQGETQSPQK NTKISQVWWHVPEVLAP*KAEAKG LLEPGRQRLPPTLHSLRGSETL
1290	6787	C	1363	79	153	MPDMIRQHSSCLIKRVYLTRWFGR*
1291	6788	A	1364	4776	9134	WLHDSVNILKNIEHFFFFFFWROSL APSSRLECSGAISAHCNLHLPSSDS PASASQVAGITGAHHHAQLIFVFLV ETSSHHVGQASLKLLTSSDPLALAS QNAGITGMSHHTWPNH*IEHF*WV NCMVWEHYLNKAILKFYKEIKSRR DPTPKAYLIWGR*C*/TVL*NKEQVT DTKFLT*LFKGVGRM*KFTVPAPPEV VRVS*LYLA*DKCLVIIVAMLMDRN VIFLKGPLMGFVG*LCSGFQGKEWF LFESYPSLPTSPITLSPALPKYFL*VN VTKANFLQ*SIPFYIMVLTFPST*S QYTNFFFFSF/HFFFFFF/CFFETESH VTQAGVQW*DLGSL*PLPPRFQ*FS CLSLSSWDYRHAPLRPANFCIF**R /SGVSPCWPGWS*TPDLK
1292	6789	A	1365	3	287	
1293	6790	A	1366	75	301	AHKKLRAAPLAPMTGTH*K\VFVK AGDKVKAGN\PSWVMFPMKMEHTI KSPKDGTVKKVFYREGAQANRHS FSRV
1294	6791	C	1367	155	377	MKASSFKKLQKFYIDPYKLLPLQRF LPRPPGEKGPPRGGRGGRGGRG GGGRGGGRGGGFXXXXXXXXXG RG*
1295	6792	A	1368	363	423	SIKGTENGFLIVL*PKSQV

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1296	6793	A	1369	157	723	KTLWRYGNRG/GFQRGGST/RAGGC/GAQQGGPEGHVAPY*GEFLHPCE/DDIVCKCTTDENKVP\YFNAPVY*ETKEQMGKVDAIFGQLRDFYFSVKW/SENMRLLSSFKKLQKFYIDPYKLLPLQRFLPARSPGEKGPPK\SGGRGGRGGRGGGGRRGGGGFRGGRGR\EGGGFRGGRGGGFRGRRTLSETC
1297	6794	A	1370	1	810	ASPPLVCTHARSFVLAFLHFPPLL/PDRRSRSFRAVHFWGPRSSPPHAAVRLREARRGRDRREKAESPTGEKSTS/PSSSRQRGPPTKVRPPAPFTMQP/ASAKWY\DRRDYVLKWEFVFLNTLRDV\NVNFIEKSKTYNFSCLG\SDNF*GILNEIDL\FH\CID\PNDSKHKRT\DRSIL\CCLRKRIWASSWPGLTK\ERGKGLIWV\SVDFNNW\KD\WEDDSDEDMSNFDRFSE\MMNNMGGD\EVVDYPEVDG\ADDDSQSDDEKMPDLE
1298	6795	A	1371	1	588	
1299	6796	A	1372	179	989	KWRNQSWRWPKPGTNWMLSCSVC/WRRVTWTGSVWMRKLGKHPQTPT/IKDCSIAATGKRPSARFPHQRRKKR/REMDDGLAEGGPQRSNTYVIKLFDRSVDLAQFSENTPLYPICRAWMRNS/PSVRDAECSPSS\PLPPLPEDEEG\SEVTNSKSR*CVQACPPHTPGGQPKN/ACR\SRIP\SPLAALRMQGT*RWSPF/EPEPSPSTLIYRNMQRWKIRQR\WRPPACPLPVGPFATAESPLCLSRWK/EASHRNQLRYSESMKILREMYERQ
1300	6797	A	1373	245	336	HIPSQQQDGK*VKNRARKIVSYSRG/GWHSG
1301	6798	A	1374	127	872	EATGQTVGTVPSSLSRPRPLHSSSG/GVRIQTLFATSRLDKTASIFLVLSN/ACIF*KILIA*KEIQDS*SHH*K*LLLI/RLDFLSSFFPP*LIN*FFFFPGNSLVH/RLFFFFNLGMVAHTYNPSTLGGQSG/RIA*A*EFKASLGNLVGPHFFFLGGG/VGYKSPFIKPILNKKKTKSLQKKKR/YRKRIPLLHMVPKREKNKGDNRQH/AQQIKASFSYFFNVQNTSKGYTYLK/QELSDAGHAGPGKPFQ
1302	6799	A	1375	37	80	
1303	6800	A	1376	1452	1700	
1304	6801	A	1377	316	373	
1305	6802	A	1378	144	356	FQFRLTSLRNSTDVHRCQQLPPPPPS/PPPYPGPWGMGCGRFPKGQQGPRP/RLSGLG*FLSFFALGFSDG
1306	6803	A	1379	860	924	
1307	6804	A	1380	263	616	TTCFSFESRASCFHVASAVSPPTPL/CSPATLMAQDKAGKPSPRK/PSLAP/EKPLSPLPSQ*RHSPKPKAPHVESP/SGPSPTRAKKRV*FSSPPSLWGQEP/SHAECPLPYLGEGAPA
1308	6805	A	1381	152	272	YSVLKFNYEILKNCFSFFV*VSEPF

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						KTILVYFTLTEKL
1309	6806	C	1382	71	316	MCHHSQTLFLYFVKTKSHCVAQAG LELLASSDPLDSTSQSVGITGMSHH TQPLILFFNFSVSVKYTKIMVLKNGF RNSYKK*
1310	6807	B	1383	165	520	XNLKLLDNWDSVTSTFSKLREQLG PVTQEFWDNLEKETEGLRQEMSKD LEEVKAKVQPYLDDFQKKWQEEM ELYRQKVEPLRAELQEGARQKLLP VLESFKVSFLSALEEYTKKLNQ*
1311	6808	A	1384	3	558	
1312	6809	A	1385	3	118	
1313	6810	B	1386	28	384	MKAAVLTAVLFLTGSQARHFWQ QDEPPQSPWDRVKDLATVYVDVLK DSGKDSVTSTFSKLREQLGPVTQEF WDNLEKETEGLRQEMSKDLEEVKA KVQPYLDDFQKKWQEEMELYRQK *
1314	6811	A	1387	2	1093	GGASCCLPRSLWLPSSRFRPCPRPG LWVPEVFSRSVPFSSPGCNEWGSTG LLHAEGTPLSQALLLQVPHGPFMR KAAVLTAVLFS DG*ARRRHFWQG G*SPPRAAWDRV\K\DLATRVPTV LKEQRTETYVSQFEG\SALGK\QLNL KAPLTTGDSVDLPPFS\KLREQF\GP C*PRDFLGINLGKRETEGP*GKGR*G KDLWKEVKAKVAALTDDFQERS WQEEIGAFTQK\VEPLARKNFQEG\ ARPESLHELARRSLSPGGEEMRDRA RAHVDA LRT\HLAPYSDEL RQRLG AR\LGALRENGGARMGQYHA\QAT EHLSTLSEKAKPALEDLRQGLLPVL ESFKVSFLSALEEYTKKLNQ
1315	6812	A	1388	1	2076	
1316	6813	B	1389	560	752	XSVAAVTALNSES NFARAYAQGISR TKYWELIYEDSMDLI AKLPCVAAKI YRNLYREGSVTRGH*
1317	6814	A	1391	1031	1407	CVGGRAQVEKEGAALRLRPATVPR ALMSLSSLVKPETA\ALCGTEMQDF FTPLLCDFKS\PGISFCKGT*MCLRSC *HNVRWR\DQPTPVSTVTPVPTLT CVPSPHFPVPER\GAGCLHLCLKFM VH
1318	6815	B	1392	97	880	MAPRTVLLLLSAALALTETWAGSH SMRYFYTSVSRPGRGEPRFISVGYV DDTQFVRFDSDAASPREPRAPWIE QEGPEYWDRNTQICKTNTQTDRES LRTAARLLQPERGRMYGCDVGPD GRLLRGHNQFAYDGKDYIALNEDL SSWTAADTAAQITQRKWEAARVAE QLRTYLEGTCVEWLRRLYLENGKET LQRADPPKTHVTHHPISDHEATLRC WALGFYPAGDHTDLAAGMPRTKL RNTEL VETRPAGR*
1319	6816	A	1401	1380	2180	EIQSEWNLQDL\ELQLEERLAGAWE E\LSFRAVRMPSPFRSSALMG\MCG SRSADNLSWPFFH*NVMEPVTELM

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						QE QSYLKSELGLGLGEMGFEIPPE SSVESVFSRAQQDSFCECSGPSNATR KMGVPSVTASVGKSKTPLVARKKVF RASVALTPTAPSR\TGSVQTP\PDLE SSE\EVDAAE\EGSPRKL*GPKSESEV/ EKEGHGKLP\MPAAEEMHKNV EARRLSLQQVIR\EIKESIVGEIR\REIGKL DFWAAVSS\SKASNSR\QDYH
1320	6817	A	1402	119	301	INDKRKKKRPARPGAGGLHLQLCL SQPPQPRGHPAPIPTGQAGPRDSGP GASP*/GRDPPSD*WTPADLGSDPW AGPLPTPQEP*GSRWPSSATVSLAS TATGTPCTYSHGTGWTQRLWTRGL PLSRDPPSD
1321	6818	A	1403	1451	2495	RGLAGNFEDRKSAHYVFQTFRGGE RRSLELEAHLEGWSLGLRFLGPLK GPPA\QGHFHP\SLPISSWRGAGVPHS R/SPFP\TLGIPG*IFPPKPGRRPRGP KEDLGPGMVG/RPSG\PLQLPSAVL SADPAGPRPHVPFCEP/SPSHGVRAS PGSKWVEEIGGEEGRQ/PKCRQAF QEA\WLMQG/GARGQGLPGS/GCWR INKPSKPSKRGKGLTCQTFSTNIC* SPPLMPRSLP\GPSFILHLISSQP*SG LLFIDPIPEKGRGGLSERWGRAFG DSVACSFQKPTPGPWEVFEQDAWP NPWP/QGPPPENFPKGNPSHSRNIHK GDEQSPVRTKTEPTWGGKHSQFA SR
1322	6819	A	1404	3222	5798	PLLTPLVSKVTAAGVPLFFFFFFF* DIVSLCHPGWSAVV*P*LTAASNS\ VKQSSHL\SLPSSWDNRYAPRPANY FYFYFL*RLDLALFPKLLNCWAQ VILPSQPPKVLGL*AQSSEGGIHSGL SLPSPCFLLCNPI
1323	6820	A	1405	38	402	
1324	6821	A	1406	2	380	
1325	6822	A	1407	1	477	
1326	6823	A	1408	1	1104	
1327	6824	A	1409	524	1584	IVKMEKYSIMKSMNMHLTERKKDH FRNDTNTQSFYREKWIYVHKESTKE RHGYCTLGEAFNRLDFSSAIQDIRTF NYVVKLLQLIAKSQ\TSLSGVA\QK NYFNILDKIVQKVLDLHISLLFKDL PQVLSSNLCTLIRGVGKSVLVGNIN IWICRLETILAW\QQQLQGLQMD*G K*TMGLT\ASDLPLAHGWNNILLPV FQDGWGHSTFRPR*PPRLYMAVG EDRQLWKKL\CQYHF\AEKQFCR\H LILSEKHS/VEWEVGCNFATFRKH YPAKEQYGRQHCIFCRHCSILFWKD SGHP\CTAADPDSCFTPVSSQQFIAL FQVLRACPLPIPYWRFVNPCCPVQG LIVSVL
1328	6825	A	1411	588	855	VLLSSYLQYSLVFICWLFICLFICIFI FMYVTM*IWFVAVFVWNLVFPYKV VK/TPWRSRIHVHCLYF**NYSYAF



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						LYSA*CYSLCVH
1329	6826	A	1415	277	509	YMLSCHHTFVQTHRMYNKHEP*C KLWTLC*DNLSM*VHQL*KFPTLVG DVDS/ERRLCMYGDRGYMGNYLIL LSILL
1330	6827	A	1417	15717	16041	
1331	6828	A	1418	41	544	TKLVMMQKLLKCSRLVLALALILV LESSVQGYPTRKPRHQWVRCPDS SSAHCLEEKGHMFELLPGESNKP L\RTDLFPKTRIQ\DLNRIFPLSEDYS GSGFGSGSGSG\SGS\GSWFLTGN RNYQL\VDE\SDAFQ*QPLGSLDRNL P\SDSQDLGQHGLEEDSMV
1332	6829	A	1419	168	467	
1333	6830	A	1420	2	196	ASTRSRRSGSRGLTRRAAFGVRA GWVCGGPAGSRRRRKLPLTGP SFQCRSRGGRGSVNMKGDPNKP GKMSSYAFFVQTCREEHKKKHPD FSVNF\AEF\SKKCSER\WKTMSCKG RSSKF*RIWAKS*QSFADR\EMENL RFLPKGDKKGKKKDPN\APKRPPS AFFLFCSEHRPKIK\IEHPGLSIGDTA KKLGEMWSESAKDKQPYEQKAA KLK\EKYEKDIAAYRAKGKSEAGK KGP\SRPTG\SKKKNPPRSWRGWEG *EA**DPASGIWGAGRRGLGLWRA GGQSEEAETAPDRARFWEFSMSVT RWTRICQHG
1334	6831	A	1421	3	107	
1335	6832	A	1422	450	851	KTEFTQNYFWKSCTGVDGFFFSILF CLFV*DGVLCHPGWECGCDLHS LATSASQVQAILVPHQPSK*AWDYR RAPPQLG*LYC\CRDRVFTMFVPG LSNFW\PHV\HLPQ\PPKVLRIIGREP TCAPASMAF
1336	6833	A	1423	6	461	AEMTPLHSSVGSRVRLHLKKKNYI KKPRKALFISIFGIFFHLIYVSTYIYL STFSFTSLILMEFILCVV*VLHLQLK NAILMAYWY/TFILITWLPSEEDLK VL*LFMPKNELIFSCKFHFLFIVPKFT LLDHLAFLRLKLAFWRLGWHST
1337	6834	A	1424	222	350	GAHTWTGISQAALQPTAPGRLSRTL LFLC*KCGEICNLLSGC
1338	6835	A	1425	198	385	
1339	6836	C	1426	207	385	MFFYKLAQMXQISVSTLKFKLVLFV PTGXQVNGGEPSTLYGRWGRXGSA PSWRYQFPCP*
1340	6837	A	1427	327	516	
1341	6838	A	1428	58	255	FSPDFYRGYIYFYHYFGFEKFFFTPS NFFISQSR*FFCVKMFSFFNLRFKIPL PNHVDFALCFFVV
1342	6839	B	1429	242	509	MRPRKAFLLLLLGLVQLLAVAGA EGPDEDSSNRENAIEDEEEEEEDD DXGENDLEVKEENGVLVNDANFD NFVADKDMDTARDLPPX*
1343	6840	A	1430	338	511	NSFSKSKTPCVAHGRGVHAEAGNK RQYLGFLFFF*FFILWCFTSCSEY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
1344	6841	A	1431	2	454	
1345	6842	A	1432	671	955	FFFF*IFTLGCFITSCSEY*ITMNDVK* FSPEFLPEGYLLFLSLFGV*KIFFYTL LISLFLKAD/RFFCVKMFSFFNLRFKI PLPNHADFALCFFVV
1346	6843	B	1433	46	3152	MRPRKAFLLLLLGLVQLLAVAGA EGPDEDSSNRENAIEDEEEEEEDD DEEEDDLEVKEENGVLVLNDANFD NFVADKDTVLLEFYAPWCGHCKQF APEYEKIANILKDKDPPPIPAKIDAT SASVLASRFDVSGYPTIKILKKGQA VDYEGSRTQEEIVAKVREVSQPDW TPPPEVTLVLTKEFNDEVVNDADIL VEFYAPWCGHCKKLAPEYEKAKE LSKRSPPIPLAKVDATAETDLAKRF DVSGYPTLKIFRKGRPYDNGPREK YGIVDYMIEQSGPPSKEILTLKQVQE FLKDGDDVIIIIGVFKGESDPA YQQY QDAANNLREDYKFHHTFSTEIAKFL KVSQQLVVMQPEKFQSKYEPRSH MMDVQGSTQDSAIDFVLKYALPL VGHKVSNDKRYTRRPLVVVYYS VDFSFDYRAATQFWRSKVLEVAKD FPEYTFIAIDEEDYAGEVKDLGLSE SGEDVNAAILDESGKKFAMEPEEFD SDTLREFVTAFKKGKLPVKSQPV PKNNKGPVKVVVGKTFDSIVMDPK KDVLIIFYAPWCGHCKQLEPVYNS LAKKYKGQKGLVIKMDATANDV PSDRYKVEGFPTIYFAPSGDKKNPV KFEGGDRDLEHLSKFIEEHATKLSR TKEELMDVQGSTQDSAIDFVLKY ALPLVGHKVSNDKRYTRRPLVV VYYSVDFSFDYRAATQFWRSKVLE VAKDFPEYTFIAIDEEDYAGEVKD LGLSESGEDVNAAILDESGKKFAME PEEFDSDTLREFVTAFKKGKLPVI KSQPVKNNKGPVKVVVGKTFDSI VMDPKKDVLIIFYAPWCGHCKQLE PVYNSLAKKYKGQKGLVIKMDAT ANDVPSDRYKVEGFPTIYFAPSGDK KNPVKFEGGDRDLEHLSKFIEEHAT KLSRTKEEL*
1347	6844	A	1434	785	1271	LCTDQLHNFNNYFQDKDKCFYFPM FWSFLGLETEAACFKPDSKGKALQ NRKYFN/VYLPSATSRDLWISPGWS QPFFFFFFFFFFFF*RA
1348	6845	A	1446	549	791	GLLSN*NFFFSILIFFFQTESRSVA ECNGAISAHCKLRLPGSRHSPASAS RVAGTTGAHHHAWLIFFVFLVETG FHHVSQDGLDLL/NLVIHLPRPPKVL G*QAGVQWCDLRSLQAPPPGFTPPS CLSLPSSWDYRCPPPCLANFFCIFS DRVSPC
1349	6846	A	1447	59	485	NSPCSGSSIATASPERRKGINPAPPST PAAPCRS*ACTAAAAAAVR\DDRLN VTEELTSNDKTRILNVQSRLTDAKR INWRTVLSGGSLYIEIPGGALPEGSK

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						DSFAVLLEFAEEQLRADHVFICFHK NREDRAALLRTFSFL
1350	6847	A	1448	125	927	NPPCSGSSIGPCSPKRRKGIKPGPPH RKPAPSGS*ACTAAAAA\VRVPGS PSTAV\VTRVRGLGGAPDAPHPLK DPRVGEQNSQRNPNL\ANLFYS\DD RLNEQKEL\TSHDKDEHSRRPSSRLT DGKTPLNWRNNC*SGGSLFNIKPA GRRWPEGSKGQLLQFLLEFA*GATC GADPKVFICFQTRTREKAEPPLLRIT FSFFGLCRLVRPGGIPLVPKETPDAC FMALQRSRESLPGEVEVGARLRG WAIPPPWGHPLVCTGG
1351	6848	A	1449	1	866	ESVDLAAEAVRIRRSPLIFSKAVHIM AAAFRKA AKSRQREHRERSQPGFR KHLGLLEKKKDYKLRADDYRKKT RITSKALRK\KALEK\NPDEFYKMT RVKLQGWSYILLRETKGRK*PQEQL KADEELQDVKYIEMKRVAEAKKIE RLKSELHL/VWDFQGKQKNKHVFF FDTKKEVEQFDV\ATHLQTAPELV DRVFNRPRIETLQKEVKGVNTNQT GLKRIAKERQKQYNCPAHQRIE\RE KKLIPLLPQKIQTRKDLMDKTQKVK \VKKETVNSP\AIYKFQKSVENR
1352	6849	A	1450	3	896	LRAVRVGLLLGGGGVYGSRRFR\TF PGCRA\SPWRVRVQRRCEMSTM FADTLIVFISVCTALLAEG\TWVL \VYRTDK\YTRL*AEVEKQSKKLK GRKET\TEFSWFGQKKKIERQEEE T*RNNNRDLS\MVR\MKSMFAIGFC FTAL\MGMFNSIFDGRVVAKASF*P LFSYIQ\GLSH\RNLLG\DDTHRLVPF IFLYILCTMSIR\QNIQKILGLAP\SR A\ATKQGRVDFLGPPPPSGEVLLEL KELFIFYSFFLGHTHIRMGQLFCSQE PIGSLYYLGLFLVLNYFLSLLGYD
1353	6850	A	1451	2	125	
1354	6851	A	1452	18	1374	LAEQIVPRGVGIRPPDKADQAPCRS PIRTPAPESWHCDRQFRQDSSRM KMRVLGLVVCLVLWTLHSESGG KLTA VDPETNMNVSEIISYWGFPSE EYL VETEDGYILCLNRIPHGRKNHS\ DKGPKPVVFLQHGLLADSSNWVT\ NLGNSRLGFILADAAIDVWMGNTR GNTWSPKHKTLSVSQDEFWAFSYD EMAKYDLPASINFL\LNKTG\QEQV YYVGHSQGTIGFIA\FSQMLELAK GLKMFFAWGPVASVAFCTSPMAKL GRLPDHLIKDLFGDEEFLPQSAFWK VAGVPHLATHVIL\KELCGNLCFLL CGFNERNLNMSRVDVYTTHTSPAGT FVQNM*HWSQAVKFQKFQAFDWG SSAKNYFHYNQSYPTYNVKDMLV PTAV*VTGGHDWLEDVYGVNI*LTQ ITNLVFHESIPEWEHLDFIWGLDAP WRLYNKIINLMRKYQ
1355	6852	A	1453	165	1353	LPKPRLGPGQPEKDRTESSVRMAIT

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						LEEAPWLGWLLVKALMRFAFMVV NNLVAIPSYICYVILQPLRVLSKR FWYIEGIMYKWLLGMVASWGWYA GYTEMIEWGEDIRAVSKDEAVTLV NHQATGDVCTLMMCLQDKGLVVA HMMWLMDFHFKYTNFGIVSLVHGD FFIRQGRSYRDQQLLLKKHLENNY RSRDRKWIVLFPPEGFLRKRRETSQ AFAKKNKLPFLTNVTLPRSGPTKIIL NALVAAQQKNGSPAGEDAKELASK SKGLQWIIDTR*PYPKAEPI/DNIQT WVFGYRKPTVTHV\HYGIFPAIKDV P\LETEDL\TTWLNQRFVEKEDLLSH FYETGAFFP\SKGHKEA VSREMTLS NLWIFLIQSLAFLSGYMWYNIIQYF YHCLF
1356	6853	A	1454	313	650	FVICV*TYTGMNTHSPHTKLSFLS DSG*FFYCRSL/CNIG*QKTYQPNR LHTHTHTHTHTHRGYFSHTSSTVEK ALLTRIPEGSEEDNGFYGWALRTI LVAFKSQCQMH
1357	6854	A	1455	2	401	VSVGGLVGEVACACRDCIPETMAE GDNIRSTNLLAAETASLEEQLQGWG EVMLMADKVLRWERA WFPPI/MG IIYYLDPSVLSGVSCFVMFLCLADY LPILAPRIFGSNKWTTTEQQRFHEI CSNLVKTRRRRA
1358	6855	A	1456	18	741	AACGAFSRVVVGVRVSVGGLVGEV ACACRDCIPETMAEGDNIRSTNLLA AETASLEEQLQGWGEMLMADKV LPWERA WVPPIAGVVSFLIYY LDPSVLSGVSCFVMFLCLADYLVP LAPRIFGSNKWTTTEQQRFHEICS NLVKTRRRRAVGW\WKRLFTLKEEK PKMYFMTMIVSLAA/VLLAWGQQV HNLLTYLIVTSLLLLPWT*TQHGHI FERTLGMANMEINKLLKHK**TN
1359	6856	A	1457	2	529	GRVDPKAKKEAPPPKAEAKAKA LKA/RRKAVLKGVHSHKKKKIPHV HPPFARRPGRHLRLRRQPK/YPPEEP RPRRNKLDHYAVIKFFLTTESAMK KIE\DNNTLVFIVGCLKPTKHQV*Q GC*RKLFWTLDVGAKVNTPGFGPD GRRRKAYVPTWLPDLPIAFGMFAN KIWGFI
1360	6857	A	1459	323	624	IVVHLVPTTQRSGKGKIMELVERSV VARVEVGHRGFLERGLPIAANDM KKSPEIISGRMTFVQPRNWLLFACH ATNEVAQLIQGGRLIKHEMTKTASA
1361	6858	A	1460	438	549	
1362	6859	A	1461	210	556	QFWGPVATWGLPIDAINDMKKSPEI IQWGG*HFALC\CYSLTMEILPYK V\QPSGTWASCFACHGTNEVRPSFI QGEGLIPNTRMDLKRASGINQWG KGKNKVFEGLSLCPGCC
1363	6860	C	1462	110	509	MLLICSFAPATLXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX

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						XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXVSA*
1364	6861	A	1463	93	180	
1365	6862	C	1464	128	382	MYLGISRRLSSMLTFLAYLHPRERP PHRAPXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXQQAQG TGISIPRTCTSTGL*
1366	6863	A	1465	3	140	
1367	6864	A	1466	1	609	
1368	6865	B	1467	1	690	MASWDEKDLTVPQPDTRKGSVLR GLSSRALRWAGRGHVAAGWRPLA PESAGGWGMAAAMVPGRSSEWER GEPGRPALYFCGSIRGGREDRTLYE RIVSRLRRFGTVLTHVAAAELGAR GEEAAGGDRLIHEQDLEWLQQADV VVAEVTQPSLGVGVELGRAVAFNK RILCLFRPQSGRVLSAMIRGAADGS RFQVWDYEEGEVEALLDRYFEADP PGQVAASPDPTT*
1369	6866	B	1468	1	975	MSPPGREQGLLLNLLRPSGLDNAG KTTILKKFNGEDIDTISPTLGFNIKT EHRGFKLNIWDVGGQKSLRSYWRN YFESTDGLIWWVDSADRQRMQDCQ RELQSLVVEVGSSYPLCTWRFFSY LRIEQMYNLVLYRDIQFPDFCFNSN TDWSKGLKTHARFGNTSLHVAHTD STNTTNFVDVWRGRTKSLACLLQL SSLTCIYTAGKMRLQDRIATFFFPKG MMLTTAALMLFFLHLGIFIRDVHNF CITYHYDHMSFHYTVVLMFSQVISI CWAAMGSLYAEMTENKYVCFSA TILMLNGAMFFNRLSLEFLAIEYREE HH*
1370	6867	A	1469	25	353	EVCYYSSEAFFSELIKVILRHLCV AGKGLCSIPQLNTREGSVLRRISK GSPLAVEIEEGHCLCLPLGTECLGI KPIVHLLNSEIGKPPFSPLSPCSSA AFLLLR
1371	6868	A	1470	79	467	RPESQRANGVDSGPNLKTVPQPDTR KGSVLKWKSKRGKPLAVEIEESHCL CLPLRTECLGIKPIVHLFSCTRPVIV PSLELHYDIDSIAHMFVADLLIITLL SYYIPFYLGFQAGITGINHRAWFY
1372	6869	A	1471	368	611	LCPSHFAPTTLTQSGSSLKTCVVLNS RFKACRAVPGPCLVNQMFASSILG KSHHSLVPINQGHNAWKAAGPL PLKAGY
1373	6870	A	1472	441	1178	FVALPQPLCPSHFDPTTLIQSGAHKN MCCI SRFKRDLGLCRTCLVNKMF TSSILGKSHCHSLVSINQGHNA AAGPLPFRAGYCAQGFSPCDSLKYG SWDEKDLTVPQPDTRKGSVLRWIS QRGKPLAVEIEEGHCLCLPLGTEC LGK/PIVHLFNSEIGENRPMVGG RHVLQ*CLG*FL*PLRCLGGEKH KSG/HVHIPVIVLSLELNYDIDSFA

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						HMFF/SVDLLLIITLLSYIPFC
1374	6871	A	1473	1540	1812	GKFQLIKTLQNPVVCSLPVPALWG GQRWVDHLRLGVRD*PGQHGETPS LLKNNNNNTKISWAWWHEPVIPA\ MGEAEAGESLEP\GRRRLQ
1375	6872	A	1477	1	354	
1376	6873	A	1478	1	411	
1377	6874	A	1479	2	265	RMYGKIIFVLLLSGIRNVHPK*IVSIS ASSTTGVMHTSTSSSVTKSYISSQT NGITLINWWAMARVIFEVMLVVV GMILISYCIR
1378	6875	A	1480	111	520	
1379	6876	A	1481	106	395	EEALPPLHCTWVPFSPFECLQEMS KEIVSISALSTTEVAMHTSTSSSVTK SYIS\QTNGRKRDNLSDRFHCTSSC SDNTSLFLCVMGWYYWERSS
1380	6877	A	1483	3	1078	TRAAGLRAGVRVPRSPGSRMPA RSGAQFCRRMGQKKQRPARGQP HSSSDAAQAPAEQPHSSS\NPAQAP CPRERCL\GPPTTPGPYR\SIYFSSPK GHLTRLGV\EFFDQPAVPLARAF LG QVLVRRLPN\GTELRGPHRWETEA/ YTLGPED\EAAPLQGGWPGKTPR\N RGMFH*KPGD/LWVVYIYGYMYFC MNISSQGDGA\CVFL\RALEAPGKS WRPMPQLRS\TLR\KGTRQARVLKG PPKLCSP\SKLACQA\LPINKSF*PEG TLAQDEAVWLERGPLEPSEPAVVG S/APRVGVGHAGEWARK\PLRFYV\ RGSPWASVVDRVAEQDTQACAKG LPRQDFLHCLKTRINVLFEKKKKK
1381	6878	A	1484	3	452	
1382	6879	A	1485	26	493	NSTDERTHPWLLSPARQRPTSRPA WGKVGHAHVRSMCAEALERMFLS FPT\TKTYFPHFDL\SHGFPCG*RATG KKVDDSDAQTPWPTWDDMPKRRC PP*SDLHAHKLS/RLDPVNFKAPKA TCLAG*PLAAHLPAEFQPLAVARLP WGQISWGFC
1383	6880	C	1486	30	200	MCISYTKGHFVVVWVVPFGFSKILF RYISCPAPCRSSRMQSQCAHSSQSE VPGHRA*
1384	6881	A	1487	31	664	APALPGCEHMMMAIRELKVCLLGD TVGKSSIVWRFVQDHFHDNISPTIG\ ASFMTKTVPCGNELHKFLIWDTAG QERFHS LAPMYRGSAAAIVYDF TEAGFHFHPLKKWV\KRLKELGPE\ NIVMAIAGNKCDLSD\REVPPGML KEYAESIGAIVVETSAKNAY*YRKS SFKEISRDPHPWTPHENGNGTIKS *EANPCKPVRRC
1385	6882	A	1488	124	1180	DLGKPLFKVQEEGGRPPTLNQSEVV ALCPQGPANHDARSLIMDSPRAG THQPLDAKTEVGADRCTSTAYQE QRPOVEQDGKQAPLSPGLPAMGGP GPGPKDPAGCGGAGA\GGSEPLVT VTVQCAFTVALRARRGADLSSLRA

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						LLGQAFPHQ\AQLGQLSYLAPGEDG HWVPIPEEESLQRAWQDAACPRG LQLQCRGAGGRPVLYQVVAPPPK RGTPKPKRALDPFPPSPPPPKGPE DLGFRQGD TVDVLCE\VGWAWPFP GSTVVPGVWGA*SSACAVSRRGTQ KATPG*RPAEPDVPLAVDQAWLEG HCDGRIGIFPKCFVVPAGPRMSGAP GRLPRSQQGDQP
1386	6883	A	1489	1	229	
1387	6884	A	1490	3	461	AASTRFRASGQFVMAGAGSAAVSG AGTPV\AGPTGRDLFAEGLLEFLRP AVQQLDSHGHA VRESQVELRDQID NLATELCRJN*GQKVAL\DLDPYVK KA\ILNARRRV\VLVNNILQ\NAQE\R LRRVNHR\VAREQPARRAMLDSGIY PPGSPGK
1388	6885	A	1491	1274	1416	FGIFSQFSVLH*SGK*A*N\YYYYYY YYYCYFYKMEYGSFFNLQVTF
1389	6886	A	1492	243	1125	FQQRLYRAARRFTMVKIAFNTPTA VQKEEARQDV EALLSRTVRTQILT G\KELRVCHPGKKEGSSGEMLWFTL FRAFQFILG\GLYLFGGACIYK/YTF MPKRHHFTVGEMCFFDSED PANFPF GGGEP*LSCLVT*/EEADIREDDNIAI IDVPVPSFS\SDSPAANYFMTFEKG MTA\YL\DLLG\NC\YLMPLQYFYL LWPPKKIWVELFGQTGRVGRYLP\ QTYVVR\EDLVA VSRKIRDVSNLGIF IYQLCN\NRKSFRLRRRDLLGFNK RAIDKCWKIRHFPNEFIVETKICQE
1390	6887	B	1493	28	282	MYHDWRLVPKHEEEAFTAFTPAPE DSLASVPYPPLLRAMIAERQKNGD TSTEPM LN VQRIRMEPWDYPAKQ EDKGRAKGPV*
1391	6888	A	1494	2	187	QNDRKMETQA/PEEPMLNVQRIRM EPWDYPAKQEDKGRAKGTPTPTPR AHAGESGKRSLPFPH
1392	6889	A	1495	302	771	RKRGVCTHLLCRRRSASNCRAPALP SLTFEGQDAPGLPVVQVLRVVG HPREAPVARLVVLPQPLARDQAA QAEEREAAEQLO/AGGSRGARRPRP GPAAGVQRTAASRSRSPRRAGSRA ACSVAPAGRARGGPAPRSAADAPS SAPWRVRVLSG
1393	6890	A	1496	497	1212	SWPGGEAGTARRPGCLPAPA*TR*R PPRAWAPAASHGT*RVRSPAPRSQ SSLMKKKRR\FEGQDAPGLPVVQV VQSHKQAGSARKALGPRGQEVGAS /DHANLQGGGEAGRPAGCRVGVRT GCTHLLRVVGHPPREAPVARLVVL PQPLARDQAAQAEEREASEQLQQ SGSRGARRPRPGPAAGVQRTAASRS RSPRRSGSRAACSVAPAGRARGGP APRSAADAPSSAPWRVRVLS
1394	6891	A	1497	852	1562	FGKAGWELNRRERGSWRVEEKDL QRWGVCGGLCLPKPVRRSGVCLS

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						LKHISGGLRTLSQAPNWRNNSNGR VRGKHSNLNAQPFHPSLSYELKPCC VSQGLQRGILPPPQVSGPTFCSPKAL TPPSVRVLPPPPPP*CASVCMVNSP PALPTPLAKVSPADLAPRD*AHISG* RG*PLGHPHLSPLMLFTSPEPSE/PPP YPPSAP\SSSFSPARPAPTVPWPPPM QHRLWLPFPSS
1395	6892	C	1498	127	355	MKNRILQRNGXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXX*
1396	6893	A	1499	529	2082	FLDLLHFTTSLIIPHYKRIRDLTYTIR HFPFVHLSPKCLDRPLSLFIHLGV/ VIL*ALEPIH*SSSFLFH*LKIFSSPLW NI*VSPTFDSHF/CFLILNLFLLSFPL SALI/NFQLQF*IKNETFHTLLIG*SEH *I/HT*MISTLFWLKF/LLLTGSLV*A RIFSCVHTQYHHACAIEKEMYLSSL FLFMNNSKSLILFCSIIGPEFFDILL IC/LFFFLD*IIFSSIPALQ*YYLWALN AHSSQKARDSMLS/F*/ILVCWIAVT LG*DTLLAVTLE*DILSKVHCFMDPI SSSFLVFNPHFGWENFPQRYFPQVR VQRRLS*KFA*QEKCPPLWMFLPEQ SALTMKFLGYQKISLKALKDVPDID FWAFSVG**QIC*QSISHPFLC*ANR DDLICFLPGHFNIFLLSLIFQNFTILC LDVRLYWALSIWRLSL/RLFFN/IFFF LFLHLTSLASLPGTPNITY*MTMSL FFLY\FYYLSLFALYLGEIPSTLFFQT VYQILLAVLFYFQRDLPSYSSLSFP
1397	6894	A	1500	3	930	SSRGRAGGVWRFERDEDGTGAGCG QWTRFCREPKMAVNVYSTSVTSDN LSRHDMLA\WINESLQLNLTKIEQL CSGAAYCQFMDMLFPGSIALKKVK FQAKLEHAEYIQNFKILQAGFK\RMG VDKIIPVDKLLKGK\FQDNFEFVQW VKKFFDANYDGKDYDPVA\ARIQG QETA\AVPSLVAPALNPKPKPLTSSS AAPQR\PISTQRTA\AAPKAG/PLGV VRKNPGVGNGDDEAAELMQQGQR I*NLFFEDLGGKERDFYFGKLRNIEL ICQENEGENDPVLQRIVDILYATDE GFVILDEGGPQEEQEY
1398	6895	A	1501	3	87	
1399	6896	A	1502	1	667	RRSSARRGGRSEPGRAAGGGAAED TRRRAGMDRGEQGLRTDPVPEE GEDVAATISATETLSEEEQEELRREL \AKVEEIQTLASVKQQRKHLA EIQAGNLGINSLQELKQNIAGGW*D VTVT\SAYKKT\SETLS\QAGQKA\SA AFSSVGSVITKKLEDVKNFPNFLNH FEEKVENLKS\VRGH/TKPAGGDF GEVLNSAANASATTTEPLPEKTQES L
1400	6897	A	1503	1	395	AKAKMADVLDLHEAGGEDFAMDE DGDESIHKLKEKAKKRKGRGFG/SR



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						*VWGKWGRVA**GRSYGFWSPHPP HRNNGRKEEFSVISCMSLIEEGSRA RMREDYDSVEHDGDEPGPQRSVEG WILFVTGVHEEA
1401	6898	A	1504	146	833	CLSGTDEISIEGEMADVLDLHEAGG EDFAMDEDGDESIHKLKEKAKKRK GRGFGSEEGSRARMREDYDSVEQD GDEPGPQRSVEGWILFVTGSP*RKP PEEDIHDKFARIMGEIKNISSSTFDR RTG/YILKGYTSLNIETYKEAQA MEGLNG\QDLMGQLGGVDWCFVR GPPK\GKRRGGRRRSR\SPDRRPSLT GPLLSRCSLQDSIWTMAALGQIGLG WELCCVYI
1402	6899	A	1505	717	1563	APLPAVLTQTIHLVTGTAFHSGKVD IVTIGYPFIDLNDMVCMSQYDSTHG *FHSTVKTEGKLVINGNCITHHPR RDPTKIK*DDAGTEYVVESTGVFMT MEKAEAHAPSADG\LNDKEYENSL KIIGNASCATKGFAP/LPAKVIHDNF GIVEGLMAMVHAITATQKTVDGPS KK\WHDSHGALQNIIPASTGATK/A GMAFLVSTTNVLVMDLTLEGILGY TEHQVVASDFNSITHSSTFKAGVGI ALNNHFVKLISWYENEFGYSNRVV DLMVHMASKGSS
1403	6900	A	1506	625	2919	
1404	6901	A	1507	2	76	HHYAKLGTRAVRRARRCAGWQSY VDNLMCDGCCQEAIAIGYCDAY VWAATAGGV\FQSITPIEIDMIVGKD VRKGF\FTSGLTLGA\KKCSVIRDSLY VDGDCTMDIRDKQS/QGGEPTYNV A\VGRSGRALV\VMGKGKVFHRR HTLTRKAYETPLYT*RQAWHEGSA KGSKMCLAEALRG
1405	6902	A	1509	63	290	GGILLSISRPYKTKPTHGIGKYKHLI KAEEPKKKKGKVAVRAINLGTDY NYGVLNIHLTAYDMTLAESYAQY VHN
1406	6903	A	1510	315	1092	RPRSSKRMSGTSEKVLCLRNNTIFK QAFSLRFRSAGEKPIYSVGILLSIS RPYKSK\PTHGIGKYKHLIKAEEP KKGKVEVRAINLGTDYEYGVNLN HLTAYDMTLAESYAPLSTTFCNLS SH*KSEESYAMPTQNHKKWLPVCR DQGQPKCLGLKCLPHERV\VQIS GLSATFARKFSWKIPKPVLP*RESG LFS*REHTERKTSRGRFQRFDP ELGRTFWAKFEVATVDPFHCQQWSYLSA KEKSLLGS
1407	6904	A	1511	284	758	KQNPSSPLQRLIAGSNLDSEPIRIQTD ILKQATKDRVSDFHKLKQSRFFDEN ESPVD PQHGSKLADYNGDDGNVGE YEADKQAEALAYNEEEDGDGGEEDV PPDEEREL/PNGKKQAMESNISMMS FKS*RNAENLKCCCKMKSFYFVLS D FCKDELYQL
1408	6905	A	1512	148	476	

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1409	6906	A	1513	204	620	GDAMAAVTPRPPLPEGCRAPSSAPT VSLPELRSLLASGRARLFDVRSREE AAAGTIPGALNIPVSELESALQMDQ LAFQGFIFLLEKPKLGR*ASSFSFLFR WGKRGLQATQLARSLGYTGGFATY AGAY*\EWLEKES
1410	6907	A	1514	1386	1711	FPKSIMGLVTIQDMNLCIKFIGLSHL PALVLLYC/DVRACVMSGC/LRKTS EKNLKSRRPSFFACSILSRNVQCQNW KIGMFKDI*GFFCFPYFYLFVSCIFA YLCRFSGF
1411	6908	A	1515	481	1380	TSKQNAAPLVKYFQEKGLIMTFDA DRDEDEVFYDISMAVDNKLFPNKE AAAGSSDLDPMSILDTEIIDTGSDY EDQGDDQLNVFGEDTMGGFMEDL RKCKIIFIGPGSGKGTQCEKLVEK YGFTHLSTGELLREELAS*SERSKLI KDIMERGDLVPSGIVLELLKEAMVG \SLGDTRGFLID\GYPREVKQGEF\ GRRWRPHSWVICME\CSADTMTN RL\LRSSRLPVD\DTTK\TMAKRLE AYYR\ASIPVIAYYETKTQLHKINAE GTPEDVFLQLCTS*LTLFSEGKNA CLG
1412	6909	A	1516	47	416	NSYIYMCISYINTIYIHIYLESNLSL LNIYISTPT/HIY*RHTV*VHTKAYV HML*HVYIHFCLCVHKSFKGTIYRD ASFLESCSKVNTECHKLRKVVKRYS RIHHTGIHQSSLIITSPFTF
1413	6910	A	1520	1386	1666	SLMAPQKMGRITSCSPSERLGN*GPE TGSDSHKTPQQGCKGGRTRGSIVSL GDRRPLAP/GACFAGDKDFLGLRSP GVGTALLGCTSIQRLWA
1414	6911	A	1521	304	1253	VTNEMSQGVGKYDFYIGLGLAMSS SIFIGGSFILKKGLRLARKGSMRA GQGGHAYLKEWLWWAGLLSMGA GEVANFAA\YAFAPANSSGLHLGAL \SVLVKCPFFLSYFLNERLNLHGKIG CLLSILGSIVMVIHAPKEEIEITLNE MSHKLGDPGFVVFATLVVIVALILIF VVGPRHGQTNILVYITICSVIGAFSV SCVKGLGIAIKELFEGSLCCGIPWA WILLLSLIVCVSTQINYNRAL\DIFN TSIVTPIYYVFFTTSVLTCSAILFKGV GKDMPVGRCPVL*SGFFTHVGGY SCCMPLKTSALA
1415	6912	A	1522	20	131	KEILPKQAFAVAPTYITEPVEIKFFFF SRIRL*VPPG
1416	6913	C	1523	7	348	MSKLYIMQFXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX TV*
1417	6914	A	1524	1103	1388	VLLIFNLFPMALYFVCFSF/CFFETEA HSVT*ARVQWHDLGSLQPLPP*FK* FSCFSLPCS*YYRHLPYPANFCIFSR DGVSPCCPGWS*TPNLR

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1418	6915	A	1525	149	421	
1419	6916	A	1526	1	1107	
1420	6917	A	1527	25	1486	GPQQPHSRSTHASGRPQSLSPVLSLS PDSMSFTTRSTFSTNYRSLGSVQAPS YGARPVSSAASVYAGAGGSGSRISA SRSTSFRGGMGSGGLATGVVAGG/L AGMGGIQNEKETMQSLNDRLASYL DRVRSLETENRRLAESKIREVHLEKK GPQVVDWWSHYFKINEDLARAQIFA NTCGTMPRIRSARIDNARLA\ADDF RVKYEDRSWPMCPVLWRTDIHGLP KVH/IDDTNYHTDLQLETEEALKE ELLFQ*RRNHEEGS*KALRRQ\SSS GMNAWRLD\APKSQDLAK\IMADIR \AQ\YDELGSKKNPRGSLDKY\WSQ Q\NEESTTGGSPQKSAEVG\AVETHA HRSCLKRTVPVLGRSTLDSMARNLKG QLWRTSLREG*RPAYALTRLEPAPT GSL\HLESELAQTRARGTAARPRE YEALLNIK\VKLEAEIATYRRLLED GEDFNLDALDSSNSMQTIQKTTTR RIVDGKVVSETNDTKVLRH
1421	6918	A	1530	277	693	PWHCPDSHYSQQPGSTASSSVPART GGPCWSSSCSPN*CCTSCCSTTPTPT LDPR/GSRHCQLPWLKQLPKGM/CT STCLHGSCGCICGSCGPGCIDGPTL GRNHNEPHHHSHGDLPYRFPPEHAH HGHA\TMGLMDTPLV
1422	6919	A	1531	1	364	PFVSLGLMCFGALIGLCACICRSLYP TIATGILHLLADTML*SPGHMEVSC VDAPAEIPS*APN*QPTSFPAMCGSH PGCPALTS\QRTSATAILLHPCETLI KNQLAEPNQPMELIEIK
1423	6920	A	1532	1	898	RGESRVLWSELEGEAGGAGGWASS LNARMDNRFATAFVIACVLSLISTIY MEG\SIGTDFWYEURSPQENSSDL NKSIWDEFISDEADDATYN\DALF\R YNGTVGFLRRVYSPYPKTLHWVLA HHERTESFDVVTK\CVSFTLATEQFM EKF\VDPGK/HTNSRGLDLLRTYL\W RCQFLLPFVSLGFDVLWGALIGLC A\CICRSLYPTIATGILHLLAGLCTLG SVSCYVAGIELLHQKLELPD\NVSGE FG\WSFCLACVSAP*QF/LWASALFI WAAHTNRKE\YTLMK\AYRVGMSK KPACF
1424	6921	A	1533	939	1591	LQSLCRVLLQMESGSRDTIPGVCKR ERENREDTEVLQPRFPYQGGQLVG KAATPQPF*STVGWTLQPQ*P*YP AGQGCPP\RCPPAPSS*GSKRPPEPQ QGR\GPKPGSPQA*GNASPPKCPA PVPTPC\PTLCTGEKTGGARAGPW VGAGSPW*DPR*DGPIPCVGDPLSP HPCCVIVALLPFNVSVPGGRGGAPP QPP*T*PKAMAVAPPFV
1425	6922	A	1534	34	912	GRIRMQRQSTTGGRGIMEGPRGWL VLSVLAISLASMVTE\DLCRAPDGKK GEAGRPGRRGRPGLKGEQGEPGAP

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						GIRTGIQGL\KGDQGEPPGSPGNPGK VGYPGSPGLGARGIPGIKGTKGSP GNIK\DQPRPAFSAIR\RNPPMGG\NV V\FDTV\ITNQEEP\VDPSG\RLVCP EPGYYYFT\FQGAGPQWEICLSIVSL LQGARVRRSPGAF\*HPPTRGFLFQV VSGGMGL\QLQQGDQ\WVEKKPP QKGSHFYQGSE\ADSVFTGFL\IFPIC LSQGRTPSPPTSLASMLRL
1426	6923	A	1535	919	1260	YSVSEFRGQTLTAKFCFFERESHV PRLECRGTILAHCNLCPLGSSDSPAS ASRVAG\TTGACHNARLIFVFLVET GFHHVVQAGLNS*PQVIHPPCPPKV LGLQACTWHLAH
1427	6924	C	1536	130	441	MVQNKQQLPANSQRGTEAXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXD*
1428	6925	C	1537	5	316	MVQNKQQLPANSQRGTEAXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXD*
1429	6926	C	1538	74	91	MTLAM*
1430	6927	A	1539	368	430	
1431	6928	C	1540	191	592	MGQQPGQARAPSYCRCPLSPGSGR ALRWERPGGGQGPKEIVLSGCVPE KGPQTPAQPHSLRHLQNPPEATARTG EEATSAAGGPWASPSFGGTQLCSDT MPALLGARSTCWIATHVCTLPLS ECGPINILLE*
1432	6929	A	1541	58	1531	VIAVTSALPGRTOAAWTRVVKMDL LAAKMAVGGGSLMTDLTSSISKPL VPVGNKPLIWYPLNLLERVGFEEVI VVTTRDVQKALCAEFKMKMKPDIV CISDDADMGTADSLRYIYPKTKTD VLVLSCDLITDVALHEVVDLFRAYD ASLAMLMRKGQDSIEPVPGQGKK KAVEQRDFIGVDSTGKRLLFMANE ADLDEELVIKGSILQKHPRIRFHTGL VDAHLYCLKKYIVDFLMENG\ITSI RSEL\IPYL\RGKQFSSASSQGTRK EKEGGSKGKRGLKSFRISYSFY*KE ANYTGTGAPY\DAC*NACRGDRWE DLRSQVRCYVHIMKEGLCSRSTL GLYMEANRQ\VPKFLSALCPGRTHQ SISSSPDCQHYTWVGVD\SLIGPRDH RLGEKVIPLSASVIGSSL\CLIKDRVT IT\NCL\LMNSVTFWRKEANIQGSVI L\NNAVIEKGADIK\DCLIKWARRI EA\KAKRSVCR*S*GNDQLMEI
1433	6930	A	1542	315	644	EEETPKDQCLGAHFSSDTFPRQSRL LGVHGRGAGSLCTGLLSEHCPSTPP SGSPRVTYLPH\PLPPSP\SWAFTP PAHR*KPSTEPFPGPSTQVV*PLPMF TTKGAPP

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1434	6931	A	1545	1	364	FFFFF*DGVSLWPRLERNGVISAHC NLCLPASNDSPASASLVAGITSAC/R PLPPKQK*LFFFLRWSLALSPGWSA VARSWLNATSPGYF**KQGFHHAG QDGLGLLIHPPWPPEVLGLQA
1435	6932	A	1546	1	391	
1436	6933	A	1547	2	2371	GPPGRARARGLRRAPAAFLRRSLSL PAAFSSAAGPSSPQRSQEGRRPRT RSSRGSRGSRPRRLRLRRGRSAIH GEGRTAKGSAAWSARTFRSPPGVG RDPMRRAHEGREIPSLGGARRREVL QAGRSQRAAGRRRRRQELEGVGS GRPGGPPPGPGRRGTCAAALPPEWP RRRTGLPRRGPRPLAMAKWLNKY FSLGNSKTKSPQPAPRPDYREQRRR GERPSQPPQAVP\QASSAASASC ATASCFSASSGSLPDDSGSTSDLIRA YRAQKERHFQDPYNGPGSSLRKLR AMCRLDYCGGSGEPGGVQRAFSAS SASGAAGCCASSGAGAAASSSSSS GSPHLRSSSERRPATPAEVRYISPK HRLIKVESAAAGGAGDPLGGACAG GRTWSPTACGG*KLLNKCSSSSAEE SGAGMKDKVTIADDYLDPFDAKND LKSISGKGESAGYMEPYEEQRIMTE Y*RQECVRSQH*GIQLYETP*EPEGQ NFESESESTVNPRMRENKLPQDYEQ /RPAD*YDQPLELNPV/TQFPALAA QFNGNEKPQSSPSR\DRRRQLARA PGGGF\KPIKHGSPEFCGILGERVDP AVPL\EKQIWYHGAISRGAEN/LCL RLCKECSYLVNSQTSKHDYPLSLR SNQGFMHMKLAKTKEYVLGQKS PP\FDSVPEVIHYTT\RKLP\IKGAE HLSLLYPVAVRTLLSGPDSALLCDR AWRLARCQRPTNQPATVAGCVV CVVCMVLAHHCMSLECCCHLRGLE KAWIKTEGRQHTTSPNPNEALEFL
1437	6934	A	1548	304	678	PQVILPPLVSQGCWELPDVSPLRPSL VW*FL/RK*KLDLPCDPAIPLLGVP RKIKACFHTKTCIQIFIATLFGIAKKK GKQPKQPSAGEWINTWW/HIHTMK HCSAVKKEQTETISLFRSRIWRI
1438	6935	A	1549	80	623	LGGVTRGFNMRIKCYFCSGPIYPG HGMMFVRNDCKVFRFCKSKCHKN FKKKRNP\RKVRWTKAFRKAAGKE LTVDNSFEFEKRRK*TYSNYQRDLL GIKT\IDAMKRVEEIKQKPPS*IYNEQ IE/GKIKSYRKFDIKRSPSQNIPSL RAPPCQAKGKQLGEEMGTARLQGG CGHGKMPP
1439	6936	A	1550	1021	1544	EPTKKCCVYYAQFLSLPSLFFPTGSE EQDSIYFILFFEMEFRS\VTQAGVQW CDLGSLOPPPGFKRFSCSLSPSSWD NRLLPQGPANFCIFSR/GWGFHRVG QAGLFSRDGVSPS*SGWSRTPDLVI RPPWPPRVLECSGQYIIFPWLFSRFS LSIFSKFDCNLSQGF\WICLFYSS

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1440	6937	A	1551	2	210	
1441	6938	A	1552	2	310	IGVKMEEYAREPCPWRIVDDCGGA FTMGTIAGGGIFQAIKGFRNSPVGVN HRLRGS�TAIKTRAPQLGGSFAVW GGLFSMIDCSMVQVRGKEDPW\NSI TSGCLNGEPYWQARNGTQWPMVG VSPQWVGIFPSF*FEGSWYLCCLTRF ASGTVFPMGP\QFA\EDPSPVCLSTQ LPSL\PFGGGIFQAIKGFRNSPVGVN HRLRGS�TAIKTRAPQLGGSFAVW GGLFSMIDCSMVQVRGKEDPWELH HKWVP
1442	6939	A	1553	1	4629	
1443	6940	A	1554	96	721	PGQLSSLTPPRPASLLPWRAAYLFLA LFLPAGLLAQGGYDLDPFPFDHG QYTHYMDQIDNPDDYDYQEGTPR\ PSEQQFQ\QSQQEVQQGVIPSPNPR AQGNAEL\EPTEPGPLDCREEQYPC\ TRL\YSIHRPCK\QCLNEVC FYSLRR VYVINKEICV\RTVC\AHEELLRA\D LCSGTSFSKCGR*WASSGL\QCSV\A ASCA\RSCGSF
1444	6941	A	1555	262	732	FQNKGNFFSTKRTEVSPSTQFNIFA RKNTTLIRISHSSLGQVRIRLVWFG LVWFWFLETGV\CTLVIRGWEFQW\ CDQNSLQP*TPGLQRIFPTSASQSTG ITGVSHHSLVRYVFTVTEIQLKFWILI TKITVLLVYN*L*NKGY*YIFITFFL NLQN
1445	6942	A	1556	162	496	HSYIHIVHVCNFFMYSFAVFVFKKH LLLCLYNRTVIIYNNLGKL*INS*FK QPVYMH*VLYC\INLCFTYMVKAA RILLICNYTHKIYICMIHEIYLEMFII LMDILWCE
1446	6943	A	1557	2	247	GEIVVFKVEGRDIPVHRVIKVHEKD NGDIKFLTKGDNNEVDDRGLYKEG QNWLEKKDVVGRAR/GYALLAVM GAYVLLKRES
1447	6944	A	1558	1	503	VRAGAVGAHLPASGLDIFGDLKKM NKRQLYYQVLTAMIVSSALMIWK GLIVLTGSESPIVVLSGSMEPAFHR GDLLFLT NFREDPIRA/GDNGDIKFL TKGDNNEVDDRGLSKEGQNWLEK KD\VVGRARGFLPYVGMVTIIMND YPKFKYALLAVMGAYVLLKRES
1448	6945	A	1559	180	257	
1449	6946	A	1560	2	676	FVRCSAAVCATQSRRAARSPENPA MVRAGPPWGLNLPASRLGISSADL KKMNKRQLYYQSFKPSPWIVSSAL MIWKGLIVLTGSESPIVVLSGSME PAFHRGDL\FLT NFREDPIRAGEIV VFKV*RPRTFPISQR*SKVHEKD\N GDIKFLDLKGDN*SLMD*EALYK KARNWLEKKDVVGRARGFLPYVG MVTIKMNDYPKFKYALLAVMGA\ YVFLKR
1450	6947	C	1561	449	820	MVIXGQISPMTATSGQKAFLAGPLG

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						SLGTLPRSQAVKRRLLLKLTKDRIF RDVLLLMLFKGHRETHGQCLQRQQ TKESTSIVVLALCGLYGKQVVTLLN VGIPFSINVYFTTPKSPLIMKLI*
1451	6948	A	1562	251	473	
1452	6949	A	1563	22	212	
1453	6950	A	1564	160	397	
1454	6951	A	1565	17	262	LFWAKALNRHFSKKHIQMANQH MKRCSTSSAIREIQVKIAMVYN*YTI *HSQYSLQLPFPLWKTWVKFLTIV KLLNCSVK
1455	6952	A	1566	2	294	GNKMAAPKGSWVVRTQLGLPPLLL LTMALAGGSGTASAEAFDSVLGDT ASCHRAQLTYPLHTYPKVGPRVS GLRPFPCSPFLGSPHVCRLWQPGC
1456	6953	A	1567	366	1412	QRGTRWRRERGSWVVRTQLGLPPL LLTMALAGGSGTASAEAFDSVLG DTASCHRAQLTYPLHTYPKEEL YACQRCRLFSICQFVDD\GIDLTRT KLECESACTEAYSQSDEQYALPFL GCQNSACHFAELRQEQLYVPRWP KMAPTFFL*LLGEGSFWELT*WDSA QSFITSSWTFYLQA\DDGKIVIFPV* SQKSQYAPHFGAREPTNFEENHLLS KMSSDLQMGKFHQAHQGIFLKNEE RDGLFKKPSILNSGWILTTVLVLSV MVLLWICCATVATAVEQYVPSGE AGVTMGDLEFMNEQKLNRYPASF SCGLVRSKTE\DH EEA GPSYLPKVN LAPFLEI
1457	6954	B	1568	76	384	MSGWGVLSGRLNPAAREKDVERFF KGYGRIRDIDLKRGFGFVEFEDPRD ADDAVYELDGKELCSERV TIEHAR ARSRGGRGRGRYSDRFSSRRPRND RRNAPP*
1458	6955	A	1569	3	229	
1459	6956	A	1570	152	536	PDIMSGCRVFIGRLNPAAREKDVER FFKGYGRIRDIDLKRGFGFVEFEDP K\ADDAVYELDGKELCSERV TIEH ARARSRGGRGRGRYSDRFSSRRPR NDRRNAPPVRTENRLIVENLSSRVS WQVC
1460	6957	A	1571	771	1383	ILIEYKCGKCHVCTLSNIFSFSSLVFF ISCDCLCVFPPLCLTQLSCVKDLK DFMRPAGE\VTFA\DAHRPKILNEGV VEFASYGDLKNAIEK\SEKEINGRK IKLIEGSKRHSRHSRHSRHSRHSR RSRHSRHSRHSRHSRHSRHSRHSR DVPVLLSRSPRA*EPRNRGSSSRSK SPASVDRQSRHSRHSRHSRSDSGN
1461	6958	A	1572	236	1377	PDIMSGCRVFIGRLNPAAREKDVER FFKGYGRIRDIDLKRGFGFVEFEDPR DADDAVYELDGKELCSERV TIEHA RARSRGGRGRGRYSDRFSSRRPRN DR/RVCEGWMAALNNYW*G*PFKI QESLAVMILGPAV*SVLLFPR*PIVL DESI*VIEKSIDGSH*NGL*YLMA*

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						TCPQLNTSAVIAFLPL*IRIFFLRNAP PVRTENRLIVENLSSRVSWQDLKDF MRQAGEVTFADHRPKLNEGVEF ASYGDLKNAIEKLSGKEINGRKIKLI EGSKRHRSSRSRSTRSSSRSSRS RSRSRKSYSRSTRSSRSRKSRSV SRSSPCPEKS\QKRGSS\SR\SKSPSHL WNRPEVPGPRSSRSQIQLDQWPIKPV K
1462	6959	A	1573	568	770	PDIMSGCRVFIGRLNPAAREKDVER FFKGYGRIRDIDLKRGFGFVEFEDPR DADDAVYELDGKELCS\ERV TIEHA RARFTRLGRGRGRYSDRFNNSAEL RNDRRNAPPVR\ENRLIVENLSSRV SWQDLKDFMRQAGEVTLPTDTRL NL\NEGVVEFASMGDLRNAIEKLSG RELNGRKIKLIERPAKRPO*VQQSRS SDPGTQKSPGPRSSRSPVAVANLN SRSKK/RRGSREPGSPEPSRSC*VGS SPVP*ERFFKGYGRIRDIDLKRGFGF VEFEDPRDADDAVYELDGKELCS
1463	6960	A	1574	22	202	TKSSS*CDSVATCGHIFSCPHNLSKI HDSISPRVC\SICKPHGSIHKLCKIKIF HIFAR
1464	6961	A	1575	1	1878	MQYSHHCEHLLERLNKQREAGFLC DCTIVIGEFQKAHRNVLASFSEYFG AIYRSTSENNVFLDQSQVKADGFQK LLEFIYTGTNLDSWNVKEIHQAAD YLKVEEVVTKCKIKMEDFAFIANPS STEISSITGNIELNQQTCLLTRDYN NREKSEVSTDLIQANPKQALAKKS SQTKKKKKAFNSPKTGQNKTVQYP SDILENASVELFLDANKLPTPVVEQ VAQINDNSELELTAVVENTFPAQDI VHTVTVKRKRKGSQPNCALKEHSM SNIASVKSPYEAENSGEELDQRYSK AKPMCNTCGKVFSEASSLRHMRI HKGVPKYVCHLCGKAF\TQCNOLE NACKELHTGEKPYKCGICVIKGAQ KC\QLVFHSRMHGEEKPYKCDVC NLQFATSSNLKIHARKHSGEKPYVC DRCG\QRFQAQASTLT\Y\HVR\YHW EEKPYV\CDTCG\KAFVLLVLFHS FLRK\HTGEKPYICGICGKSFSSGEL NKHFRSHTGERPFICELCGNSYADI KNLKKHKTKV\HS\GADKTPRTPSA\ EDPNLGVKQDP\IQKSPFNPETYGCE SPS*YELYPALPLGTED\HHMLLPV TDTQSPTSDTLLRSTVNGYSEPLIF LQQLY
1465	6962	A	1576	42	134	
1466	6963	A	1577	154	768	HVACGLLWYVSPSAHLNLDGTITT K/ENLGTVNEILLGSPTEAELQDMI NEVMSDNGGTIDF\PEFLTMMARK MK\DTDSE/EKEIRRKHSRVFGLRVG NGLYLACRNFHVM\TNLGRKF NQIEEV*WN*SRGSQILDG*WSKLT YEEFVQMMTAKVRPLSRNVNLFLV



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						QNCFICLFLWFVTLSCCKVFSPTCQ KKNMHVIGN
1467	6964	A	1578	3	202	RRMVSAFSCRCMPSEPCIAVTAPCM MAGQAPAERTAQ*PLYF/CTLFQGS LSPT*REVGWPLGPAGM
1468	6965	A	1579	133	378	
1469	6966	A	1580	891	1744	DMFPITPSRSVLPSFLLTYLPRQSL/N SVAQAGVHWC DLSSLQPPPGFKQ FSCLSLPSTW*LGLQACTTVP*FFV VVVCIFFFFLVETGF/TLGWARLVLN L*LQ/CDPPTWASQSAG/ITDVSHHA QPILRFKCLS*CIRSFNEGRIKGTRO NKVELSL/CFLRQESHVSTQAGVQW CNLSSLQPLPPGFKQFSLTG/LPKC WDYRSKRPRPANQTSILGC*RKDPY *LHWAKKATEDIKLESCRLTPGKAR PTANFLRQGQFFWGPILGGLGPQE GFPFLFFKGF
1470	6967	A	1581	2119	2436	TTRYLKKTSTTGQRKKRGRNGSF PTENLVPSGTVTGSQQLGPPFR*N/H TEECWGPPTADGRAGKGPRQPGR AQRIYRWDPSDGTTWHHHRPCGSR GTDQPETK
1471	6968	A	1582	208	296	
1472	6969	A	1583	185	947	SHCSSGMEIPVDQLPSLPRAALVAQ NYINYQQGTPHRVFEVQKVKQSQA WKDI\PGKEGHKYS/HLKFAV*KKL YKKQVKG*TCTA\EVLLPFQRGQET LHQEVNFHILKEKLGKNPD\EEDNT FYQRLKSMKEPLQAQNI\PDNFGN VSQEMTLVLNLAWVACGLI**WQK FLLKTTWYK\MVKI\QTCQARCQRI DDF\ELDYPFFYFINIASQEII\WQM QVLWHPQYGTKVKHNSRLPKEVHL GYTPKPLTLEV
1473	6970	A	1584	5060	5662	ESQAAPPPRSTLHRPARATAITAC WSSQASGPQAVRRRLLTPLSSPAAR DLVSKEGFRRARHVVG EIRRTAQ AAALRRGDYRAFGRLMVESHRLR *GPLGAPLLPGTGRPRPTPSISLQ\D DYEVSCELDQLVEAALAVPGVYG SRMTGGGFGGCTVTLEASAAPHA MRHIQEHYGGTATFYLSQAADGAK VLCL
1474	6971	A	1585	2	987	LREGCPQR*RQPTQLDWPYF/CPFSP VC*KTKTKKPYPCAPKLGHVRCPT ASTLQAHTGPCPPSPQTGPQTRAGL LHICVGVGARFLFLLSLSPFGDIPL
1475	6972	A	1586	318	382	
1476	6973	B	1587	106	293	MAGRVCCLCQGSAGSGAIGPVEAAI RTKLEEALSPEVLELSFRGTEPPTTT PAGPRSAGRAGS*
1477	6974	A	1588	442	905	PMLSGRLVLGLVSMAGRVCCLCQGS AGSGAIGPVEAAIRTKLE\EALSPEV LELRNESGGHAVPAWAVRLHFRVG CW*ALVFEGLSPLTTDTGLFHAALA EELGRFRSHALA\IPGTDPPQWREN

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						\SQLEQLAPPCLG\GKQENFLGTPLE PPKRG
1478	6975	A	1589	1206	1335	KTQERYFNLKQN*TGQAWWLMH/WEAEAKGSLEPRSLRPAWAT
1479	6976	A	1590	136	837	PSEKTSFDRDKKKRAVRSILFLELQ NIIQDHDQGEKENESQIMKEENT GAGAEAKREEDMNPVKSSKKHKS EEHNDKEHSSDKGRERLNSSENGE/ AQAQTPRKEGH/RKGRGHSRSRSRE RRHRIRGRERKKSRSRSRERKKSR SRERKKSRSRSRERKRRRSRSRSR IQRHRA*D*KAGVGPRSRSDRKKR IEKPRRFSRKFKPDSQVHLPLEGRTQ PWDAQEAFS
1480	6977	A	1591	209	1545	PYYFLQANSPPGPLLTPALLPHRILS DVTQGLPHAHSACLEKLKRSYEFY RYFETQHQSV\QCLSKTQOKSREL NNVHTAVR/SLWQLHLKALLNEVII LEDELEKLGCTKETQELVSEAYPILE QKLK\LIQPHVQASNNCWEEAISQV DKLLRR\NTDKKG\KPEIAC*KPTCY SSTF*RQPTLHIADQDPIEEQE\LEA YVDDIDIDSAFQNRHDFYYLSQEDK ERQKREHEESKRVLQELKSVLGFK ASEAEQKW\KQLLFSG\HVLK\SL FPVGPQWEPISNSEPSMNSDMGKVS KNDTEESNKSATTDNEISRTEYLC ENSLEGKNKDNSSNEVFPQGAER MCYQCESEDEPQSKIGSLTTAPPT P\RD\SLQPSIKQRL\ARLQ\SPDFTT AGPCWQEVGCLDLLLPFTTMAGNR LFGDEEEEQIIEEN\KNEIEEK
1481	6978	A	1592	1	296	DFPLPTLLKTGPGPGF/YNGPP*GER FYVASPG*IWAPQGFF*KGPPSSSSS SSSQSKPLFPFCFANKTG*VGCFLVI SQRDQIPYPRPTPPTLPWLQ
1482	6979	C	1593	15	350	MLISLNINQTLLYCNKTENCXXXXX XXXXXXXXGGPFKRTPGGPKFNRG WQGIKIFPLKGGLLKPWWGIFXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXEKGEKQPEKPGG*
1483	6980	A	1594	11	129	APWLSVLY*SESPEAQPPYMMGPLE SP*AQRCPGLERGR
1484	6981	A	1595	2	660	NFPTARLFRLFYPLFPLKIFIPKAFN FCREVGPFCPPPK*GFFPKIPK*VFN RPP/SKGKSFTLPAPVKFGPPRGPFK RAPSSSSSSSPVV*APWPTVLY*SE SPEAQPPYMMGPLESP*APHEGVTA WVES*GPCPA*PWGRQAAPQPPPP QERAG*EPESKFGPGSK/PPERPVYA GNSPVLRSGLTSPSPSPAPPGGFKY MEERSKADLGPGMEKG
1485	6982	A	1597	1	680	ESRIRRRSSRRPREPPGPSRRRRRRR PDPRTMPSEKTFKQRTFEQRVEDV RL\REQHPTQIPR**LERSKGNNQPP \VLDK\TKFLVPDHVNMSELIR\IR RRLQLNANQAFFLLVNGHSMVS VSPHPISEVYE\SEKDEADGFLYMV

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						LCPPE/YGLR*TLNV*N*KKKNAAS S*NCLNPLPKEKICEYPTIDQFIPI TDHETSSVPTLGLVSCVCVSSRKT
1486	6983	A	1598	2	508	PDSSGPHRLRENPPMVAVSCPTKTN VKGPPGGKVGAGAHAG\EYGESEALE MFLSFPTTKTYFPHFDL\SHGLCPR LKGHG\KKVADALTNAVAHVDD MP\NGVVRP*SDLH\AHKL\RVDPVN FKLLSH\CLLVTLA\AHLPAEF\TPA VPRPPWDKFPWLSVKHRCCLTFKYR
1487	6984	A	1599	295	758	VLSRKCQRSLTAFSSKCPNSWFSITQ TECKTMTCGMPQHVTQQ*RPIINTS HQYSVKLGHP\DTL\NQGEFKELVR KDLQNFLKKENKNEKVIE\HIMRGP GTQNAQAELSRFIMLMGEA*PG AFPRRKIARGLTEGPHPNK*PGPG GGAPP
1488	6985	A	1600	411	1259	SQGTTSRGSWFPHSPEIEETSCLAE LFEKAAHLQGLIQVAKQGATLCT LYAKYKQVKVGNCTPKPSFFDFE GKQKWEA\WKALGDSSPH\QAMQE YIAVVIKLDPGW\ISSDIQRRNGKEA NTGFGGPVISSLYHEETIREEDKNIF DYCRGKQH*PYNQKPSNPKNVDVN VKDEEGRAPLHWGL*SEDIKELVH SVAANIELTLNCQD\NERPKQALHY ASACGVSGIL*ELAAPSLGADPDSR PGWLPARGGDRLQNSFFGAAAAHN WQGLIKRLENCSL
1489	6986	A	1601	177	409	FLQASGILKGFEPNLLNLVLTVTI*Y MRDPDDQYKLTGGHPGKLGVLVFR G\TSLVL\ICPDGMEAI\PNPFIQQQ DA
1490	6987	A	1602	1	165	PLKRSDGCDGRPTRPPTPTDTTVF TSNLKQTRMVHLTPVEKSAVTAL WGKVNVD\VGKALGRLLVVLVLP WDPKRSFQSPLGESVPTP*MVHLTP VERVCRYCPVGQGERG
1491	6988	A	1603	240	461	
1492	6989	A	1604	2	206	
1493	6990	A	1605	2940	3296	
1494	6991	A	1606	189	736	ENKISSVFKADFLPPAPCSLPGLEVS VSPKGKNTSGRESGFGWAIWMEGL VFSRLSPEYYELA\RPHLRDEEKS\CP C\LAQEGPQG\DLLTKTPELGP*ITR TC\LTIVQKT*RKMVDKP\TQRSVS NAATRVCRTRGRSRWRDVCNFM RYQSRVTQGLV\AG\ELAQQNLVST SRLCIPSTGPL
1495	6992	A	1607	3	452	
1496	6993	A	1608	3	485	PTLLVPTDSERTHPWLLSPADK\TN VKGPPGGKVGAGHAVRSMCAEAL RMFLSFPTTKTYFPHFDLSHG\SAQ V*GPRARKVADALTNAVAHVGR LPNALVPPLSDLHAHKL\RVGPGSTF KLLKATCLAGLTL\AAHLPARVQPL AVASLPWDKVSWSAC

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1497	6994	A	1612	77	636	QPQTDTMVHLTPVEKSAVTALWG\KVNLD\VGKALGRLL\VV\YPWD POKVL*NPLGESVPTP*MLVKWGP PKGEKAQWQKKKCSGAL*VNGPGL T/HGQPSKGTFGPH*SE\HCDKLH\ VDP\ENFRLPGQQCLVCVAGPITLG KEFTP\QLQACLFRKLVA\GVANAL GPTSNHLSLAFLAGPISN
1498	6995	C	1613	167	391	MNVFMCRLGTTFHLVLLPSVLPSL RKTVFLNPFSSIKQRFQRWKHWVFQ VASELTDAILSSCGHLFLPGSHNLS*
1499	6996	A	1614	1402	1871	GLQGSQSLHIPSLTGLRHACITLGKT AHSSRLHSPAPPPYL*STDTRDNN APEPTPPRSWTWRA*/PMGRGSSQE GQASQQPWPGEGKSGCEMPPPLVY KVKPEP*P/SPDPWGL*QSMPLDYL HLSVILRWRRGGGQWQGATKISRR DRRGGALLHL
1500	6997	A	1615	8	551	SAQMAVTTADPRVRPRVRTQLCSL ASLIQTLLVHLTPVE\KSAVTALWG KVNVD\VGEDLSRLLPVYPWTQ TFFD\SFADQSTPDAAMGNPKVKAH S\KKVLG\AFSGGPGCTWDNLKGTf AHTEVSLHC*QACTWDP\ENFRLG\ NVLVCCCWAHSLLGKEFQPHQLQA CLIKKIGWLGVG
1501	6998	A	1616	3	389	
1502	6999	A	1617	1	672	
1503	7000	A	1618	18	621	RSLRCSRHSCLATSSPLPCARRAH PARGKADQPCRSAGPSVPAAPR GENREKEETTRIGPGVMESKEKRAV NSLSMENANQENEEKEQVANKGEP LALPLDAGEYCVPRGNRRRFRVRQ PILQYRWDMHRLGEPTGQGMKR RE*WKRIGEEVRQLMEKSWRGKSQ L\SH\SLRGESGTDPPSPMTHD*VF ALMPLNP
1504	7001	A	1621	3	700	HASDRRHGSHACSRVSSGHQAGL LGGWEEDRECGQRAEGMMFWA ALALAAATSPSRLLLSPGKGPVPSRL PLSDAASPTWLKLT*RR*RSQIYQT G\QEGPLLPSQIGVILRDSHGVA\QV RF\VTGNKIL\RLKS*GTCS*IFLIDL YHLN*ESQFAVRKGILRREQERDKG G*NFPSPDF*IGEAGFHPFWLRYKQ QAESSLPNWEIWNHLTASALGRINL VWCTPSN
1505	7002	A	1622	1	340	GEHSMAPPAHFRALLYHPGTATLV PHPASISQHSPPWGN\RG*PV*RQ RHLTAPRSPPHPRFRHKPGKDPREN PSRWPEVPSLPQTHVVPQGAAWDT VNTTVCKNRSTKPQD
1506	7003	A	1623	3	1076	HPVPSSSYSVHTLSPAAMTEQMTLR GTLKGHNG\WVTQ\IATTPQFPENNL PASRIEKAIIIRKPARGWSQPMNFQ RRSRIHSHLLRMVVIS*DGQFC/AF QGFWDWKPCALGDLTNG/TPTRGR

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						FCGPIPKDVLSVAFSSDNQRQLSLGS RE*THQSLWN\TLGVCKFNLSRNES H/SESWVLCV\RFAPTTSKPLSIGLP VAWDKLVQV\WKPLNCKADAPN PHLATTGFL\NTGDLSSSRWDPLCA SGG\KDGGQ\MLWDL\NEGQPPLQR *NGGD\N\ALCFSPNRY\WLCVAAT GPS\IKIWDLEGKI\VDLQKQEVISTS SKAEPQCTSLAWSADGQTLFAGY TDNLVRVWQVTIGTR
1507	7004	A	1624	1	1189	LQGGGRRGCGASFSKPSSAILVAAA THALAAAMTEQMTLRGTLKGHNG\ WVTQ\IATTPQFPENNLPA\SEKAI LRKPARGWSQPMNFQRRSRRIHSF V\SDVVIS*DGQFC/AFQGFWDWKP CALGDLTNGHPHEGDFVGPYPRNV LSVA\SSDNQRQLSLGSRE*THQSL WNTPGWCANTTVPG*EPTQEWV\S CVPLPRPNNQQTPII\LLWPGNNLV QVMETWANCKLKDPT/NHWPTPGY SETPVTVLSRMDPFCA\SGGQGMAQ AHVYGD\NEG\KHLHARMVGTSI N\ALCFSP*PATWLCAATGPS\IKIW GFRGERSIVDELQKQEVISTSSKAEP QCTSLAWSADGQTLFAGYTDNLVR VWQVTIGTRLEVYGRALPIKKKTGF SEKKKK
1508	7005	A	1625	3	445	GEFADSF/SSMGSPVNAQDFCTDLA VSSANFIPTVTAISTSPDLQWL\QPA LVSSVAPSQTRAPHFPGVPAPSSGA YSRAGVVKTMTGGRAQSIGRRGKV EQETDQLEDEKSALQTEIANLLKEK EKLEFILAAHRPACKNPDDLGFPE
1509	7006	A	1626	7	514	
1510	7007	A	1627	3	462	RRSERAVTVLLPSSASQRPPVSAPRP LARLCLTATMMFSGFNADYEASSS RCSSA\SPAGNSLSYYHSPRRPPFSA WGSPVNAQ\DFCTGPGPFSSANFIP TGHLP\SWTSPD\QWL\VQ\PALVSS V\APSQTRAPSTFSESPPPTAGA\YSR AGVVKTMTGGRAKSIG\RRGKVEQ LSPEEEEEKRRIRRERNKMAAAKC\R NR\RELTDTLQ\ETEQL*DERTAF WTRMSHPVEEEGKLEFILAAHR\PA \CKIPDDLGLPRKMSVASLDLTGG LPRGLPPRRSEEAFTL\PLLNDP*/DP KPSVEPVK\SISSMELKTEPFDDFLFP ASSRPSGSETARV\PDMDLSGSFYA ADWEPLHSGSLGMGAHGHRGWEP LCTPVVTCTPSCNCLHVFLRLHLPR G*LLPQLCSCPPQGGQQQ*AFL*LA QLTHAAGPVRGQGRGGRHPQV\PL PELVHYREEKHIFP*RVPRGIASLT TTHPADLLFQHGARLSTRRDFCTGP GPFSSANFHSGLAILDQSGPCSG WCKPALVSSVGPIADQSPFNLFQVP TPYRWGLAPGLAL
1511	7008	B	1628	43	674	MDWTWSILFLVAATTGVHSQVHLV

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						QSGAEVKKPGASVKVSCKASFSNF DTYGFNWVRQAPGQGLEWMGWV SAFNGDTNYIRKLQGRVTMTDSST STAYLELRSLKSDDSAIYYCAATNS DKYFWGQGTLVTVSAASPTSPKVF PLSLCSTQPDGNVVIACL VQGFPPQ EPLSVTWSESGQGV TARNFPPSQDA FGDLYTTSSQLTPATH*
1512	7009	A	1629	3	1639	SPGIFRGFQSVIRTEQRELTMESGLN WLLLVAVLKGVQCEVQILESGGGQ VQPGGSRTLSCAASGFIFSNYVMTW VRQAPGKGLEWVSSTAASGANTFY AESVKGRFTVSRESENMMYLQMS SLRDEDTGIYYCAKDGDVPNLGVA WIVAGPGNVRPRKWFDWVWGQTT VTVSSASPTSPKVFPLSLCSTQPDGN VVIA\ SCLVQGFPPQEPLSVTWSESG QGV TARNFPPSQ\ MASGDLYTTSSQ LTLPATQCLA\ PKSVTCHVKHYTNP HPDVDG\ PCVPSTPPTP\ CSLNSTYP ISLMLPPPTVTAPTGPSKDLFLGSEA NLTCTLTGLE\ NASGCHFQSEGLQV GKSAVQGP\ PEA*PSVAAYSVVQLS CRGWREAMEPLVRPFTCTAA\ HPV VQGPALTAHPLQNPNTFPGRVHP FAPAVGRVCPFNDLLTLHCLAR\ AF SPQGPCWVRWLQGS PKLPPRKST* L G\ PFPAGA QARAPTTFAVTSILGR\ V QPEDWEE\ EGT\ PFSCMAGH\ EALAL AFTQKTIDRLARKPTHVNV\ SAVMP EVDGTCY
1513	7010	A	1630	3	497	SSGPTRLRENHPWLLSPADKTTVKG PL\WGKVGAAHAAEYG\ SEALGEGFS LSFPQPKTYFPATSDLE\ HNGFAPG LKGHGQRKFGRTR*PKSRGGNVD\ D MPQTALSAPERPCTAHKL\ RVDPV\ NFQASLSHC\ LCLVTLAAHLPAEFT PAVRRLWSKFLAS\ VSTVL
1514	7011	A	1631	9	489	NSARATDSERTHHGARLLPDKTKA QRPPRLKLGANA\ GEYG\ SEALERM FLSFPNPPKTYFRQFRP*ANGFAQG* RGHGQRRWPDALTQ\ AVA\ HVDEH APNGAVRP*SDLH\ AHKL\ RVDPVN FQASLSHCLAW*PWP AHLPRPSSTP GGATPSLEQSSWASC
1515	7012	A	1632	2291	2960	INCPAQAKVADILQFNFKKFVCLF/D FLRQSLALSPRLQVQWYDLSSLQSP SPRFKQFSCRLRPSS*NYRCASPRPT NFLIF/M*RWGFTMLARLVFVLLTSS DPPTSA/SHSAGITSVSHCTRPLQSIFI *PLEQVS*VKDKNNKKT HFFVLFC FLRQSHS\ VTQAGMQWHDQSSLLL QPPRLKQFSHFRLSSWYYRCLANF *IFCKDGVLLCCPW*SQTPGLK
1516	7013	A	1633	1	1233	
1517	7014	A	1634	233	884	ESPGVGCSARRGPRRSPGPPPAAP GTPRPHGIPLYTRAGHQ**GEIRRRP CTFISKFLRPQGSASERQLPDLQAR

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						AWQELLGRP FNKH\HWFPR*SPCKG IGVTRC\IRINP*KWIPLIGPGQHS AIGLSSQELFRLLP\SEL\TLWG*PIEVS SYRIGEDGSHLCACMKPSPA\GGST\QN QTNVQMV\DS\RISCKEELLGRTEP FPKTTNMMTVSG
1518	7015	A	1635	2	402	SQTQREPTMVLSPADKTNVCAA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKLRVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTISKYR
1519	7016	A	1636	2	522	GLEFGTSHRLRENPPWCLSPADKTN VKA\AWGKVGAGAHAGEYGAELER MFLSFPTTKTYFPHFDLSHG\SAQG *RAHGK\KVA\DALTK\AVA\HVDD MP/HNGAVPPLSDLHGAQAFGWDP VQLQSS*SHLPCW*PLARPPSPAEFQ PLAVATSSLGQSFLGFLKHKRCLNL PNYR
1520	7017	A	1637	344	742	GFLIGVNEKTCFFTSPMLHDSYFFFL VNVIRCHFICGTLYLYWAKHIFSVPF FLSFLFTSFISLFLPFPFFLFFFFFFW* LLLPTPFYVSF\MKG*SFNF*FFIFKC RLLTLLQNIK*TREMTTFDYFLSVFL
1521	7018	A	1638	1	519	PLKRS DGCNDGRPTRPPTRADTTAY TSNLKQTL LVHLT\TEEKSAVTALW GKVNVEKVG GKALGRLLVVPWT QRF\FESFGDLSTPDVAMGNPKVKA HSQESSPRGL*WWAWLTWDNLKG TFAHTEVSLHCDK\LRGSLKNFRL LGQRAWSVVAGPIHFWQKNFNPTS CRLA
1522	7019	A	1639	3	452	
1523	7020	A	1640	3	484	PTLLVPTDSERTHPWLLSPADKDQR QGPWVGKVGAGHAVRSMCAELER MFLSFPTTKTYFPHFDLSHG\SAQV* GPRARKVADALD/TNAVAVNGRTL PNALVRPL\SDLHAHKLRVDPVQF SSFL\SHCLLG*PWAHLPRPSFNPW RLQGFLGDKVSWAFC
1524	7021	A	1641	180	613	SFAGISNGLAGRSVKDSGKAQAKA VSR\SQRAGLQSQWGR\INRH*KSRD AS\HERGGATA\AVYSA\AILE\YLPQ KVLELAGKASKDFKGKAYYPLRHL Q\LAIRG\DEE\LDLIK\ATIAGGGVI PTTSHQISDRGGKKKDNQKTV
1525	7022	A	1642	107	368	IYIILRD*VLSTFVCFILCKAIYKNIW TAFWKCS*ILICSI/LCNYVCTCTSVY ALCYIYIIDLR*QQTYLCESKCTCIC MYVCIFLC
1526	7023	A	1643	790	1252	CAKPETQNNGNLRLVRLRPLHFGHT LN*VRT*LKRRIFFFLRQSLALSPRV ECSGMISAHCKFCFLGSGHSPASAS* VAGTTARRQHA WFLC VFSRDEFH RISKDGLNLL/NLVICPPRPPKVLGL QHEPPCPAKRRNFLSKIMGGHCFEL

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						SSCN
1527	7024	C	1645	171	329	MGARASGRSPLCQVGRQEQGLRGR NGPLPASRLPQQPVVPATPQSPRD DLA*
1528	7025	B	1646	196	514	MGRDTGPCLHDSLPAADDGPSL PTKQNEEFRPFIRRLPEFKFWHAAT KGILVAMVCTFFDAFNVPVFWPILV MYFIMLFCITMKRQIKHMIKYRYPF THGKRX*
1529	7026	A	1647	43	321	
1530	7027	A	1648	35	821	GRPRLGRGAASYRMSEGDSVGES VHGKPSVVYRFFTRLGQIYQSWLD KSTPYTAVRWVTLGLSFVYMIRV YLLQGWYIVTYALGIYHLNLFIAFL SPKVDPSLMEDSDDGPSLPTKQNEE FRPFIRRLPEFKFWDASVCGDGRC CKAGGGRQCPVLAADAALTFSPHL KHAATKGILVAMVCTFFDAFNVPV FWPILVMYFIMLFCITMKRQIKHMI KYRYPFTHGKRYYRGKEDAGKAF GQLEAGRLRPHVLQEQF
1531	7028	A	1649	156	818	HSYRMSEGDSVGESVHGKPSVVYR FFTRLGQIYQSWLDKSTPYTAVRW VVTGLGLSFVYIDSEFTCLQGWYIC* PMPLGIYHLNLFHKLFSFSPKWDP SLMEGLQDDGSFGYPTKQERREF/RA PFIRKGSFVNLFWHAGYPRASLVA LWCTFFDAFQTSPVFWPILVMYF HHASSCITDGRRANSRHMDSLRY MPVSHMGK/RGRYRGKEDAGKAF AS
1532	7029	A	1650	154	685	PPLHLRDCFSPPGRALSPVGFYPYR RSVPATWLKLTSDDDVKEQIYKLGQ EGPLLSQIGVILRDSHGVAQVRL GTGHDTFKNLKSKGLAPDLPEDLY HLIKKA\AVRKH\LERNRKD*GC* NSRLILIESRISPFWLRYYK\TKR\VL PPNWEIWNHLTASAPGRINLVWCT QAIK
1533	7030	C	1651	127	435	MAASXNPEVLDITEETLHSRFLGV RNVASVCLQIGYPTXASVPHSIINGY KRVLALSVETDYTFPLAEKVKAFLA DPSAFVAAAXLGCCHSCSXCCCSP S*
1534	7031	A	1652	1	689	KCFI/VGADNVASKQMQQIRMSFRG KAVC*WGKNTMMRKPIRGHLENNP ALEKLLPHIRGNVGVFTKEDLTEIR DMLLANKVPAAARAGAIAPCEVTV PAQNTGLGPEKTSFFQALGITTISR GTIEILGVRNVASVCLQIGYPTVASV PHSIINGYKRVLALSVETDYTFPLAE KVKAFLADPSAF/VAAAP/VAAATT AAPRAAAAPAKVEAKEESESEDE MGFGLFD
1535	7032	A	1653	68	1110	RTAVMPREDRATWKSNYFLKIIQLL DDYPKCFIVGADNVGSKQMQQIRI VPWGEACVLMGQKTMMGQAHPK



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						GTL*NNPSLWRKLLPHIRG\NLGFC FTQGGPSLEIKGHVCLANKGLPSWL PVVGANCPHGEVTGGQPQNTG/LSG PEKTSFFPGL*AITTKVISQGAPIENPE VNVPAESRTGDQSGKPSEANAA*TC SNISPF\SFGAGSSQPGVSTNGSHLPP LKGLDIHRRNLCIFWLSWRGVRNV AKCLSARLAYPTVA\SVP\HSIINGY KRVLA\LSV\EPDYTFPLAEKVKAFL \ADPSAFVVA\VPVG\VAPPAAPGG\ VAAPAKVEAKEESESEDEDMGFGL FD
1536	7033	A	1654	1	364	
1537	7034	A	1655	70	253	
1538	7035	A	1656	151	657	APTTPTGPGDPLDLVALAEQVQKA DEFIRANATNKLTVIA\DLQ\HLPE QARKVLEEHRDANLHHVACNIVK KPGDIYYLL*TG RVGQYFHSISPK LGDKFVHIDFLGAYKLQHDLSWTP V*GH*EGKMLKISMMGHVAKPVSG PASVHWNPTFQGTDSLEEWGF
1539	7036	A	1657	345	547	GFKPPDFFLCNENKWRKINTSSFSE Y*CLMHIHLLIFNITIFSS/LHTYIHKH THTHTPFSVFIMEGC
1540	7037	A	1658	228	900	PSQAGNTSPSGARSSFPKDMKLEN SSFEAINSQLTVETGDAHIIGRIESYS CKMAGDDKHMFKQFCQEGQPHVL EALSPQTSGLSPSRLSKSQGEEEG PLSDKCSRKTLFYLIATLNESFQA*L *LQHSPQLSSAGSPALSWLG*MQS TAVCSQLCGEDFKDLKPQLWNAV RGDLPGLKCDIYSYNPYLDSDFG EDGSLWSFNFFYNKRLKRNRL
1541	7038	A	1659	35	1288	
1542	7039	A	1660	1	1641	
1543	7040	A	1661	212	369	HPVTVYLLGYLLFQLPCGSEFSTSE THGHSADRLG\AAFAVSRLEQDEYA PG
1544	7041	A	1662	63	255	VLMFSSSHG*GYQSSRLQCKLQIVQ LIQDILLFFSF*IPE*LLS*LTPLKIFPL HQNGPSDFVS
1545	7042	A	1663	169	391	
1546	7043	A	1664	85	1534	KSSHCIKMGPQIFHKTSSELVLPATSC PSCPDQNEEDVSQTQYKECCG\GG WCSHSIFAVWHFI*RPDAT*FGLEQ RLTGLLASGPVSLREV*LYSSLGT VISGK*KTSNVG*RGLALGSAFSD KYSWFTMTWACISGPTKAL\TTGV \GLIAFGQCDVIVAGGVELMSDVPI RHSRKMIMKMLDLNKA KSMGQRLS LISKFRFNFLAPELPAVSEFSTSETM GHSADRLAAAFV\SF\AQDEYALR SHSLSKKAQDEGLLSDVVPFKVPGK DTVTKDNGIRPSSLEQMAKLPKPAFI KPYGTVTAANSSF/LLTDGASAMLI MAEEKALAMGYKPKAYL/RRDFM YVSQDPKDQLLLGPTYATPKVLEK

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						AGL\TMNDIDAFEFHEAFSG\QILAN FKPMDSDWFAE\NYMG*KKPRFGL PPLWRRFNNWG\GSLSLGHFPFGT\T GCR\LVMTAANRLRKKGGQYGLV AACAPG\GQGSATDYVEAYPK
1547	7044	A	1665	294	823	
1548	7045	A	1666	3	1171	
1549	7046	A	1667	1419	1801	TMEIHPIEQLDPSDHLESTAAGQEA LFTYHSF*STFISFFETGPHFVTRLK CSSAIITHYSVELLGSSHPPTSASWV AGNTGVCPhVQLIFLFFVEMGSHY VARLVFNS\GLVIFLPWLPKVLGLQ V
1550	7047	B	1668	68	471	MVRKLIVPRAEAAEAGGLPELGHH RPQPARAARAAALTGCSGGEDYTR YNQLSRAVPVCSRLGAHARVRWEL CDFVTASSFCRRRLPTVLLKLRLMAQ HLQGSIAL*
1551	7048	A	1669	2	359	
1552	7049	A	1670	1	585	PRGVIGHGPLGTSFIGKYGCGDYW VKAFLDRPSQPN\QGPKNFEVWD LVDVNTPADLMA\PVSAKKERKVC MFIPDGRVSVSARIDRKGFCGEDEIS IHADFENTCSRIVVPKAAIVARHTY LANGQTKVLTQKLSSVRGNHISGT CASWRGKSLRVQKIRPSILGCNLR VEYSLLIYVSVPGSKQVFIKAL
1553	7050	B	1672	21	410	MPSKVRCXSVQVFDAMKTATAVA HCKRGNGLIKLLEPVLLLGKERFAG VDTRVRVKGGGHVAQIYAIROSISK ALVAYYQKYVDEASKKEIKDILIQY DRTLLVADPRRCESKKFGGPGARA RYQKSYR*
1554	7051	A	1673	1	456	MPS/KGPLQSVQVFGRRKKTATAVA H/CKRGNGLIKVNGRPLEM/IEPRTL QYKVLGSGTGVSGWRTLGD RDVV ALESWGAGISNGMFRSCVGCQWA AGASSASRQERFAGVDIRVRVKG GPWPRFMSKKFGGPGARARYQKST DKPIVTQNSLV
1555	7052	A	1674	172	661	LLEPVLLLGKERFAGVDIRVRVKG GHVAQIYGESQELGAWRRWLWEG GLHSAPVPFNCVSFSQSVSPIS\KAL VAYYQK\WSEHGSFP*GRWVCGDQ VKDSV*LSKSSLLFLPDVDEASKK EIKDIL\QYDRTLLVADPRRCESKK FGGPGARARYQKSYR
1556	7053	A	1675	27	554	STLGAMPSK/GVPLQSVQ\VFGRKK DSGQLLAH\CKRA\NGLIQ*TGGPL EMIEARARLQYK\LEPVLLLGK\IE RFAG\VDIPCPV*KGGWSTWPQIYAI RQS\ISQKPLVAYYPEM*VSMGPPH E\YVDEAFQRREIKDILHPSY\DRNP AGLAGPFVRCE\SKKFGGPGAIRAR YQKSYR
1557	7054	A	1676	192	836	ALIMSFIFEWIYNGFSSVLQFLGLYK KSGKLVFL\GLDNAGKTTLLHMLK

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						DDRLGQHVPTLHLTSEELTVIAGM TFTTFDLVGHE\QARRVWKNYLPS QLMGFVFLVDCA\DHFSPSWNPKE LNALMTE*NNIPMCPIILGNKIDR TDAISEEKLREIFGLYGTGPQERGEL *PLKEL\NARPM\EVFHVAVLLKEG KVYGRGFSAGLLPVLF
1558	7055	A	1677	196	520	DTVSRKNKSGKIFQLSSRV*YIERSQ SGVKVYKCKTFGKAFTQ/HF*AHM RMYTGEKPYKY*ECGKFFILVLLL LMIQKYFHLLIKIVRLYLIRKKVSCQ PSNKILQS
1559	7056	B	1678	1	1521	MGIRVTSVIVSRPVPHSEAVFCCWL LGATDVWIPEHPANPRLTFPLFPESP GRHLREIKLQSARDASVKSANKTR VIPKPQRVIHPGGQPTDKMDLDDLD LNPRIIAAIKAKLKSVEVLHFSGP DLKRLTNLSSPEVWHLRLTASLHLR GSSILTALQLHQKERFPTQHQRLS LGCPVLDALLRGGLPLDGITELAGR SSAGKTQLALQLCLAVQFPRQHGG LEAGAVYICTEDAFPHKRLQQLMA QQPRLRTDVPCELLQKLRFSGQIFIE HVADVDTLLECYNKKVPVLLSRGM ARLVVIDSVAAPFRCEFDSSQASAPR ARHLQSLGAMRELSSAFQSPVLCI NQVTEAMEEQGAHGLGFWDER VSPALGITWANQLLVRLLADRLREE EAALGCPARTLRVLSAPHLPPSSCS YTISAEGSWGNTCKQNTLHISPET AGPAHAACWPQQDTVRAGHSES WHASCCNPDTMQGQTISTSVNQ QEAQAKPPPTPL*
1560	7057	A	1679	991	1367	AVLVFNNGEANEGSGPRGP*GERS SRARPP/SGPGPWNCAPRPWCPL RGWSSVSWD*TAQAKPVCKSP/AG GSSPGTGSPSAPSPGAGTEPAWAG PAELPGVFSLNVLPLSLCLIF*SLAC LA
1561	7058	A	1680	313	429	CIESMVHGGENIFPAGHGGSHL*SQ HFGRPRQVDHLRSG
1562	7059	A	1681	552	792	GSASDYQSGIRTVGPRDWLCRRRA LDLDAARTQSVRAAEGKCAFLQMQ GPRVYTGPGRPRRADHLRSGV*DQ PGQHGETP
1563	7060	A	1682	508	1085	CQHFGRPRRADHLRS\GVRAQPGQ HGETPSLLKILKLA/GHGGAPL*SQL LGRLRQENHLNPGGRGCGEPRSHH CTPAWETERDSISKKTKTQVVICI* SLNLVREIKNKIGLTAE*ILQKNSL EDVSIIEI*NEGQRDGKMDRAFLRS MQQYQAVQYMCNQSPRRVGDRL GRINSQKKCKTYTMNTIKHC
1564	7061	C	1683	46	516	MLSDPPARIRTRKGPTETVSRIPRPN SPNGQGPVDSSPSGXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX

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						XXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXX*
1565	7062	A	1684	2	100	
1566	7063	A	1685	2	814	PGYKKGPQETGSRIPRPNSPNPLRVL WTAHLVAMAPGSRTSLLLAFALLC LALGFKEAGCPSQTPV\LSRLF\DHG MVQGPSRV\TSCAID\TYQGFEETYIP KDQKYSFLHDSQTSFCFS\DSIPTPS NMEGSATRNPILELLR\SLLLIE\SW LEPV\RLRSIVPPTTWVYEHLGTAI DYHLL\KDLEGGHPTV*WGRLEDG KPPDLGKILKQTYSKFDTNSHNHDA LLK\NYGLLYCFRKDM\DKVE\TFLR MVQCR\SVEGSCWLLGCPSSIL
1567	7064	A	1686	3	452	
1568	7065	A	1687	3	516	PTLLVPTDSERTHHGACLLPDKTNV \KAAWG\KVGAGAG\EYGAELER MFLSFPT\TKTYFPFHD\SHGF\CPGL RATGKKVADALTKRRG\HTWDDM PKRRCP*SDLHAHLR\DPVQLS SS*SHLPCWVTPGPAHLRPSSTPGG CKASLGQSFLGFL\KHRLNLPNNV
1569	7066	A	1688	3	409	SNFRSNFGYNIP\KHLADRVAMYV HAYTL\YSAVRPFGC\SGYWGCAIGK ARQAAKTEIEKLQMKEMTCRDIVK EVAKIYIVHDEVKDKAFELELSWV GELTNGRHEIVPKDIREEAKEYAKE SLKEEDESDDDNM
1570	7067	A	1689	2	437	
1571	7068	A	1690	126	409	ILLWMDILICTDFGSVNYFNVWRL PKSYLSLFYSRIYIVHDEVKDKAFEL ELSWVG\ELTNGRHEIVPKDIREAE KYAKESLKEEDESDDDNM
1572	7069	A	1691	516	564	
1573	7070	A	1692	224	344	ILLGFLVLASDHLQSKYAL*CPLR HLP\ELNPSLREGSVL
1574	7071	A	1693	1	1237	MGCRPVGQAGLELLTSARTCFVSD LKRGLKIQAAKF\NIDGNNECPIDTR KQLAENLVVIGGTSMLPGFLHRLLA EIRYLVEKPKYKKALG\TKTFRIHTPP AKANCVAWL\GARSLLGYNRFLMF QPF\RGEE\TVWSLLPKIQA\YCCPFL KYDLSASTFSPDGRV\FQVEYAMKA VENSSTAIGIRCKDG\VV\LG\VEK*VL SKLYERRVPNKKTF\LMFDR\HVGM A\VAG\LLADA\RLADIAREEASNF RSNFG\YTIPLKHLADRV\AHVWCHA \YTTLPVAVRPFGCQFPC*GPYSVN\ DGA\QLYHD*PHPGVSIPVNWGCAI GQRPQAWQRRKLEK\LQMKEMT\ C\RDIVKEVAKIYIVHDEVKDKAFE LEPSW\VGELTK\GRHEIVPKDIREE AEKYAKESLKEEDESDDDNV
1575	7072	A	1694	1	1083	
1576	7073	A	1695	138	545	RPGMWSTRSPNSTAWPLSLEPDGP MASASTTMHTTTIAEPDPGVS\GLP\ DGRMETPTPHP*LTMVVMAGCDV\

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						AAVPIVLVSLLFVMLRYMYRHKGT YHTNEAKGTEFAESADAALQGDP ALAQDAGDSSRK\EYFI
1577	7074	A	1696	2	498	
1578	7075	A	1697	41	510	APSPRRPWGHFTEEDQGLLSTSLWG KGEMWKKCWEGRNPWERLPGCPT PWTPRGSEQLWQPCPSA/ILAHWP ANPQSPRHHGK\KVLTSLGRCP*STL DDLKGTFAQL\SELHCDKLHVDPEN FKLLG\NVLVTVLAIHFVGKDFTPGG CRASWAEDG
1579	7076	A	1701	153	744	AVNLVPSKDRHLTQSRSQGGGVAN PNSGVYSARPSSPPPQIALPAWGTG QPQTLQTSPGEGFSVQTGAEVGVG RG*PRRRPPRARQGGKGVHSTLKKL KHYRFHIADGLDRGOAPPLGRPLFL GPGWLRTH*GRAGK/QNPQTVGDH PGAGAPPSSPALAVSL*/H/CTGLC*I PSPACSPGSPSPRRRGSHSPDAWV DP
1580	7077	A	1702	35	569	
1581	7078	A	1703	509	2455	LPAATVLTSSPNFQIQPNRTNGD VTKKIHDSLESSKISTLKGNLERYF QPSWMTLRGVRLQLEEVPAIVEIA RELELEVPEDEVTEFLQSHDQTLAD QKLLLMAEQRKWFLEMETTPGGD AMNIVEITINNLEYNINFVDKGAAG FERIDSNFERSSTAEWVTVKQTQAH PSGGIQEGIVIIRDGSRPYTTPEHLPV RPNVEEEDSDIDESSPFLRNYYKA AHSFIGRIRFKHSTSLLEAFYIITSK EFFSAIRKLASSPEKGKGGIIFTAINP FTRSINEIYKIQRRRGKERQLNDCV HRSDDANKGPESLGSAGSGQSHDV AQGHLQGLVLGQLFILAPLGKFHPE EDVKQATSNFENLQKQLARKMKLP IFIADAFTARAFRGNPAAVCLLENE LDEDMHQKIAREMNLSETAFIRKLH PTDNFAQKNMNSTLTFVTLSGELRA RRAEDGIVLDLPLYPAHPQDFHEVE DLIKTAIGNTLVQDICYSPDTQKLLV RLSDVYNRSFLGEPGKLNTENLLQV ENTGKVKGLILTLKGEPGGQTQAFD FYSRYFAPWVGVAEDPVTGSAHAV LSSYWSQHLGKKEMHAFQ/SFPPE ESWEFPFVQT*RVDIRGCAPVVLEG TLTAYRWLCCDAAVSNHQVFA
1582	7079	A	1704	1	1503	
1583	7080	A	1705	1	635	
1584	7081	A	1706	1	804	LQFSSALGGGRCRASASSPRRARRR GQRPRHPAPRRPQAARPSAAPRARR FLSQRPAAAAAAQRAALMQAIK\ VVVGKPKL*GKT\CLLI\SYTTQCHF LGEYIPTVFDNYSANVMVDGKTG EIWGLWDTAVQEDYDRVTPYPYP A/QADVFLFCFPFVSPASFENVRK WYLNVRHHCPN\TP\ILVGTKLDLR DDKDTIEKLKEKKLT\PIYPQGLA\

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						MAKEIGAVKYLAECSALTQRLKTV FDEAIRAVLCPPPVKKRKRKCLLL
1585	7082	A	1707	1	848	RPRVRAGAENMMFSAARLSPWE GSPSFAENMNDWMPKAEYDPLKA GSIDGTDEDPHDRAVWRA\MLARY VPNKGVIGDPL\TLFVARLNLQTK EG\K*KEV\FPRYGDRLRLVRDLV TGFSKG\YAFIEYKEERAVIKAYRD ADGLVIDQ\HEIFVDYELERTLKGW IPRRL\GGGL\GGKKESG\QLEFGGR DR\PRKP\INLPVVKNDLYREGNRE RRERSRSRERHWDSTRDRDRHDRG REKRWQEREPIRVWPDND\WRRER DFRDDRIGREKKER GK
1586	7083	A	1708	3	3067	
1587	7084	A	1709	148	4435	GIQRKYLKGSIMVSSGCRMRLWFI IVISFLPNTGFSRAALPFGLVRRELS CEGYSIDLRCPSDVIMIESANYGRT DDKICDADPFQMENTDCYLPDAFKI MTQRCNNRTQCIVVTGSDVFPDPCP GTYKYLEVQYECVPYIFVCPGTLKA IVDSPCIYEAQKAGAWCKDPLQA ADKIYFMPWTPYRTDTLIEYASLED FQNSRQTTTYKLPNRVDGTGFVVY DGAVFFNKERTRNIVKFDLRTRIKS GEAIINYANYHDTSPYRWGGKTDID LAVDENGLWVIYATEQNNGMIVIS QLNPYTLRFEATWETVYDKRAASN AFMICGVLYVVRVSYQDNESETGK NSIDIYNTRLNRGEYVDVFPNQY QYIAAVDYNPRDNQLYVWNNFIL RYSLEFGPPDPAQVPTTAVTITSSAE LFKTIISTTTSQKGPMTTVAGSQ EGSKGTKPPPAVSTTKIPPITNIFLP ERFCEALDSKGIKWPQTQRGMMVE RPCPKGTRGTASYLCMISTGTWNP GPDLSNCTSHWVNQLAQKIRSGEN AASLANELAKHTKGPVFAGDVSS VRLMEQLVDILDAQLQELKPSEKDS AGRSYNKAIVDTVDNLLRPEALES WKHMNSSEQAHTATMLLDLLEEG AFVLADNLLPTRVSMPTENIVLEV AVLSTEGQIQDFKFLGIKAGGSSIQ LSANTYKQNSRNLAKLVFIYRSL GQFLSTENATIKLGADFIGRNSTIAV NSHVISVSINKESSRVYLTDPVLFLL PHIDPDNYFNANCSFWNYSERTMM GYWSTQGCKLVDTNKTRTTCACSH LTNFAILMAHREIAYKDGVEHLLT VITWGVIVISLVCLAICIFTFCFRGL QSDRNTIHKNLCLNLFIAEFILIGID KTKYAIACPIFAGLLHFFFLAAFAW MCLEGVQLYMLVEVFESEYSRKK YYYVAGYLFPA TVVGVSAAIDYKS YGTEKACWLHVDNYFIWSFIGPVTF IILLNIIFLVITLCKMVKHSNTLKPDS SRLENIKSWVLGAFALLCLLGLTW SFG\LLFINEETIVDGHISFTIFNCFP

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						GGVFHFPSPFHCALPKGKVRKRIMAKCL/RRHLHTACGGP/LPT*ESPHSSVKASTHPEPSARYS\SGTQS\RIRRMWNDTVRKQSESSFISGDINSTSTLNQGHSLNNA\RDTSAMDTLPLNGNFNNSYSLHKGDYNDVQVVDCGLSLNDTAFEK\MIISELVHNNLRGSSKTHNLELTLPVKPVIGGSSSEDDAIVADASSL\MHSDNPG/VWELHHK\ELEAPL\IPQRTHSLLYQPQKKVKSEGTDSYVSQLTAEADHLQSPNRDSLYTSMPNLR\DSPYPESSPDMEEDLSPSRSENEDIYYKSMPNLGAGHQLQMCYQISRGNSDGYIIPINKEGCIPEGDVREGQMQLVTSL
1588	7085	B	1710	98	264	XQVVCKKYRGFTIPEAFRGVHRYLSNAYAREEFASCTPDDEEIELAYEQVAKALK*
1589	7086	A	1711	155	1217	DPPSPVPAPPSSPRDGHFLVPDATMAEEQPQV\ELFVKAGSDGAKIGNCPSQRLFMVLWLKGVTFNVTTVDTKRRTETVQKLCPPGQLPFLLYGTEVHP\DTTKIEEFLEAVL\CPPRYPK\LAALNPEVQHSWGWDFAKFFLPNIQEFQTPALN*QSGRRGFLESP*KVLDNYLT\SPSPPEEVDETSC*KIEGVSQRF\LDGQRRPHPWLDLQTCCPKVTH*VQVVCKRK*PGNSPHPPKAFPGKCHRV*SKMPYAPGKNPSHPVPDDEIELRPMKSKVAKALQISPSLGLPSTPSIFSTKAPGGFHATPMGHTPKLASGQGILGDIEPAKGVVEEGMRERNGP GSDF
1590	7087	A	1712	39	256	LSVKMEEGILPCSLYETTITDSKT*QG*YI/EDFRLVFLINLNA YILKKMLVNHLR*NMRDNSETYRRIVRIV
1591	7088	A	1713	1193	1436	PQSDFLDTLPQTSPIIP/I*EVPTGLVCYSSRVNKRAPPASIPVPACSPSPVSNPPHPVSNPPHVSAPLPCSSHQTQ QAP
1592	7089	A	1715	2	533	ARDSFLAAMASHR\LLLLCLAGLVFVSEAGPTGTG\ESKCPLMVKVLDAVRGSPA HQMW*HVFRKPR**PPWEAILPSGTRKTQLSLGELAHGAHKLREGICTNGIYKSGK*DTKFFTGGKTLGIFPHFPLRHCQEVGISTGQRTSGPRLTPLAALLEPLTPISTTGCSFTNSQGN
1593	7090	A	1716	38	661	APSPRRPWVISQRRTKATITSLWGK\VNVE\ DAGGETLGR\LVVYPMDPRGFFDSFGNLSSASAIMGNPKVKAHG\KKVLT\SLGDAIK\HL\DDLKG/T PFAQA*SELHC*QACNVGS*GTFKL PGEILLVT/LFWAIPFSGKEFHPLRCQVFLGQEQKMAEDGD\WS\GQCPCSFQITTELTP*MQSFSRIWLYSCKQLQIINLFLLRDHQ
1594	7091	A	1717	32	487	SRRHGSSLWGKVNVEDAGGETLGR

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						LLVVYPWTQRFFDSFGNLSSASAIM GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG
1595	7092	A	1718	41	597	APSPRRPWVISQRRTKATITSLW GK \VNVE\DAGGETLGRLLVVYPWT QRFFD\SFG\NLSSASAIHGQPPKVQ GTWSKKVLTFLGEMP*KHLDDLK GHLLPKPEVNLHC\DKPAMWDPIEN FKAPGEMLLVTRFWAIPFSAKEFHP WRLAGLPGQKDG*LGVGQCPCSFQ IPLKPLGP*IQ\SFQG
1596	7093	A	1719	3	573	HSLFGTSEVINKLLVPDAHGSFHRG GPRLSTSLWGKGECGKMEEKPL GRLLVVYPWTQRFFESFGNLVLLP SCPSMGQPPKVKAHGKRRCLSLG RCQ*STLDDLKGTFCPSLKRNLHC* QACNVGS*RTSKLLGENVAG*PVFG QHFRAKNFTPEGCKASWQKQKM AEDGDWSWPVPLFLPDYH
1597	7094	A	1720	676	1283	QRKILYTHNTTENKWEGINFT*SFR IFLFLRRSFTLVAQAGVQ\WLDLGS LQPLPPRFKQFSCGLPSSWDYR/RC VPAHPANFCIF**RWGFTMLARLLS NS*PQGDPPASASQ\SAGITGVSA/H APVRASFFLSLTVSGVQWRDLGSLQ PLPSGFKGFSCLSLPSSWDYGCPPPS PANFCIFSRHGFSPCWSGWSQTPDL K
1598	7095	A	1721	41	669	APSSRRPWVISQRRTKATITSLW GK \VNVE\DAGGRKPLGKAPWLSTPWT \QRFFDSFGNLSSASA/LSMGKPPKS KAHGK\KVL\TSLGDA\TKHLDDLK G\TFAQA*SATCTVDKL\HVDPGGT FKLLGENVAG*PVFGQHFRAKNFT PGGCRASWQKQKMAEDGDWS\GQ CP\VLQIPLKLNCP*MQSFSRIQLLFL QAITNNKSISAKRSP
1599	7096	A	1722	2	307	TPYLVGQVVAGAQLQLFESHAGH LGPQLFNKFALPYIRDVAKQVKARL REAGLAPVPMIIFAKDGHFALEELA QAGYEVV/GDDFGPHRYIANLGHG LYPDM
1600	7097	A	1723	20	473	AVEFEANGLGPQGFPPELKNDIFL*A AWGEETDYTPVWCMRQAGRYLPE FRETRAQAQDFSTCRSPEACCELTL QPLRRFPLDAAIIFSDILVVPQWTLM TYMVEGGGSSTMAQAKRWLYQRP QASHQLLRILTDALVPYLVGQVVA GAQAL
1601	7098	A	1724	3	1170	CKHSLGHTCYSPRGSSYRQLTMEA NGLGPQGFPPELKNDIFLRAAWGEE TDYTPVWCMRQAGRYLPEFRETRA AQDFSTCRSPEACCELTLQALGME VTMVPKGKPSFPEPLREEQDLERLR DPEVVASELGYVFQAITLTRQRLAG



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						RVPLIGFAGAPWTLMTYMVEGGGS STMAQAKRWLYQRPOASHQLLRIL TDALVPYLVGQVVAGAALQLFES HAGHLGPQLFNKFALPYIRDVAKQ VKARL\REAGLAPVPSIIFAKDGHF ALEELAQAGY\EVVGLD\WTVAPKK ARECLGKTVTLQGNLDPCALYASE EEIGQLVKQNLDTFGPHRYIANLG HGLYPDMDPEHVGAFVDAGHKHS RLV*QNMWGPLWMLGINTHVWFD KTECIPLSRTPNPDDWLFSGP
1602	7099	B	1725	92	846	IIFAMDGHFALEELAQAGYEVVGLD WTVAPKKARECVGKTVTLQGNLDP CALYASEEEIGQLVKHMLDDFGPH RYIANLGHGLYPDMDPQHVGA FVD AVHKHLRLV*
1603	7100	A	1726	1	804	
1604	7101	A	1727	178	1093	TFLLPACLLAALLPLRHHVRGRAW VQGSILNEG VG*ALKD\LINEACWG Y*APAGVNLQSMGHRPTVSL\VQLT LRV*GASTPYRC\DRNLGHGR*NL T S\MSKILKMAAGNED\ISLTLRAEDN AGYLGR*YFEGTKPGRKFSDYEMK LMDLDVEQLGIPEQEVSCVVKMPS GEYA\RICRESQPILGDVVIISCA\K DGSENFASGELGNET\IKLSQTSNV DKEEEA\VPKMNPE\VPQNFCH*GY LNFFTK\ATPLSSTVDT PVC SADGTP LVGRSIIAGYGDHLKYLLGLPKDP RIEEGSLGHS
1605	7102	A	1728	58	483	AARDRLHLRRTTEQHVPEVEVQVK RRRTASLSNQCQLYPRRSQQQVVP VVD FQAE LRQAFLAETPRGT VAAA ANAATASIAGAPTQYPPGRGTPPPP RRQTTPPPGIM\APPPGMRPPIG\PPPI GFPLARGTPISMPPSGN
1606	7103	A	1729	292	531	FQAKTSLPLGFQKHQVLTVDIGFGG TAIMTVGKSSKMLQSLFPLQW/CFV KLCRVFVSFLPHFALIIANNK CIEQ KKKKK
1607	7104	B	1730	326	419	XRLTCKRSLARSIASLNAPQTDASGI SGGPDA*
1608	7105	A	1731	774	1763	GNPRSYLLSIAFPLGLQKAFKVFNC GTLD FGWNSNHD LFGKS\SKLLQHI DYRMRCILQDGR\FIGTFKAFDKH MNLILCDCDEFKIK\PKNAKQPRA VEE/ESRVLGLVLLRGENLVSM TVE G\PPPKDTGIARVPLAGAAEGPG\V GRAAGRGVPAG\VPISGPLAGLAG PCSRGSLGGP/SPQQVMTSTGKEAL* AAAAVAATASIAGAPNTVPTQGT GTPAPTSGRATQPPGIMAPPP\GM RPPMGP\PMGLRPARGTPI\GMPAPG \MRPPPPG\IRGPPPP\GMRPHKTL SIL FDPSQSLFPLQCVLVKLCRVSAELF CSLIIAIRC
1609	7106	A	1732	32	487	SRRHGSSLWGKVNVEDAGGETLGR LLVVYPWTQRFFDSFGNLSSASAIM

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						GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLP MQSFQG
1610	7107	A	1733	1	591	NFALEAKNSARAISLVPDAHGVIS QRRTKATITSLWGVNVEADAGGE TLGRLLVVYPWTQRFFDQLLANLS SASAHGQPPKVQGHMAKKVLTFL GEMPIKHLDDLKGHLLPKPEVNCT VDKPAMWDPENFKAPGEMLLVT/L FWAIPFSGKEFTP*RLQASWAERWV TWS\GQCPCSFQIPLKPLGP*IQ\SFQ G
1611	7108	A	1734	1	477	RRPSWLVAALVRNANMQIFVKTLT GQNHHLRYETQ*HPLKNVQPKKIS KNKGGYPHPD\QQRDLNLPQKQLE GWPALLSDYKHPRKESHPAPWCLR LRGGIIEPFPGLPQKYLRQR*SC RQVLCFAFNPPCLSTGRKKKCGSH QTTLRPQEGFRK
1612	7109	C	1735	9	254	MEFHSCCPGWSAMARSQTAATAS QVQSDSPASASRVAGINRHALTHPA NFVFLVETRFLHVRQAGLELPPQPP KLLGLQV*
1613	7110	A	1736	5	290	FNLTHIESRPSRLKK/DEYE/FFTHLD KRSLPALTNIIKILRHDIGATVHEL RDKKKDTPVWFPRTIQELDRFANQI LSYGAELDADHPVSPWPVG
1614	7111	A	1737	68	312	
1615	7112	A	1738	317	916	TSSPPSSLCFLSFDICHELLGHVPLF SDRSFAQFSQEIGLASLGAPDEYIEK LATIYWFTVEFGLCKQGDSIKAYGA GLLSSFGELQYCLSEKPKLLPLELEK TGIQNYTVTEFQPLYVAESINDAK EKVGNSAATIPRPFVRYDPYTQRIE GLDNTQQAHDLG*FHLTVEIGILCS ALQKNKVKAMDRMVVCQAVE
1616	7113	A	1739	389	1881	NLQPHVLFANLPVPEALKSQRPHSR GASMSTAVLENPGLGRKLSDFGQ\E TSY\EDNCNQKWPISLDPPHLKER KLGALGPKYCALFEENDVNLTHIE SRPSRLK\KDEYGFPPFGIKRSLP/A LTNIIKILRHDIGATVHELSDKKKD TVPWFPRTIQ\ELDRFANQILSYGSG NWDADHPGFKDPVYRARRKQFAD IAYNYRHGQPIPRVEYMEEKKTW GTVFKTLKSLYKTHACYEYNHIFP/L LEKYCASHEDNIPQLAEDVSQFL/QT CTGFRLRPVAGLLSSRDFLGDLAFR VFHCTQYIRHGSKPMYTPEDICHE LLGHVPLFSDRSFAQFSQEIGLASLG APDESIEKLAPIYWFTVEFGLCKQG DSIKAYGAGLLSSFGFQYCLSEK KLLPL/ESLEKTAIQNYTVTEFQPLY YLAESFNDAQGEI*GTFAATIPRPF SVARHDPHTPQRIGGSWDNTQQLAKI LA\DSI*Q*IGIPFAVALQNIK

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1617	7114	A	1740	1	191	MQK*ITAWAPAPMKIKIIASPERKYS VWIGGSIWPQLST/FQQMWISKQEY DESGPSIVHRKCF
1618	7115	A	1741	1	360	SGACPAFLVDRNLRHHETTFNLIMK CDVDIRKDLANTVLSGGITTMYPG IADRMQKEITAL/APPSTLRFRIAPP/ ERRKYSVWIGG\SILASLSTFQQ\MC LGKQEYDESGPSIVQRKCF
1619	7116	A	1742	13	1277	INPPPLSRRRCQLSHSVLPPLRRRVSL PVAMEEEIAALVIDNGSGMCKAGF AGDDAPRAVFPSIVGRPRHQGV MV GHGPRTDSYVGDEA/QRSKRGILTL KYPHIEGIVTNWDDME\KIWHHTFY NELRVAPEKHPVL\LTEAPLNPKAN REKMTQ/ILCFETFNTPGHVPWPIQA VLSL*SLWAQPIGIVMDSGVDGVTH TV\PILRGATTLLHANLRLGPGLARD LTDYLMKILT\ERGYSFTTHGPGSKT FRNIKGEACATSPLDFEQ\EMGTAA SSSSLEKSYELPDGQVITIGNERFRC PEALFQPSFLGMESCGIHETTFNSIM KCDVDIRKDLANT\ALSGGTTMDP GVADKIAEGRSTALAAPAP*KIR\IIA PP\ERK\YSVWIGGSILASLSTFPARF W\SKQE\YDESGPSIVHRKCF
1620	7117	A	1745	644	844	ELSPTTFMPFSEGAEHL\YLPQGPG* GSESPGGCPA/PPYSPYSAPPATPEP IEKSQPNPIRHRFPF
1621	7118	A	1746	2	271	
1622	7119	A	1747	83	420	DSSNPSCQSPTQLSKANTLGWHVV CELALPDQSSGTSASRGGLE*THLL VA*ALEPIVL*SGAGLPGKL\GPVRP LG*AAVGPGAESLLPSVRSGSSLPQ RREGSLPDGPLP
1623	7120	A	1748	154	1030	SDISQAQLSCTGPPAIPGIPGTPG PDGQPGVTPGIKGEKGLPGLAGDHG EF\GEKGDGPVG\N\PGKKFGPKGP MGPKGGPGAPGTPGPKGDSGDYK ATQKIAFSATRTINVP/LLRRSQTVRF RPRCITNMNT\NYE\PRSGKFTLQGC PGLY*FNLSTPVS RGNLCVNLMRG RERAQKV\VTFCGLMAYNTFQ\VT GGHGSSAEE/GPQKEGGGGRKPPF LQATDKN\SLTGA WEGANSVFSGFL AFFQIWEGLTCGLASHPTAPPARN AHYTPNNNHMTKPN\AHNRDW
1624	7121	A	1749	3	607	FCPRGQEFGEKNLLSPRRPWVISQ RRTKATNTSLWGK\VKCGKNAGKE ETPGKGSLVVL/HPWTPRGSFEQLW QTCPSALCPSMGNPQSQGTMAKKV LTS\LRCP*STLD\DLKGHLLPKPEV NLHLLTSLHVGS*RTFKLPGEMLLV T/LFWAIPFSAKEFHPLKVAGFPQK DG*LGVGQCPCSFQIPLKPLGP*IQ\S FQG
1625	7122	A	1750	2	585	AAAAPAGGNPEQRLDYERAAALGG PDGRAWGGRSPLPPAP*AQGAPGP RWPPPRAGSPAPSPAGCGGKGKGGG

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						LVTPGRGGPRAAGREL/RAVRCPCP VRPRPPSKPALGGSLPQPEPAAAPG PSIR/PVLPPIQTGS/PWRRPKSLRPVL GTRVGRTPLPPP/PDPAGPPPLPLPG P\HPSRPPPTGPWRPARADGRV
1626	7123	A	1751	25	1295	KLCATKDLSYLAASPTAFAYLG GLFSPKLPVMAHRFPALTPEQKK ELSEIAQSIVANGKGLAADES VGT MGNRLQRIKV\ENTTEENRRQFR\EIL FLLWDSSIQPGGIGGC*FLFRR/YPL TQKGTARGKLFPGNIPSREKGD SW VGNQV*DQGRLLFCREPNKGNHH FKGLDGLFERFVQYKKGVDGFK WRAVLRADS\CPSSLAIHENANAL ARYASICQQNGLVPIVEPQVIPDGD HDLEHCQYVTEKVLAAVYKALND HHVYLEGTLLKPNMVTAGHACTK KYTPEQVGYGSP*QALHRTGPAAV PG\ICFLSGGMSEEDATLNLNAYQTF A/TSTKSPWKLSFSYG\RGLQAQCTG LPWGGKAANKGGNPRTA FMKRAH GLTCQAAQRDSMFTRVLLGAASHP SRLHHPCLYPT
1627	7124	A	1752	1	186	IFSRDGA\HRVTQDGLDLLTS*SARL SLPKCSDYSREPPRAQTPILIRHFIH NSKHEKTME
1628	7125	A	1754	74	595	RGGQGLLSTSLWGK\VNVEDAGGE TPGKGSLLVYPMPGQRFDFSG\NL SSASAIHGQTPKV\AHGKKGADFP WDDAIKHLADDLKGHLLPKPEVNLH C*QACNVGSLRTFKLPGENVAGLT VFGNPIFGKRISPLKVAGFPGQKDG* LGVGQCPCSFQ\PLKPLGP*IQ\SFQ G
1629	7126	A	1755	21	457	NPRVRGALTMELSES VQKGFQMLA DPRSFDSNAFTLLLRAAFQSLLDAQ ADEAVL\DNKNSLEILLGSGRSLPHI TDVSWRLEYQIKTNQLHRMYRPAY LVTLSVQNTDSPSYPEISSSCSMEQL QDLGGKLDASKSLGKSTQL
1630	7127	A	1756	1	455	
1631	7128	A	1757	3	468	
1632	7129	A	1758	50	895	THASDGALTMELSES VQKGFQMLA DPRSFDSNAFTLLLRAAFQSLLDAQ AD\EA VLDHP\DLKHIDP\VV LKHC\ HAAA\ATYILEAGKHRA\DKSTL\ST YL\EDCKILTEKRIELFFAREYQ\NNK \NSLEILLGKY*GRSLPSYNRVFSW ALWIIQVKDQSTFHRM\YRPA\YLG DLKV VQNTGIPPS\YPREL VFSCQPW NQL\QDL\VG ETLKDASKKPWK R AT SVVTLGKVNRSPSSRRKTQKPPLP FSWNHRLCRAGCPFSVEKNFSLNL YPFIHFGHFKNV
1633	7130	A	1759	470	737	RKSFFLAQTVLKWCCCKMSSPGKK LFPGEIWGVKGNKNKLWLPDP S IR HRFERVPSHKRPLPGWVRWLTPIPS TLGGQSAVDHLRSGVRDQPGQHGE

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						TPSVLKI*KLGRGGRQL*SQLFGRL RQENCLNTGG\RGCEPRSHCTPA WATE*NSWDYSCLPPRPANFYIFST DGVSPCWPGWSRTPDLK
1634	7131	A	1760	1	297	
1635	7132	A	1761	1	162	
1636	7133	A	1762	54	504	YTAIMSIMSNGGAVMAMKGKNC VAIAADRRFGIQAQMVTTDFQKIFP MGDRLYIGLAGLATDVQTVARLK FRLNLYELKEGRQIKPYTLMSMVA NLLYEK/RDPDHLFETISQAMLNAV DRDAVSGMGVIVHIEKDKITRTL KARMD
1637	7134	A	1763	51	748	YTAIMSIMSNGGAVMAMKGKNC VAIAADRRFGIQAARLLTTFQKIFP MGDRLYIGLGPASPLDVQTS/VAQR LQVSGNLNY*V*REGIRQITFITLM EAWLANLFVMRKRFGLLTLRPVH LPGLGPERPFKALSIC/SL*DLIRVGP MGDLNDFCGSSGNLAPNQMLRECV ESLWGGPTWVPDSTVLKTIFPRPW NAVGPWQCSGMGSSLFHIEKDKI TTRTLKARMD
1638	7135	A	1764	433	851	KPQPFILCSKYNQMILLHLRAPGHA DASTQKQQLWL*NLLTSLGQRLFN FFETESHVST*/L/QCSGMISAYCNIC LPDSSNPPTSASRVAGTAKRQHTQ LIFCIF/VVQTGFCHVGPGLGFTEAR AIHPPWV\PKVLGLQV
1639	7136	A	1765	213	617	KRFLV*KVASVLKGLHAIVVSDRD GSTLLKWARDNAPEHAF/RGPGFL \STFALATDQKQQTWDFSKNKSINIC LLTPYQGGFNFSFYLVWGEFS*A QAGSAQLQGLICSA*EKGTWFPLF* RN*GQVVEVSLI
1640	7137	A	1766	2	140	
1641	7138	A	1767	157	371	
1642	7139	A	1768	3	135	
1643	7140	A	1769	1	1431	MHKAGLLGLCARAWNSVRMASSG MTRRDPLANKVALVTASTDGIGFAI ARRLAQDGAHVVSRRKQQNVQDQ AVATLQGEGLSVTGTVCHVGKAED RERLVATAVKLHGGIDILVSNAAVN PFFGSIMDVTEEVWDKTLINVKAP ALMTKAVVPEMEKRGGSVVIVSSI AAFSPSPGFSPYNVSKTALLGLNNT LAIELAPRNIRVNC/LAPGLIKTSFSR MLGEPEDCAGIVSFLCSEDASYITG ETVVNLSVMFTGGGVCRAASWKE GGTGTPTPRESPRQREPGETSSTD QENKVWNGLPANPQRPAAEGPVRR KTNKQKGIASAKDSINIRTKGDIH TKTPSIGHQHQRPKVDKTTKMERN QSKKAETSRNQNVSSLPKEYKSSPA REQNWMEKFDLTDVSFRRSVIT NYTQLKEHVLTHCKEAKNLDKML NEWLTRMKNLEKSLNDLMELITTV

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						QELHEGYTSFNS
1644	7141	A	1770	53	582	RKETVSVSPQQSRHLIGVRSPKGLS EVALAGLIHAQGAATSVHCARAGK SVRLASSGMTRRDPLTNKVALVTA STD*ALHRLSLDLTTTQARQGLFSR SAVALAQIAGATSQGPT/CQ*GKTQT SQAPFLYWLPVDYQAAKPYGGIDIL SSKAVVNPLFEA*RVSPPEARDLTL DIIG
1645	7142	A	1771	44	1059	AMHKTGLLGLCARAWNSVRMASS GMTRRDPLANKVALVTASTDGIGF AIARRLAQDGAHVVSRRKQQNVND QAVATL/QGEGLSVTGTVCHVQKA EDRGAAWPPAVKLHGGIDILVSN AAVNPFFGSIMDVTEEVWDKTLDA NVKGPKP*MTKAVVPEMEKRGGGS VVIGLSIAAPSPSPGFSLYNVSKPAL LGLAQTLPIEL\APRNIRVNCLAPG\ LIKTSF\SRML\WMDKEKEESMKE\T LRIKKV*ASPEDCAG\IVSFLCSEDAS LHSLGKTVVVGGGTPVPASEGTGK TAQRPKVGLLSFLVLFPAIQPNWPF PTSCSTLLFHPHSNQFLPL
1646	7143	C	1772	1	174	MWIFIFNKYYQHVKSPMTSRTGKS ATCDGCGMAAHCSRCWGLSWGLG EALSYSKNVS*
1647	7144	A	1773	154	765	RAGLEELTAAVMVRLNCIVAVSQ NMGIGKNGDLPWPPLKNEFIYFQR MTTSSVEGKQNLVIMGKKTWFSI PE/RRNRPFKG*EFNLVLSRELQGNL PQGA\HFLFQKF*D\AMPLKLTEQPE LANKVDMVWIVGGSSVYKEAMN HLGHLKLFVTRIMQDFESDTFFSEID LEKYKLLPEYPGILSDVQEGKHIKY KFEVCEKDD
1648	7145	A	1774	1	676	DRPNSGRPRAALAAGSTFPVLACSS AMAPKGSSKQQSEEDLLLQDFSRN LSAKSSALFFGN\AFIVFAIPWLYW RIWHMDLFKSAVLYSVMT*LSTYL VAFAYKNVKFVLKHKVAAQKEGK DAVSK\EVTRKLFWKLDY*ERCSRE GRKD\ERILWK\NEVADYEATNIF PIFYNNTLFLVLVIVASFFILKNFQ PHSVSFSRNYILSISG\SSGLIALFTG SK
1649	7146	A	1775	99	362	
1650	7147	A	1776	3	403	
1651	7148	A	1777	184	360	
1652	7149	A	1778	1	885	EFGTRWDFSMVAFADLDLRAGSDL KALRGLVETAAHLGYSVVAINHIV DFKEKKQEIEKPAV\SELFITLPIVQ GKSRIKILTRLTIIVSDP\SHCNGFER QLLRGARLYDVVAVFAPKGQEKSLF HIA\CTHLGCGDLVCITVTEETTIFT SKRPPINVAIDRGLAFDLALIPLLSR TPTMRKVYNFSPAPPILMPNLAKGK NVNYYLGGWQERAFREIR\GPYDV

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						GKS*ACLFPGPF*K*TPRVRVSTWNCRAALLHGETRKTAFGHISTVKKPRPAS EGDEDCLPASKKAKCEG
1653	7150	A	1779	175	534	DCSLPSVCHFPPLPSPHTHPPTHPWVG /CPSGGPEGLPIT*RHQVGSCPTAPPP VPAPSRQSDCGAVHSQDENTVNALI GGFLVLLHIMCNVVALTFYATIYED LCCTCNKYIEKAHTSVW
1654	7151	A	1780	190	390	TKRGAGEGNSKVVLGLQVGCQSQR GNHQGMFTWA/CCGKDSGGACSCSL GV*CSWGQKSIRVSLWGF
1655	7152	A	1781	805	1325	ASKLEGSPCGKGGVGLGGCFPKRPE PRNHPHFVLWYLPPLPQTRLEPKPLP PQLPSVG*KGPGPSFGLSLTAGPLP LQERLVPTQLLPVGKPGPGPPACA TSSGKPKLRPLCAKSTMP*THPPT VPKPPGQEAVERNQAPMASEFPSSP SVSGDLKPWGFRSFLCQGGAWS
1656	7153	A	1782	1016	1560	KDPELQASHFPCFSYCTPPAHFASLL DFAFSDPHLLGFLSSFLERSSI/CGKT DLSKTFSLD*SFGLNFSRLRESSYRP FGVQDAID*HPPAMFFSASQTLQGP SCGVPICAFIPAVPSTFQLPMFLWVR FLSLPSFSFPNPPVSSGPSLFPHTPFL TTP/LPHG*LFPSAPPALHHATHFRT
1657	7154	C	1783	68	223	MSPSSVFFVXXXXXXXXXXXXXXX XKASFIFFPLDLXXXXFFLSFQMKSI DF*
1658	7155	A	1784	1373	1651	LSVLCHCVCVCVCV/CCD*KGLHSY LFPWTWKKIFFYLFK*NLLISSNHI*I NVKAYIVLYVN*ILKITKYMLLSTT
1659	7156	A	1785	6	140	
1660	7157	A	1786	223	397	QTPP*KSKQPFRTSS*DQVPSQP*PPI PPINNPPIPPPFGEVYYFEPILRKWV KGR
1661	7158	A	1787	2287	2854	
1662	7159	A	1788	1	610	SGRPFFFFLGGARATAQLAESWRG GQHLQSSPPPPASPGGPSSSDQRS PCSNARW/NTSIYSLVADGTC*D TALVGNKDPASIWAIPGKTFLNIT PAEVGVL/VGKDWWKLLSLNGLDT GGPRNYNLLVPGDFHWLAGWGN* TVDL\QLKSIGGSP\TFNVIVTMTAK TLGLLMGKEGIHGNFIDK*CYEMAS HLQRSQY
1663	7160	A	1789	157	610	GYSKKQLRGDRRWAIHRIRITLTSR NVKSLEK\VCA*L**RRRKKEKNLK S*KGP\VRMPTKT\LRITTKKT\PCG*/ EGSKDRWDRFPD*GFHK\RLHLTLH SSFLRFV*GRFTSFSYLRPGFEVGSS PFADALSQSIHTIDDQLKKKKKK KI
1664	7161	A	1790	1367	1582	METRWEPPPDNFIAPVTP*FCSNS D/CVLSVPDSSRLPRHFPPSHCTRKR PHLPTQQQPFKCALQEKWFF
1665	7162	A	1791	122	344	ALGPLPLFFPPSPLPVQKG*YSNQKL EGAGPGQGGFQPVFP*LGGTSNFPP

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						FRKSPSQVQAH*PGSDEDPRPL*EDPRPL
1666	7163	A	1792	656	1068	NQINFCLNGKYTYVCIDTLPYMFN IHTLKHINTSVIISLEFAI*HKGQVEL HIKITYRSN*MWLGHNQRRN/LCPQ EGEEIPNEA*IFSIIKRQSWPGTVAH ACNLITLGG*DGRIS*DQVFKTSLINI VETPSLLKK
1667	7164	A	1793	138	396	
1668	7165	A	1794	143	327	CGVQLLPDRRRESRDIIIVEL*AAVA AAGGNPDGKKGSGGWEAGQRKER KESEDPDAEPDCV
1669	7166	A	1795	23	483	KAIVLLHIICTEVISIILFNDFIQDKRP CRLFTCCSLLRASPVSSAANMP FSSTSSSTVSWLSLSSSLSSCFLSFR FGNSSCMSFSIIIPFVRPEDWKRMLL AK*GPLMALMLCALFFSSSSRLKPL FMSTTILSLKYGGGVQDVGGWQ
1670	7167	A	1796	429	1394	TISFEADHMYKT*ETD*TIFLEPYD YLLQLPAGKQVRTQT/LSQAFNHW LKVPEAKLTDYLFEDVRKLFGLMP LLNDDIEDNSKLPTWAFVVAHSIYGI PSVINSANYVYFLGLEKVLTDHPD AAKLFTRQLLELHHGQGLDIYWRD NYTCPT*EYKAMELKQKTGGLFGLS KCLKHIVSDYQEYLKPLLNTLGLFF QIRDDYANLHSKEYSENKSFCEDLT EGKFSFPTIHAIWSRPESTQVQNILR QRTENIDIKKYCVHYLEDIEGSFEYT RNTLKELEAKAYKQIDARGGEPLS LVALVKHLK*RCSKEGKWNV
1671	7168	A	1797	145	172	GGCLLESVDTSHGQSLISASLNTK HPTGMHSTCWFHVELCGKGLGSRH TLKQHQSAF*SMPA/PPAPCHIVPQE PTS*VHPCWVFCVETG
1672	7169	A	1798	197	378	VLMSVLPALGYPPRSMWLYVRGLN ADTP*PPSTTFPLALPPSSTWNQ/PS* VHPLLGVCVET
1673	7170	A	1799	32	377	SSMPPTPGPSILSSLVPIVSPFHPCPP VLYLWPAPI/Y*KLLPVPDLAHSPPS TPTLHVSHYPMVGITLTPVPLFFIPS NSLPNGGDPEPSSDQVEPVQPGLLS LPSSKSGGFCF
1674	7171	A	1800	168	224	
1675	7172	A	1801	224	527	CHQLRQELAIFTSFVILQLFSGHLDV YMQAWAQRPDKYEYDNK*FIEIKKI IQFTLISKRMK/YVGINLTR*VKDLH NENYKTLMEIEEDTSEWKDISCSW
1676	7173	A	1802	22	430	SPGCRRAESEKSGSERGVGPSYRI WVGSGKLQSKGVVLWQAGAGVIR CSAGELLSQEKGFHKVMSSVKAGT SHLHFFCDSSVTSGHVDVYVQAWA QRPDYRSHVCSGDGCTKVSEITTKN LFM*PKTTCTPKTTE
1677	7174	A	1803	386	511	
1678	7175	A	1804	362	439	
1679	7176	A	1805	776	1376	GAPWAFGGLPWVHGLAKEGVTAIV



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						AEHGLWNIGVHEGHGTLQLQHMH HYAVALRRHPFIQAQARGVLAG GGMGTRRE*VRARGQPRVHSNNCH TGQNRYSVPSEGLWT*YLL*GPK MTQDAEQAGRDGGDDGGLALVGE ALLEAHRDAIEQALPWGLRQLSLTV SQIGGHTVGPVHFPGLSHIGEEHGL RGQLSTV
1680	7177	A	1806	420	508	
1681	7178	A	1807	735	841	
1682	7179	A	1808	796	1123	IQWICHNTISAPKNYLEISPHINNKKQ F*KKI*KHFPPA*RT*SKKYLGINVQ SLRSLYLEIYK/SLIKMIKN/DT*RYN PY**FGKINIVK*LYNPM*FRFNTVPI KMPIS
1683	7180	A	1809	137	303	
1684	7181	A	1810	122	385	YPALEHILKAQAIQSRCGCDSCLP APWDHPGPTTP\SPGRRAAADPWHL SPIDGREHLR*VPVLPVTPPSPTLGH WVTDPSPGVGG
1685	7182	A	1811	77	1181	PLEKCYDLFSQNWSGFLPCFQEFQF QFKRILINRLKPDLEKSRKMGRK/R AEEYRQTFLTADV*RSPPKSRSPRE SPKKAKKLEVIIGKPGSSSF*QRIR KRERTPATRA*SQKREKARRRSRSI DRGFERMR\SDVRNRLTSPSRSDR KGDRRDRDREKENERGRRDRD YDKERGNEREKERERSERSKEQRS RGEVEEKKHREDKDDRRHRDDKR DSKKEKKHSRERSRERKHSRERSR NAGKRSRERSKEKSSKHKNESKEKS NKRSRSGSQGRDTSVEKSKKREHSP SKEKSRKRS*/ASKERSHKRDHSDS KDQSDKHDRRRSPKYRTREPRKTSI KNKDETV*KYFVKCGSH*ILLND
1686	7183	A	1812	1	585	PLKRS DGCNDGRPTRPPTRPDTTVF TSNLKQTRMVHLPVEK\SAVTAL WGQA*TWMKVGGKALGK/RCWVV LPWDPKRSFEVLWGNLSQLPDAVN GANP*R*KASMAKEKVLGCPLVNG PWL/HWTTLKGHPLPHTEVSLHCD KLHRGSLKNFRAPGATVGLCCLA HSLLAKEFNPKNLQGLPIQEKLVGW VVG
1687	7184	A	1813	505	671	QKNKVYFFETYEIYWPGTVAHAC NPSTLGS*G/GWIT*AQEFETSLANM LKPCLC
1688	7185	B	1814	277	480	GTGHFYGRTPSDTNCQEQYTHRKL CQIKSKADLVLMKNSKSLTRVIRNI LAPQDQNHQQNPLNSQFLQ*
1689	7186	A	1815	32	1386	VLLGPKAERTNSRRNYQRRDYFSA PRSITSNQSAKSSSRGVYSAYQAP DIHECCHFRSASFLLDKMATPAVPV SAPPATPTPVPAAPASAPASVPAPT PAPAAAPVPAAPASSSDPAAASAT TAAPGQTPASQAQAPQTPAPALPG PALPGPFPGGRVVRLHPVILASIVD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						\SYERRNEGACPS*SGTLFGKLVDK\           HSEV\VTN\CFSVPHNESEDEV\AVD           MEFAK\NMYETGIKKVS\PNKLILG\           WYATGHDITEHSVL\IHEYYSREAP           NPIHLTV\DTSLPGTGRMSIKA\YVST           \LMGIPLGRT/LWGVMTPLTV\KY\           AYYDTERIRRLTLIMK\TCF*PPTRVI           WTSQVDLQQEGGGIQLRNPGMPLS           TSVANMPEGCTCLGKVSADNTIRK           VGHFLMSL\VN\QVPENRKPMTFET           MLNSNINDLF\MTYLANLTQSR\IA           LNEELVNL
1690	7187	A	1816	273	748	VIQNLFNKMDVGTGQVRVVHACNP           RHFRRLRQEPRSGVQDQPDQHGET           PSLLKIQKLARR/GGVVHL*SQLLR           LKQENRLNPGGGGCSEPRSHHCTPV           *VTQ*DSVPPAPRKKKMYVVLTKK           FHIWHISFTLPNIKRSDSLRNKVT           NFSCYCSKVS
1691	7188	A	1817	1	406	LCQLETYPPISQCTASDFPGPVTAS           WAIQEAARSGQAKAGA/GSATLS/M           AYAGARFVFSLV DAMNGKEGVVE           CSFVKSQETECTYFSTPLLLGKKGIE           KNLGIGKVSSFEEKMISDAIPELKAS           IKKGEDFVKTLK
1692	7189	A	1818	1	1222	FRQRAGAGQCGRWWSHFRVTSSCA           CYVDAPPAPAMLSALARAVPSACS/           LARSFSTSA\QNNAKVAVLGASGGI           GQPLSLLLKNSPLVSRLTYDIAHTP           \GSGPQDLS\HIETKSRK*KAYLGTW           NSLPDCL\KGL*WW*VIPAGVPTKP           GMDRD\DLFTTNATIVGTLTAACAQ           HCPEAMICV\ANPVNST\ISPITSKK           VFKKAWGQHPQKKSSGVTTLNIVR           AKTFVAELKGLDPAGVNVPIITGGH           AGKTIPLISQVHAYDPVRGFECTPK           VDFPQDQL\AALTG\RIQEAAGTEVV           KAKAGA\GSATLSQCRNAGA\RFVF           SLVDANELEKERCLWECSLPLSPQE           TECTYFSTPLLLGKKGIEKKKAKT\           LGIGKSLPFEEKMISDAIPELKASI           KKGEDFVKTLK
1693	7190	C	1819	876	1124	MALGLRQRGIVSLAASITGPCPMSP           APSPHGTQVLLPTKRHPQVCLSHTC           VEMRQVTKRLSAFKVRNKPDRFY           SALLCSTE*
1694	7191	A	1821	103	483	
1695	7192	B	1822	1	798	MAFLDNPTIILAHIRQSHVTSDDTG           MCEMVLIDHDVDLEKIHPSPMPGDS           GSEIQGSNGETQGYVYAQSVDITSS           WDFGIRRRSNTESPKPEQLRNLFIG           GLSFETTNEKSRSHCEQWGTLPCDV           VMKDSNTRSGGFVFTYATVEEV           DAAMNARPHKRRKKYPLLKNTN           DKQLDLGPEKGRKHALNCHRMKP           ALFSVLCEIKEKTGGATQAFAKENN           QKAYKETYGVSHITRHDMLQIPKL           AQNEKSQVPSIRSIQRLKII*

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
1696	7193	A	1823	3	545	
1697	7194	A	1824	1	440	VYLHLHSSQDRLLPMTVVTMASAR VQDLIGLICWQYTSEGRKPKLNDN VSAYCLHIAEDDGEWTHDFTLDS NEPIHKFGFSTLALVEKYSSPGLTSK ESLFVR\INAAHGFSLIQVD\TQKVT MKEILLKAVKRRKGSQKVSGACD
1698	7195	A	1825	293	2142	GNWPTERMAFLDNPTILAHIRQSH VTSDDTGMCEMVLIDHDVDLEKIH PPSMPGDSGSEIQGSNGETQGYVYA QSVDTSSWDFGIRRRSNTAQRLE LRKERQNQIKCKNIQWK\ERNKQS AQELKSLF*KKNLSKEKPPISG\KQSI LSVRLEQCPLQLNPFNEYSKFDGK GHVGTATTKK\TDVYLPLHSSQDRLL LPMTVATMASARVQDLIGLIC*QYT SEGREPKLKDNDVSDYCLHIAEDDGE VDTDFPPLDSNEPIHKFGFSTLALVE KNSSPGLTSKESLFVRINAAHGFSLI QVDNTKVTMKDILLKAVKRRKKGFQ NVSGPQYRLEKHSEPNVPADLDSTL ESHSAREFCLVRENSRADGVFEED SQIDIATVQDMLSTLHYKSFPVSMI HRLRFTTDVQLGISGDKVEIDPVTN QKASTKFWIKQKPISIDSDLLCACDL AEEKSPS\HALF*LTYLASNHDYKHS TFESDAATANEIVLKVNYIL\ESRAS TARADYFAQKQRKLEQTVRAFSFQ KEKEIPGSIEQLAFQPQILVPVASEP ACPGPSALRSPGVLSFGGEAHPL GPLGTGAGGLFGEGVGGLRREAA GDIAMGRKFALAMGF
1699	7196	A	1826	436	917	RLSSKLLHGAYQCFKAKIENYLLSW LNRKFRISFKKEKFSKAVCLKNDIW LGTVARDCNPTVRLKWEDHLSPG I*DQPGKQ*DL/PSLQKNKKLPRHGG \HTLWSQLLGRRLWENHLSLGDQG CIEVSSRHCTRAWVTEQDPI*KQLG PQGVYHHA WVIFCFFVEMQVSLFS RLVSNSWAQVILPLQPHSVGIAVTS HCTQPYVIL
1700	7197	A	1827	46	573	SQTPMGHFTEED\KATITSLWGK\NVE DAGGE\TPGKGSLLVVPWTQ RFFD\SFGNLSSASAIHGQTPKVKAH GKKVLTFLGTMPKHL\DDLKGHL LPKPEVNCTFDKLACGILEELSSFLG KMLLG*PVFGNPIFGKRISPLEGARF FLGRKMGDLELASALVPSRLPLKPL GP
1701	7198	A	1828	1	388	
1702	7199	A	1829	75	520	TPERGSAYPRPLLCGAPPGEATVIM SDQEAKPSTEDLGDKKEGEYIKLKV IGSGF\SEIHFKVKMTTHLKKL\*ES YCQRQG\VPM\NSLRFL\EGQRIAD\ NHTSNKNWGM\EEEEVD*SFREQT GGSFQQFRIFLFFFFSLKSFFIF
1703	7200	B	1830	78	236	MSYIPGQPVTAVVQRVEIHKLRQGE NLILGFSIGGGIDQDPSQNPFSDEKT

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						DK*
1704	7201	A	1831	67	587	IRVEMSYIPGQPGTAVVQRGGEIHKLRQGENLILGFSIGGGIDQDPSQNPFS EDKTDKGIYVTRVSEGGPAEIAGLQIGDKIMQVNGWDMTMVTHDQVARKRL\TKR\SEEVVRLG*RGSRMQK\AVQQSMLFLRQPPPSCDSCPLPLCTVTPLPHSGPHLASADRWAPASEGL
1705	7202	A	1832	3	420	HSLSGTSEVINKLLVQTPMGHFTEDKATITSLWGK\VNVEDAGGETLGRLLVVYPWTQRF\DFSFGNLSSASAI\MGNPKVKAHGKKVLTFLGEMPLKHL\DDLQGAFAQA*SELALVDKPA MWD*GTSKLLGEMLLG
1706	7203	A	1833	3092	3227	ERQ/WPGTVAHACNPSTLGG*GGGAGIT*GQEFKTSANTVNPSLL
1707	7204	A	1836	3	1088	SMAAVAAESACICRWRRCSTGQFEELLRLKAKSLLVVHFWAPWAPQ\CAQMNEV\MAELAKELPQVSFVKLEAEGVPEVSEKYEISSVPTFL\FFKNSQK\NDRLGWVHMPQELTKKVQADM HLSGLLPTQALMEHL*RKILQPFGL EGNLTSWLAPLAWLFYWKGLPSK EPR\CGFSK\QMVEILHKHNIQASSF DIFS\DEEVRQGLKAYSSWPTYPQLAYGSGELIGGLDIIKELEASEELDTICPKAPKLEERLKV\TNKASVMLFMK GNKQEA\CGFSKPNSSGKYLNSTWC*NLETFRIILEDERKFGQGLKSLTP NWPNIPLSLYVKGE\LVGGLDIVKE\LRKRLGEFAAL*LRGEN
1708	7205	A	1837	3	703	VEFFSSQRAELYATPLTPAPGPNNGIPGWT\WLALPRPGNLRKGPGLSLQEVDEQPQHPLHVTYAGAAV/DDELGKVLTPQVKNRPT\SISWDGLD/SKGKLYTLVLT\DPDAPKQKDP\KYRE\WHHFLGWSTLKGQMTSATGTVLS\DYVGLGGLPKGTGLHR\YVWL\YEQ\DRPLK\CDEPHPSATRS\GDHRRGKIQRWASLPVKK**SSRAPGGWAP CYPQPEVGMNQCAPKL
1709	7206	A	1838	717	1390	ASTTSSVHCARTYMGSVYNTPARVRLRVGWRAADQLLLAASSTSAIVSTRALECAKMQNAEAADATLVFIGYVVPALATLYAAGATLPRSAGKDTTPGTGDHGPAGALGTQAAGGHRVHAVWALDATLSDPAGAHGHHLAR EARGCTLPGGYCTL*RISPNSWPSPAL*HHFSTAT*TRASPASSNG**KSC PAG/APALLPGPHGGAAGAGVGGP ALLGET
1710	7207	A	1839	1	310	RTSPHSPRNILL\EPENADSLMLVDFEYSSYNRGRFDIGNHFCEWVYDYTHEEWPFYKARPTDYPTQEQLHFIRHYLA EAKKGETLSQEEQRKLEEDLLCM
1711	7208	A	1840	3	375	HYLA EAKKGETLSQEEQRKLEEDL LEMYSLKDEMGNLRKLLSTSPV

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						VFCHNDIHSSS*LHPPTPWISPGASR AGPWREEQRAEGPGDWAEPPESET VQETGLFLSLSRSPWLAGQSPVLCM
1712	7209	A	1841	94	429	
1713	7210	B	1842	96	979	XVGEEPREVLLRLYGAILQGVDLSV LESVMFAILAERSLGPQLYGVFPEG RLEQYIPVRAQSYPLLKAPPPNPPT PVPNVCLHIPHPNPITTLIASWVQSR PLKTQELREPVLSAAIATKMAQFHG MEMPFKEPHWLFGTMER*
1714	7211	A	1843	5	1463	PEKPRPAGRGAERGRKEPSPSEGSG AHPGLGPGRARAMAAEATAVAGS GAVGRCLAKNGLQSKCPDTPKR RRASSLSRDAERRAYQWCREYLGG AWRRVQTEELKVYPVSGGLSNLLF RCSLPDHLPSVGEEPREVLLRLYGAI LQGLDSLVLLESVMFAILAERSLGPQ LYGVFPEGRLEQY/IPTSWVQSRPLK TQELREPVLS/SQAIATKMAQFHGM EMPFTKEPHWLFGTMSRTLKQIQD RPPTGLPEMKLRGNVRLKDEMGN LRKLESTPSPVVFCHNDIQEGNILL LSEPNADSLMLVDFEYSSYNRGR FDVGNHFCEWVVDLYSSEE/WPFH KKAGPPSPSPHQRRQVHFIRQLPLA RGK*KVESLPPRRSQKKNWKEDLL VRKSSRVMFVQSHFLWGLWSILQ\ ASMSTNEFGYLDLCPSLRFQFLLPS KKGQA*PSVHSCILDSTLPLLGFLLE PPGQGPWRGGTTSRRPWRLG
1715	7212	A	1844	143	762	CRQERAVAPARRAMERIPSAQPPTV CLPKAPGLEHGDLPGMYPALMYQ MYKSRRGLKRSEDSKETYELPHRLI EKKRRDRINECIAQLKDLLPEHLKL TTLGHLEKAVVLELTLKHVKALTN LIDQQQLFKMHYA*LLIVF*L/SSFPV FILVLSRCLYL*SCYKYILYKIKKE NVSDVYLYNYLIHTVRKNECIPVFE EKNNFFFL
1716	7213	A	1845	203	1507	CRQERAVAPARRAMERIPSAQPPPA CLPKAPGLEHGDLPGMYPAHMYQ VYKSRRGIKRSEDSKETYKLPHRLIE KK\RRDRITNECIAQLKDLLPEHLKL TTLGHLEKAVVVFELTFEH/V*KALT NLNLSSSRQIIAL\QSGLQAGELSG RNVETGQEMFCSGFQTCAREVLQY LA\KHENTRDLKVFASTHL\HRV VSELL\QGGTSRKPSDPASKVMDFR EKPSSPAKGSE\GPRKNCVPVIQRTF AHSSGEQSGSDTDTDSGYGGESEK GDLRSEQPCFKSDHGRRFTMGERIG AIKQEESEPPTKKNRMQLWDD\EGP FQLASDLNQLPPFGPTPQHQPFFCL PFYLIPPSS/ATAYLPMLEKC\WYPTS VPVLYPGLNASAAALSSFMNPDKIS APLLMPQRLPSPLPAHPSVDSSVLL QALKPIPLNLETKD
1717	7214	A	1846	628	1061	AHRKSLYLCEACFPRSRASQETSGL

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						KEENWRLGRKTSKCRPGLSKKLGC ERKDRDCSG/CRKDEQQGPWEAPQ AARHSQKSRNARGRPFLEGGPGTE NR*QSFPKNSREQGFNDPVGPQSV EPLEQPLFPWEWQWPAALQDREL
1718	7215	A	1848	88	953	FQAPQLCYDSAFMISSVPSHILRV CFPCFHAHLRVCFPCFHAHLVCVE FPCFHAHLVCVEFPCFHAHLVCVE PCFHAHLRVASVNFHFHAHLVCVE FPCFHAHLRVCFPCFHAHLVSVN FCFHIHLVCVEFSCFHAHLRVCFPC FHAHLVCVANFRVFTPTCASVNFV FTPTVCVEFPCFHAHLRVASVCFP CFHAHLQVYEFPCFHAHLRVCFPC FHAHLRVCFPCFHAHLVCVEFPCF HAHLVCVEFPCFHAHLVCVEFPCF AHLRVASVNFHFHAHLVCVEFPCF HAHLRVCFPCFHAHLVSVNFCFH IHLVCVEFSCFHAHLRVCFPCFHA HLCVAN/CPCFHTHLCVCFPCFHT HLCL*ISVFSRPPASVCECL/CN/CPC FHAHLQ/CL*ISVFSCPPAGL*ISVFS CPPACL*ISVFSCPPVCL*ISVFSCPP ACVCEFLCFHAHLVCDFPCFHAH QSATVLV
1719	7216	A	1849	1	254	
1720	7217	A	1850	3	308	
1721	7218	A	1851	1	380	IPPLIGNFGPRGRIRHERPQKRDD RREPSSFGRKRRQ*DGTLIC/RRCGS KAIYHLQKSTCGKCGYPAKRKRKY NWSAKAKRRNTTGTGRMRHLKIV YRRFRAWDFREGTTPKPK*GSLLQH SSSS
1722	7219	A	1852	41	544	APSPRRPWGHFTEEDKATITSLWG K\VNVE\ DAGGE\TPGKGSLLVYP\W TQRFDSFGNLSSAF\AHGQTPKV KAHGK\KVL\SLGDAIK\HLDDLKG TFAQA*VNLHL*QSCNVDP\ENFQA PGEMLLVTR/VLAIHF\GK\FTPGGC KASWAEDG*LAVGQWPCSSRYH
1723	7220	A	1853	145	705	SWRNRTVSNNGSAVSASSVHLCAE CKALCGERILTDGSDVSRTIAAGG CNGTVKYL*QEVLTAPL\HDGP SHVGIPRSCPKPLDKRQAHLVCLAS \NCDEPTMYVKLVEAL\CAEHQNP *LRVD\DNKKLG\EWG*GLLLKFDR GGGKPRKSWLG\CSCFS*FKDY\GK ESQAKDVIV\EFKCKK
1724	7221	A	1854	110	776	SLASGPYL\THQQKVLGLYKRALRH LE\SWCVQRDKYRYFACLMRARF EEHKK*KRIWAKATQLALKEARGKN FWYPVKHPKSQYILPLTSLGGHPP Y*EDHD/CAYKVPRIGCL\DDWHPS E\KAMYPDYFCQRREQWKENLRR GKAWGTEGLSSLQE\ETP\PGGPL TESFAPWPEKEGD\LPPLW\WYIVT RPRERPMLEPRLSCLQVKYVT EHGTCP

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1725	7222	A	1855	1	858	
1726	7223	A	1856	165	856	PVSYHPRMCTGGCARCLGG\TLISL AFFGFL\ANILLFFPG\GKVIDDNDHL \SQEIWFFGGILGKRCL**SFPALVF LGA*RNNDCCG\CCGNEGCGKRFA\ MFTSTIFAVGWILGELGYSFIISAISI NKGPNPSMAKK\TWGLPPSNDGD/ YILNDEGLNGTKCAREPLQCGFPGN LDPLSSILLGRREGIQMV\LCANQV\ VNGPPWGTLCCGGTCQCCGCCGG\D GPVLNLRA
1727	7224	A	1857	163	1322	PGPYCGPVATMSLHGRRKKEYKYE APWTVYAMNWSVRPDKRFRWALG SFME\EHNNNEG YLDGLDEERS*V\IS KNILDRPYPTNKVMWIPDTKGVYP DLLATSGDYLRVWRVGETETRLEC LLNNNKN\SDFCAPLTSFDWNEVDP YLLGTSSIDTTCTIWGLETGQVLGR LNL\VSGHVKTQLIAHDK\EVYDIAF SRAGGGRDMF\ASVGADGSVRMFD LRHLEHSTIIYEDPQHHP LLRLCWT KQDPNYLATMAM\DGMEV VILDV RVPCTPVARLNNHRACV\NGHLLW\ APHSS\CH\CTAAG*PPGFSSWD\Q QMPRA\IEDP\LAYTAE\GEINN\Q\ WA\SNSAPNWESPIC\YNNCPWRY ECSVGGAVPHEAGAFVFPASAPPPK
1728	7225	A	1858	1	420	REDRIQLWKPPYTDENKKVGLALK DRKNLLETRLHITGRELRSKIAETFG LQENYIKIVINKKQLQLGKTL EEQG VAHNVKAMVLELKQSEEDARKNF QLEEEEQNEAKLKEKQIQR TYRGL* ILAKRAAETVVDPEMTP
1729	7226	C	1859	28	156	MMYRLMSILTRHVSSLKSYILIHQK WTICCSWGLLPKPGLV*
1730	7227	A	1860	1	315	
1731	7228	A	1861	1	119	
1732	7229	A	1862	1	1477	
1733	7230	A	1863	3	1866	PLQSGHSAGRGGSGVAQGW HKKK YLQAKM\TKFLREERQLWKPPYTD ENKKVGLALKDLAKQYSDRLECCE NEVEKVIEEIRCKAIERGTGNDNYR TTGIATIEVFLPRLKK\DRKNLLET RLHITGRELRSKIAETFG LQENYIKI VINKKQLQLGKTL EEQGV AHN VKA MVLELKQSEEDARKNFQLEEEEQN EAKLKEKQIQR TKRGLEILAKRAAE TVVDPEMTPYLDIANQTGRSIRIPPS ERKALMLAMGYHEKGRAFLKRKE YGIALPCLLDADKYFCECCRELLDT VDNYAVLQLDIVWCYFRLEQLECL DDAEKKLNLAQKCFKNCYGENHQ RLVHIKGNCGKEKVLFLRLYLLQGI RNYHSGNDVEAYEYLN RVH VSSLKS YILIHQKWTICCSWGLLPKRLGL RACDGNVDHAATHITNRREELAQIR KEEKEKKRRRL ENIRFLKGMGYST HAGQQILLSNPQMWWLND SNPET

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						DNRQESS\SQENIDRLVYMGFDALV VAEPALRVFRGNVQLAAQTLAHNG GSLPPELPLSPEDSLSPATSPSDSAG TSSASTDEDMETEAVNEILEDIPEHE EDYLDSTLEDEEIIIAEYLSYVENRK SATKKN
1734	7231	A	1864	1	727	MVVWDADTQQVIPNGIQLAGLDKS HSGFALAPPTTLFSGGGGGGAKAT AAAGAGLASPGMKTNGGRCRIRAL CWSRREWRGAGEDTAAECPRPQPQ QHCLAPRFPVRLGTSPQGWSGRG AGDLAKQYSDRLECCENEVEKVIEE IRCKAIERGTGNDNYRTTGATIEVF LPPRLKKDRKNLLETRLHITGRELR SKIAETFGLQENYIKIVINKKQLQLG KTLEEQGVAHNVKA\MVLELKQSE EDARKNFQL\QEEEQNEAKLIEERL QRTKRGL\EILAKRAA\EPVVVPEMT PYLDIANQTGRSIRIPPSEKALMLA MGYHEKGRAFLKRKEYGIALPCLL\ DADKYFCECCRELLD TVDNYAVLQ LDIVWCYFRLEQLECLDDAEKKLN LAQKCFKNCYGENHQRLVHIKGNC GKEKVLFLRLYLLQGIRNYHSGND VEAYEYLN\RHVSSLKSYLIHQKW TICCSWGLLPRKHRLGLRACDGNV DHAA THITNRREELAQIRKEEKEKK RRLENIRFLKGMGYSTHAAQQVL HAASGNLDEALKILLSNPQMWWLN DSNPETDNRQESPSQENIDRLVYMG FDALVA\EAALRVFRGKVPVAAQT PAYNGGSL\PFPELPLS\AEDSLSPAT \SPSDSAGTSSA\STDEDMETEAVNE ILEDIPEHEEDYLDSTLEDEEIIIAEY LSYVENRKSSN*RCRIRALCWSRRE WRGAGEDTAAECPRPQPQHQCLAP RFPVRLGTSPQGWSGRGAGDLAK QYSDRLECCENEVEKVIEEIRCKAIE RGTGNDNYRTTGATIEVFLLPRLK KDRKNLLETRLHITGRELRSKIAETF GLQENYIKIVINKKQLQLGKTLEEQ GVAHNVKADGCLN
1735	7232	A	1865	1	513	PRVRNLSREWLCDRHLREKMFSSV AHLARANPFDTPHLQLVHDGLGD LRSSSPGPTGQPRRPRNLAAA AVEE QYSCDYGSGRFFILCGLGGIISCGTT HTALVPLDLVKCRMKVDPQKYK GIFNG\FSVTLKEDGVRGLAKGWAP TFL\GYSMQGLLQVLAFYEVFKVLY
1736	7233	A	1866	2	1296	ALCEPQPFQSGCVAILGRKMFSS VAHLARANPFNTPHLQLVHDGLGD LRSSSPGPTGKPRRPSQ/HMAAAPV EEQYSCDYGSGRFFILCGLGGIISCG TTHTALVPLDLVK\CRMQVDPQKY KGIFNGFSVTLKEDGVRGLAKGW APTFLGYSMQGLCKFGFYEVFKSL\ YSNMLGE\ENTYL*RTSLYLAASAS\ AEFFADIALAPMEA AKVRIQTQPIG



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						YANT*EGISFPKCIKEEGLTSILQGG LLPLWMRQIPYTMN*SSPCLERTVÆ A\LYKFV\VPK\PRRE*FKRQSRLVVT IW*QVTIARVFCANCFSPLEFLG*P VLD*GKKVSQCFLWVLQRDLGFK\ GV\WKGLFA\RII\MIGTLT\ALQWFI YYSVKGYFR\LPR\PPP\EMQES\LK KKLGVNSVVRIKANCGLNLLVDPV FEESAKGTFIYLTV
1737	7234	A	1867	127	433	RPLESWIGLVRCNICRSPIAEAVFRK LVTQDNISKNNWRVDSAATSGYEIG NPPDYRGQSCMKRHGIPMSHVARQ DLNRKSNRVKTCKAKIELLGSYDP QKQL
1738	7235	A	1868	2	535	
1739	7236	A	1869	551	1299	PADPPRPSYYRHRTPPQAHWSRLRR SRLRRRGSHTRCPVGVGAGLRRRA GARLAVRLRASACGTPRCLGASAR GKMAEQATKSVLFVCLGNICRSPIA EAVFRKLVTQDNISKNNWEGRQRG NFRWVIDSGAVSDWNVGRSPDPRA VSLCRNHGIHTAHKARQITKEVFP TFDYILCMDESNLARDLNRKSNRVK TCKS*KFELPWEL*SPQKQLIED\PY YGE*LWTLETVYQQ\CVR\CCRAFL\ EKAH
1740	7237	A	1870	85	563	SSFLDIVHVCNTPNVKKMVS GSSHK VIEQDLSIGDHPVTPVQSVYCKRS PKIPKIFVKVSKTNSSETQIYLGWQV KIGFPNF*NPVAGILDRTKYRIFP*AP GIHKLKGYPREI*ASYV*KSPSTSMS TAALFPIAKPRAGP*MPTKGSWVK\ KIWYGQK
1741	7238	C	1871	604	804	MKRLRHLRXINNLAKITQPLSKTAL NLSPTQGGSKSRAILEFQLSRPGVPN PTLNWPSLNPFREPE*
1742	7239	A	1872	64	73	AFL*RWGSPPCCPRAGLK/PP*P/PSI CPPRPPKAGITRREPPGQAYFLII*F PSI*L
1743	7240	A	1873	47	225	NSHHVRGRPRCADSSSPSGDRGQPE AQPADSSAPEHAQEPGRAAVKRP DL*SHMTRRP
1744	7241	C	1874	101	232	MTMITPSSKLTLTGKNKSWSSSTAVA AALELVDPGCRNSARGF*
1745	7242	A	1875	66	723	AILHLLSSEGLWSSDQHRLVGVDSD PPQGSLLCCHFSAMATSEQSICQARA SVMVYDDTSKKWVPIKPG\QQGFSR INIIYHNTASNTFRVGVKQDQQV VINYSIVKGMKYNQATPPFPQWRD ARQVYGLNFASKEEATTFSNAMLF ALNIMNSQEGGPSSQRQVQNGPSPD EMDIQRRQVMEQHQQQRQEFLEERR TSATGPILPPGHPSSAASAPVSCSGP SPPPPPPVPPPTGA\TPPPPPPL\PAG GAQGGSHDES/SPCSGLAACH*LGPS LRRVPNGPEDASGGSSPSGTSKSDA NRASSGGGGGLMEEMNKLLAKR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RKAASQSDKPAEKKEDSQMEDPS TSPSPGTRAASQPPNSSK\AGRKPW DRNNPLRNPLSSNLVRNPLLAKGPR KLRAPFSQQPHSRMKPAGS\VSDMA \LDAFDLD\RMKQEI*KEVVRELHK GERKEIID\AIRQEA*SGISRKKNLGH RAHPPTRTSFICSQRPRLM
1746	7243	A	1876	1	668	GERGVARHDRPRGTLREYKVVGRG LTPPK\CHTPPL\YR\MRIFAP*SMSSL SPRF\WYFVSQLKKDEESLQWRFSY CAQVFEKSP\LRVK\NFGIWLRYDS RSG\THNMYREY\RDLDHPQAPVHP SCLTRDNGVAPAPAA\HEAHFHFRFI ERLEEIAGQQDCRRPGCSKQFPRIS RFKFPAPPGSLRRQDKPRF\TTKRP KTFLKVQGPSSGVCQNKQTQETPR
1747	7244	A	1877	1	1059	
1748	7245	A	1878	87	260	
1749	7246	A	1879	1	1254	
1750	7247	A	1880	160	615	PSLNITYVTSPLENFSARYRNHSND LTCVHTELQNKTKLTVLEGDILDEP FLKRACQ\DVSV\IHTACIIDVFGVIT HRESIMNVNVKGRVAVGGDKARW GNEDQKEGQEGKRSLSIEHLLCSGP SDFADHYQLGELKAAIFSFIDEKTRT EQ
1751	7248	A	1881	53	1338	CPLQGHPRVTLESDDLPSIFCFLVSD SCYFGLATMGWSCLVTGAGGLLGQ RIVRL\VEEKELKEIRALDKAFRPEL REEFSKLQ\NK\TKLTVLEGDILDEPF LKESLARDRLRSIIHTACFHLMSFGV \THREFF\MNVQC*KVPSSC*EACVQ ASVPVFIYTSSIEVAGPNSYKEIIQNG HEEPELNTWPAPYPRSKKLA\KKA VLAANGWNLK\NGGALYTCALRPM YIYGEGSRFLSVSINEALNNNGILSS VGKFST\VNPPVY\GNVAVGHILAL RALQDPKKAPSIRGQFYISDDTPH QSYDNLNYTLASKE\FGPPPLDSRWIS FPLSLMYWIGFLLGNR*GFLL\ARPIY TYRPPFNRISSHCSN*ALFHLLFIKE GFSEILGVLRPLLTAGGGKAKAGKR VGSWWVVPFVDPQAQRNLEVPRIQ
1752	7249	A	1882	3	575	HSLFGTSEVINKLLVPDA\MGHFTTE D\KATITSLWGK\VNVE\DAGGE\TP GKGSLLVVP\WTQRF\FD\SFGNLSS ASAI\MGKPPKSKAHG\KKVLTFLGT MPTKHLE*FSRGTFCPSLK*TCTC*Q ACMWDPGGTFKLPGENVAGLTVFG QSHFRQKNFTPEGARFFLGRKMGD LELASALVPSRLPLKPLGP
1753	7250	A	1883	1	960	GRPAPEDGGPLSLPNAAMARGPKK HLKRVAAPKHWM\LDKLTGVFAPR PSTGPHKLARECLPFIFLRNRLKYA LTSDEVKKICMQRFIKNDGQVRITD ITYP\AGFMDV\ISIDKDGREFSVL/Y LIDTQGVRFCL*HRITP*GRAKVQSC AKMRKILLWAPKGIPSSWVTHDAR

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						NHPATPDPPSSKVN*YHFRDLLETG KDYLISSKFDTW*PCVMVTGGAN LGRNWVLITN\REHPGIF*PLVHVK \DANGNKLLATSDFSNIFWLLGKGN KPWISL\PRGKGIPPHHLEERDKRL AAKQSSWVKWGPWVTWSDLLVP
1754	7251	A	1884	1	1218	FFQNSARGAGAGWQLPWTRFVWT SGLLEINE\TLVIQQRGVRIYDGEEKI KFDAGTLLLSTHRLIWRDQKNHEC CMAILLSQ\VFIEEQ\AAGIGSAKI VVHL\HPAPPNKEPG\FQSSKNSYI KLSFKEHGQIEFYRRLSEMTQRRW ENMPVSQLQTNRGPGQGRIRAVGI VGTERKLEEKRKETDKNISEAFEDL SKLMIKAKEMVELSKSIANKIKDKQ GDITEDETIRFKSYL\LSMGIANPVT RETYGSGTQYHMQLAQLAWNIA RVPLEERGGIMSLTEVYCLVNRARG MELLSPEDLVNACKMLEALKPLR LRVFDSGVMVIELQSHKEEMVAS ALETVSEMGLTS*EFAKLVGMSVL LAKERLLLAEKMGHLCRDDSDVEGL RFYPNLFMTQS
1755	7252	C	1885	179	361	MPKVCFVHNFLKTSSERDLFALMN TVGKKHSIMSEKGRSKKFLHLIDSK KNEDPHLDGTL*
1756	7253	A	1886	2	913	RRLLFGWARSGAVSLGSAGVSSS GFLTAPHSRRLTAAAAAAGGAWRF EAERHRGWGAEEEEQPEGGA\PCPG TERPCAMAYAYLFKYIIIGDTGGGR\ SCLLLQFTDKRFQPSAMTLTNGVEF GARMITIDGKQIKLQIWD\TAGQES\ FRSITR\SY\YRGAAGALLVYDITR\ DTSTHLTTWLEDA\ROHSHFQHGS LCLLGNKSDLAESRKE/VSKKRKEGE SFLQPRNHGLHLPWKTSCKNCFPM* KEAFINTSKRNFIEKIQEGVFDINNE A\NGIKIGP\QHAATNATHAG\NQGG QQAGGGCC
1757	7254	A	1893	138	426	FIHSHCCIVFRLFIHFSLHPKVIHSPIN SLLRIFQF*AIMNSTV*NILIHVFW*V YTFPF\GINPKKGIARL*GVYIFSFSIY CQTVFQSDCKKAPF
1758	7255	A	1894	45	1057	FLVFLVETGFHHVAQAVLELLASSD PPALAPPKCWDYRCELLRLAEFCFL RTEFWYLLFFFFWRRSLALSPRLEC SGANL\THCNLR/LPGFKQFSCLSLSS SWDYRCMPHLATFFVF/SVETGFH RVAQASLELLSSGSLPALA\FPKC\W DYRAKATV/WSPGVSSFILGL*TS* FHSLEPYLHAWKTTSHLPTKEALT W/VSH\TAKTKHLWILVSILMEF*VA LIS/SFFLGPGGK*T*VTAPQCPSLGQ DTLS*FLHAACTRSVPYPGLA/CGPS LWLTRVLLLPTPP*QQHNP/DTLEKT SFPGPHWIL*/TPQPSLSETPAPKVPP FPAFGSIPTHEEPGLP
1759	7256	A	1895	2	289	

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1760	7257	A	1896	1	397	
1761	7258	A	1897	1	410	STMISPVLILFSSFLCHVAIAGRTCPK PDDLFPSTVVPLKTFYEPGEEITYSC KPGYVSRGGM\RK FICPLTGLWPIN TLKCTPRVCPFAGNLRKMGA VRLIT DFLNYSPTRF SFSLLTWGFILEWAL DS\AKCIEGG
1762	7259	A	1898	19	1215	CQCDSSTMIFSRCSL FSSFLCHVAI AGRTCPKPDDLFPSTVVPLKTFYEP G\EEITYSCKPGYVSRGGIEESLSCPL VTGTVGPFNTSGNVTPRVCPFAGIFR KMGGRTLITTF*NYPNTDPVFSLLTL GF*FWNGALDFWPSCTGGKGKWS P\ELPGLVAPI\CPP\PSIP/TGFATLH VLLRPFR LGNNSPPIGDTAVFECLA HNMMAMFG\NDTIT\CTTHGKLDLNY PECRGSKMPPFP HQDPDNGIW* TYP CQNPNTL FTRVKAPHLGLPHDGIFS GMGPRKE\EC*PQTWGKPGSWPLA PSW*KPSLVKGTVPVKKRPTVV/YPQ GERVKDSREKFKEWECLHG**KFLS FCKNKEKKCSYTEDAQCIDGTIEVP KCFK\EHSSLAFWKT\ DAS\DVKPC
1763	7260	A	1899	58	446	
1764	7261	A	1900	1	954	MGEVSGTSDCTDDQCRQVKKALEG GKAARGHR SKIKIRFFRPGGLGPGP AITAVAGMPRVYIGRLSYQAREHA VERLLNGHAKILEVDLKNYG GFVE FDDL RDADDAVYELNGKDL CGERV IVEHARGPRRDGSYGSGRSGYGYR RSGRDKYGPPTRTEDRLIVENLTSR CSWQDLKD YMRQAGEVTYADAHK GRQKMGVIEFVSYS DMKRALEKL DGTEVNGRKIRLVEDKPGSRRRRSY SRSR\SHSRSRSRHSRKSRSRSGSS KSSH SKSRSRSGSRSRSKSRSR SQ SRSRSKKEKSRSPSKDKS\RSRSHSA\ GKSRSKSKDQAE\EFQNNNDNV\GK PKSRSPSRHKS KSKSRSRSQERRVEE GRKRGSF*QGQ/EAQEKSLRQSRSR\ SRSKAGSR*PVD RSRSKSKDKRKS KRSREESRSR SRSRSKSERSRKRGS KRDSKAS\SC KKKKKEDTDRSQSRS PSRSV\SKEREHA/RSLESSQREGRG ESENAGTNQEDPGPGPRSN\SKSKP NLPIRMHR SKIKSQASKTPISGPMSR SR\SASRSP\SRSRSKSRSRSQSRSR KKEKSRSPSKDKSLQPQP
1765	7262	A	1901	3	180	
1766	7263	A	1902	227	440	GMHNV CYVAVNE*FCGFIIR*SLAE RRQIS*EFQLFKFTLCLELILARRAC RESMA\$PVAGSWSHFPEREF
1767	7264	A	1903	2	438	HEELDTSE RKIEFDSASGTYTLYLN GDAHFEEPQSLWNVADLVHQSPPE EKAPLDLSCPQNLF\TPK\QEIQWIRI GA\NV\NFTFAP\STIIFHLGHA\AM LGLMYVYWTQLNMF\QTLKYLA IL GSVTFLAGNRMLAQQA VKRTAH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
1768	7265	A	1904	1	1660	
1769	7266	A	1905	156	2369	PVLKTHPGPQSLPRVPGVPCGGLLE PLSRAEVSPRFGRLRRDLLGGMAPP SSTVFLALTHASTWALTPHYLTK HDVERLKASLDRPFTNLESAFYISV GLSSLGAQVPDAKKACTYIRSNLDP SNVDSLIFYAAQAISQGLSGCEISISN ETKDLLLAIVSEVDSSVYPRSYHAS WQL*SGLLGLSLWAVPKESTQVAL NWL VFKQKQETVLAATVQALQTAS HLSQQADLR SIVEEIEDLVARLDEL GGLYLQ\FEEGLETTAL\FVAATYKA \LMDHVGT\PSIKE\DVQIQLMNAI F\SKKNFES\LSEAFSVAASGAAVLS HNRYHVPVVVVPEGSASDTHEQAI LRLQVTNVLSQLTQATVKLEHAK SVASRATVLQKTSFTPVGIVFELNF MNVKFSGG*CDF\LVEVEGDNRYSIS NTVELRVQDPPEVGITNVDLSTV DKDQSIAP\QTRVTYPAAKAGTFH SAGQATRNFGLVLSSW*DVNTGAE LTPHQTFVRLHNQKTGPGSGCLFAE PGQQGTCYKFELDTSERKGLNLTSR SGTYTLYLIIG*CQL*RTQILWKCGL MWVVKFP*GKEASFDCLCSQEPFSL PKQGNFRHLFPGRP*GRRAPPPWCP NTFTAPESFFGPLL/LCFLRLLWIRD WVPKCLPTFTFCFLSTIIFHPWDM AYAGTSMYVY*TQAQPCSQTLEVP WPILGQCDRFLAGQSGMLAPARQV KRIAAEQSSRLAKYRTLRTAH
1770	7267	A	1906	37	404	PQLSRCRSECMYVNPTVVM TSMGQ ATWSDPHKAKTMLNRIPLGKFAGE SGGSPASVVPAPVPCALGRGGRER WAAASFLYAPDPRPAH\VEHVVN AILFLLSDRSGMTTGSTLPVEGGFW AC
1771	7268	A	1907	271	1086	YTQCPGIEPVCVDLGDWEATERAL GSVGPVDLLVNNAAVALLQPFLEV TKEAFDR*ACEGGGTSGRGCPGGRS SPNL*PGSVPRPLDPLRVNLRAVIQV SQIVARGLI\ARGVPTGPS*NVSSQC FPAGQ*TNHVVLLPTKGVPLDMLD QG*WAL\ELGPHKLSRCRSGVNAIV NPHSGG*RSMGPGPPWSDPHK\AKI MLNRIPLGKFAGESEVEHVVN\IL FLLSDRSGMTTGSTLPVEGGFWAW LSSLHTPQAPWACFILTPNPSNKT
1772	7269	A	1908	2	305	ARESGSLVAPRSRPPWEHGLPGEHS *DAPRPHKSPTLPWLPHLHLSKEAL DTHQRSQHE\ECMPYKFTPTSEKR PQLMLPLPEQQCEQLCRFGSTPVTW A
1773	7270	A	1909	2	529	GTVAACGACYWLLGLMAVRASFE NNCEIGCFAKLTNTYCLVAIGGSEN FYSVFEGELSDTIPVVHASIAGCRIIG RMCVG\TEEILADV LKVEVFRQTV DQVLVGSYCVFSNQGLVHPKTSIE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DQDELSSLLQVPLVAGTVNRGSEVI AAGMVVNDWCAFCGLDTTSTELSV VE
1774	7271	A	1910	18	889	GVQGTVAACGACYWLLGLMAVRA SFENNAEIGCFAKLNTYCLVAIGG SENFYSVFEGELSDTIPVVHASTAG CR\IGRMCVGNRHGLL\VPNNTTD Q\EL\QHISATGLPRHSGRFRAGWKE RFLSLWGNFFNHLAIDYVGLGSNQ D\LDKGRQEEISGQMLFKGWEVFRQ TV\ADQVLVES\YCVFSNPGRAWVP SPRPFQ*RPRNELSSISFKVPLVAGT C*TKGSEVICLLGMGGEMNWCA\FC GPGTPNPAQSCQVVEECLOQS*NEAP ALAPIANRACGNSL\IDSLT
1775	7272	A	1911	132	440	
1776	7273	A	1912	149	389	FSWV*REIFSFLISLIFIYETFSKLIKIF QDHPLQKTYNYNVLMVPKPQGGLP NTALLSLVLMAGTFFFAMMLRKFK NSS
1777	7274	A	1913	3	153	
1778	7275	A	1914	94	593	LVVFSSPSQSWERTECLGFLQIFQD HPLQKTYNYNVLMVPKPQGGLPNT ALLSLVLMAGTFFFAMMLRKFKNS SYFPGKLRRVIGDFGVPIILIMVLV DFFIQDTYTQKLSVPDGFKVSNSA RGWVNHPLGLRSEFPIWMMFASAL PALLVFILIFLESQITT
1779	7276	A	1915	115	3015	TTGHSGPRHGAAGGCSLASAVLP PGGSGDLVLD SYLRWG WKSPSQPS LSGHFPQDDYEDMMEENLEQEEYE DPDIPESQMEEPAAHDTEATATDYH TTSHPGTHKVYVELQELVID\ERIPD LQWMEAAPLR\QLDENLGENGAW GRPHLSHLTFWSLLELRRVFTKGT LLDLQETSLAGVANQLLDRFIFEDQI RPQDREELLRALLKHSHAGELEAL GGVKPAVLTRSGDPSQPLLPQHSSL ETQLFCEQDGGTEGHSPSGILEKSP PDSEATLVLVGRADFLEQPVLG FVR LQEA AELEAVELPPIRFLFVLLGPE APHIDYTQLGRAAAATLMSEVFRID AYMAQSRGELLHSLEGFLDCSLVLP PTDAPSEQALLSLVPVQRELLRRRY QSSPAKPDSSFYKGLDLNGGPDDPL QQTGQLFGGLVRDIRRRYPYLSDI TDAFSPQVLA AVIFYFAALSPAITF GGLLGEKTRNQMGVSELLISTAVQ GILFALLGAQPLL VVGFSGPLLVFEE AFFSFCETNGL\EYIVGRVWIGFWLI LLVVLVVALRGVASLVRFISRYTQ EIFSFLISLIFIYETFSKLIKIFQDHPL QKTYNYNVLMVPKPQGGLPNTALL SLVLMAGTFFFAMMLRKFKNSSYF PGKLRRVIGDFGVPIILIMVLVDFF IQDTYTQKTSQVPDGFKVSNSARG WVIHPLGLRSEFPIWMMFASALPC LLVFILIFLESQITTLIVSKPERKMKV

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						GSGFHLDLLL VVGMMGGV AALFGMP WLSATT VRSVTHANAL TVMGKAST PGAA\AQIQEVK\EQRISGLLVAVLV GLSILMEPILSRIPLAVLFGIFLYMGV TSLSGIQLFDRILLLFKPPKYHPDVP YVKRVKTWRMHLFTGIQIICLAVL WVVKSTPASLALPFVLITVPLRRV LLPLIFRNVELQCLDADDAKATFDE EEGRDEYDEVAMPV
1780	7277	C	1916	20	202	MAAIKYLGISAILYKYKCPRGQGN QPEELGTGSILCGNFSLGMLFPVQM YTVKKA YRAV*
1781	7278	A	1917	1	493	
1782	7279	A	1918	214	612	
1783	7280	A	1919	287	847	SDRPTMAPGVARGPTPYWRLRLG GAALLLLIPVAAAQEPPGAACSQN TNKTCEECLKNVSLWCNTNKACL DYPDTSVLPPASLCKLSSARWVC WVNFDAIITMSVVG GTLLLGIA\NC CCCCRRKRSRKPD RSEEKAMR\ER EDR\WILQEERRAEMNTRHDEIRKK\ YGLFKEENPYARFENN
1784	7281	A	1920	61	515	
1785	7282	A	1921	1	2175	
1786	7283	A	1922	3159	3441	
1787	7284	A	1923	36	387	
1788	7285	A	1924	64	408	
1789	7286	A	1925	1	10514	
1790	7287	A	1926	64	601	VNNILGLGHTFWALLASPKMEHKE VLLLLLLFLKSGQGEPLDDYVNTQ GPSLFSVTCKQLGAGSREECAAKCE EDKEFPAGAF\QYHSKEQQCVIMA ENRKSS\IIRVRDAVLFGKGKCILF RVQDLGMERTTEGRCPKQKMASPC QKWEFHFSPADLGQTFPFIFVFIYCK VVPLCL
1791	7288	A	1927	173	491	AGEARWESQSAHLKPEFGGPTGPN NAQSPPREADAQVWREPPGPASK APHSPVGYSSPGHSHLLPGDDPA KDGSCPP\PFPLGIEAPVPGPRKRIR TCCCMN
1792	7289	A	1928	1	735	
1793	7290	B	1929	1	1026	MRARLPWALTLVAELGWD TQGG DQTSPGGNDRMSMEAECSTTVSP LSCSIPTGCGQTREEVSARATPPPSL GASLLQTLTPDTHCTGVSATIMSML VVFLLLWPFSSHSTLAKHKRIHTGE KPYKCEECKAFSRSS TLAKHKRIH TGEKPYKCEECKAFRQSSTLTKH KIIHTEEKPYKCEECDKAFKRLSTL AKHKIIHAGEKLYKCEECKAFNR SNLTIHKFIHTGEKPYKCEECKAF NWSSSLTKHKRIHTREKPFKCEECK KAFIWSSTLTRHKRIHTGEKPYKCE ECKKAFSRSSSTLTKHKTIHTGEKPY KCEECKGKLLSTPQPLLNIK*
1794	7291	A	1930	1	2832	

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1795	7292	A	1931	98	3867	PAGIGRATAKMPGTPGSLEMGLLTF RDVAIEFSPEEWQCLDTAQQLYR NVMLENYRNLAFGLIALSKPDLITY LEQGKEPWNMKQHEMVDEPTGICP HFPQDFWPEQSMEDSFQKVLRLKY EKCGHENLQLRKGCKSVDECKVHK EGYNKLNQCLTTAQSKVFQCGKYL KVIFYKFLNSNRHTIRHTGKKCFKCK KCVKSFCIRLHK\TQHKCVYTEKSC KCKECKTSLW\SSLT\NHKEIHTE KPYKCEECGKAFKQLSTLTTHKIIC AKEKIYKCEECGKAFLWSSLTTRHK RIHTGEKPYKCEECGKAFFSHSSTLA KHKRIHTGEKPYKCEECGKAFFSHS ALAKHKRIHTGEKPYKCKEKGKAF SNSSTLANHKITHTEKPYKCKECD KTFKRLSTLTKHKIIHAGEKLYKCE ECGKAFFNRSSNLTIHKFIHTGEKPY KCEECGKAFFWSSSLTKHKRFHTR EKPFKCKEKGKGFWSSTLTRHKRI HTGEKPYKCEECGKAFFQSSTLT KIIHTGEKPYKFEECGKAFFQSSTLT KHKIIHSREKPYKCKEKGKAFKQFS TLTTHKIIHAGKKLYKCEECGKAFF HSSSLSTHKIIHTGEKSYKCEECGKA FLWSSSLRRHKRIHTGEKPYKCE CGKAFFSHS\ALAKHKRIHTGEKPY KCKEKGKAFSNSSTLANHKITHTE KPYKCKECDKTFKRLSTLTKHKIIH AGEKLYKCEECGKAFFNRSSNLTIHK FIHTGEKPYKCEECGKAFFWSSSLT KHKRIHTREKPFKCKEKGKAFWSS TLTRHKRIHTGEKPYKCEECGKAFF RSSTLT\KHKTIHTGEKPYKCKEKGK AFKHSSALAKHKIIHAGEKLYKCEE CGKAFFNQSSNLTIHKIIHTKEKPSKS EECDKAFFWSSSLTEHKRIHTREK PYKCEECGKAFFSQPSHLTTHKRMHT GEKPYKCEECGKAFFQSSTLTTHKII HTGEKPYKCEECGKAFFRSSTLTTEH KIIHTGEKPYKCEECGKAFFQSSTLT RHTRMHTGEKPYKCEECGKAFFNR SKLTTHKIIHTGEKPYKCEECGKAFF SSSTLNGHKRIHTREKPYKCEGCG\ KAFFQSFFN\TLTGHKRLHTGEKPYK CGECGKAFFKESALT\KHKIIHTGEK PYKCEKCKAFAFNQSSILT\NHKKIHT ITPKIHTREKPYKYKEGKSFNRSST FTKHKVIHTGVKLYKCEECGKSFF WSSALTRHKIIHTGQPPYKQEKFG KAFFNQFSLTTR
1796	7293	A	1932	590	891	
1797	7294	A	1933	1	1527	
1798	7295	A	1934	13	1668	PESKMAGSRHRGLRARVRPLFCAL LLSLGRFVRGDGVGGDPAVALPHR RFEYKYSFL\GPHLVQSDGTVPFWA HAG\AISSSDQIRVAPSLKSQRGSV WTKTK\AAFENWEVEVTFRTVGRG



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RIGADGLAIWYAENQGLEGPVFGS ADLWNGVGIFDSDNDGKKNPA IVIIGNNGQIHQNDGASQALAS CQRDFRNKPYPVARAKITY\YQNTLA TVM\NNG\FTPDKNDEYFCAKVEN MIIPAQQYFGISAATGGLADDHDVL SFLTTFQLTEPGKEPPTPDKEISEKEK EKYQEEFEHFQQELDKKKEEFQKG HP\DLAQWQPAEEIFESVRD\RELRLQ VFEGQNRHLEIKQLNRQLDMILDE QRRYVSSLTEEISKRAGMPGQHG QITQQELDTVVKTQHEILRQVNEM KNSMS\EPVRLVSGMQHPGS\AGGV YG\TTQHFID\KEHLH\VKR\IDIDL VQRNMP\SNEPKCPELPPFPSCSLST VHFQIFVVVQTVLFIGYIMYRSQQ EAAAKKILLTTIFLCTSSICVQNDVV LREFKYLNCFIV
1799	7296	C	1935	238	360	MGGLGLSLRSLSSASPAXFRPAHAP VGAAGLGPASPQGPL*
1800	7297	A	1936	1	1656	
1801	7298	A	1937	83	260	
1802	7299	A	1938	1	678	
1803	7300	A	1939	1	1097	
1804	7301	A	1940	1	1706	MQLLLAECMGQSGPPGAVCHCQR VWQARAVRRSKRPVPSTTQGLKSV GAWRGSGRQLHLQPQYRIHWVKP AGLLSLVGTMENICVWPSDCKYTN RHSVSSSRLLDSLKRDYAGKPQPPI KSERRNPPSYAMAAAQLRDSEETG GSEFVFAEKTLRKCVKCPQVELENV AFAKDAEESRDAQRLGHWVPCIME TLSNASGTFAIRLLKILCQDNPSHNV FCSPVSISSALAMVLLGAKGNTATQ MAQALSLNTEEDIHRAFQSLTEVN KAGTQYLLRTANRLFGEKTCQFLST FKESCLQFYHAELKELSFIRAAEESR KHINTWV\SKKTEGKIEELLPGSSID AETRLVLVNAIFYFKGWNEPFD YTREMPFKINQEEQ\RPVQMMYQE ATFKLA\HVGGLRAQLE\LPYARK ELSL\VLLPDDGVELSTVEKSLTFE KLTAWTKPDCMKSTEVEVLLPKFK LQEDYDMESVLRHLGIVDAFQQGK ADLSAMSAERDLCLSKFVHKSFE VNEEGTEAAAASSL\WVVAECCME SGPRFCADHPFLFFIRHTRANSILFC GRFSSP
1805	7302	A	1941	3	428	ETLERIKNNDPKLEEVLNNIRKIP TLKAYAEALKENSIVKKFSIVGTRS NDPVAYALAEMLKENKELKTLNVE SNFISGAGILRPGEALPYNTYLVE MSDNQSQPPGNKVEMEIVSMLLEKN ATLLRVR*HFSQQDAR
1806	7303	A	1942	1	1258	ALARPLPAGAPRPPASICPPAPVP QPASAPAPQLCVRVLLSTEIQETQTS SSTMSYRRELEKYRDLDEDEILGAL TEELRTLENELDELDPDNALLPAG

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						LRQKDQTTKAPTGPFFKREELLDHLE KQAKEFKDREDLVPTGKRGKV WVPKQKPLDPVLESVTLEPELEEAL ANASDAELCDIAAILGMHTLMSNQ QYYQALSSSSIMNKEGLNSVIKPTQ YKPVPDEEPNSTDVEETLERIKNND PKLEEVNLLNNIRNIPIPTLKAYAEAL KENSIVKKFSIVGTRSGDG\VAAYAL AEMLKENKVLKTLNVESNFISGAWI LRLVEALPYNTSLVEMKIDNQSQPL GNKVEMEIVSMVEKDPHHFLKFGL PPYPSKEPRLR\ASTAMMNTIALVR E\RRLAAPDLGPSFPKCRSGV
1807	7304	A	1943	2	382	EIAHQIEEQMG/EG*NFVAIESVV*K IVTEQQTGQKIQIVTALDHNTQGKQ FILTNHDGSTPSKVILARQDSTPGK\ VFLTTPDAAGVNQ\LFFTTPLDSAQ HLQDVIMGAVTCEGCKGFFKRSIRK N
1808	7305	A	1944	240	454	
1809	7306	A	1945	1	1851	
1810	7307	A	1946	128	512	TAPLAAGRRPGDALGPRPLAVGVK GTPWPPPPTRSLVSPPSVSYRRFCAL LTPASGADATVPRLPLVDWGALRE ERLKKADGMWDRDSRRRELSVFG ACALATGRSGERRS*RSQGGVEGSE GRAAAL
1811	7308	A	1947	1	705	
1812	7309	A	1948	124	1583	IMATIEEIAHQIEEQMGGEIVTEQQT GQKIQIVTALDHNTQGKQFILTNHD GSTPSKVILARQDSTPGKVFLTTPD AAGVNQLFFTTPLDSAQHLQLLTD NSPDQGPKNKVF DL CVVCGDKASGR HYGAVTCEGCKGFFKRSIRKNLVYS CRGSKD\CIINKHHRNRCQYCRLQR CIAFGMKQDSVQCERKPIEVSREKS SNCAASTEKIYIRKDLRSPLTATPTF VTDSESTRSTGLLDSGMFMNIHPSG VKTESAVLMTSDKAESCQGDLSLTL ANVVTSLANLGKTKDLSQNSNEMS MIESLSNDDTSLCEFQEMQTNGDVS RAFDTLAKALNPGESTACQSSVAG MEGSVHLITGDSSINYTEKEGPLLSD SHVAFRLTMPSPMPEYLVNHYIGES ASRLFLSMHWALSIPSFQALG\QEK QP*SLVKAYWNEFLTGLAQCWQV MNVATILATFVNCLHNSLQQDAKV IAALIHFTTRAITDL
1813	7310	A	1949	6	2028	KILRTLTPQKYPRTESSLRRESRSHM PTAFLNLSCRSAPQSTRGSRGTVAS APDAGGSRAQKRREIMATIEEIAHPI IEQQMGGEIVTEQQTGQKIQIVTALD HKTQGKQVILTNDGSTPSKVILAR QDSTPGKVFLTTPDAAGVNQLFFTT PLDSAQHLQLLTDNSPDQGPKNKVF DLCVVCGDKASGRHYGAVTCEGC KGFFKRSIRKNLVYSCRGSKDCIIN KHHRNRCQYCRLQRCIAFGMRQDS

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						VQCERNPLEVSREKSSNCAASTEKI YIRKDLRSPLTATPTFVTDSESTRST GLLDSGMFMNIHPSGVKTESAVLM TSDKAESCQGDLSLANVVTSLANL GKTKDLSQNSNEMSMIESLSNDDTS LCEFQEMQTNGDVSRAFDTLAKAL NPGESTACQSSVAGMEGSVHLITGD SSINYTD\KEGPLLSDSHVAFRLTMP SPMPEYLN\VHYIGESASRLFLSMH WALSIPSFQSGRGKEN\SISLVESLLG IELFTLGLAQCWQVMNVATILATF VNCLHNSLQQDKMSTDRRKLLME HIFKLQEFCSMVKLCIDGYDYAYL KAIVLFSPDHPSLENMEQIEKFQEK AYVEFQDYITKTYPDD\TYRLSRLLL RLPALRLDGCT\TEELFFKGLIGNIR RDSVIP\HILKMEPADYN\SPIGHSI
1814	7311	C	1950	65	286	MDYCNTFLPSNPETVFGDIMPRVVK PDLGTALSRGFTHEINKTYLSHLKL GSQKTHFWFIISFYAHLTLIYP*
1815	7312	A	1951	15	82	
1816	7313	A	1952	2	1934	CVQAATSLSVGICPLPGPGSPWPY PGVSVNVWIFKQIDDEGDLRLINK EVLSGVVVISSKDSVQHQQVSLTME GTVNLQLSAKSVGVFEAFYNSVKA QLRRSVQATGLEERPALPERLQQEG SEEAGGLSGAEAALPRRARGSPIQII NSTIEMVKPGKFPSPGKTEIPFEFPLH LKGNKVLYETYHGVFVNIQYTLRC DMKRSLAKDLTKTCEFIVHSAPQK GKFTSPSPVDFTITPETLQNVKEHSHQ TEAGQQRAFQRFRSALRGRLTAR ADNSSSSNVAQGSQKSGHPCSRPSS VLPQQRQVCRVKRALLPKFLL/RRT SQLNKLCHHAATNGRAGGGELGSR HQRGAAAGARGDPGQQSRP*P*L* KTRGRRGSKSKSVAVP*Q*PRV*GK VCR\SYARDATEIQNIQIADGDVCR GLSVPIYMFVPRFLTCTLETTFNFKV GKWHSPSPHGPMPGRAAQRQGLL WVTELRTCPSVPQCQGLPQAIQLR ACCP\AAQQNLVKELLCRTGDTPT GSPGACGTSTVTWGN\TQTHISVDM GRPQPQVGTDSKAPSTAELPQCGA QHRVPSAHTMPFPPLLTLGKEMVL VCRQDQQGSPISAEESVEKESCLLK EFEVNIVVLLHPDHLITENFPLKLCR I
1817	7314	A	1953	262	1274	ATAGREGKGRGPQPSGEAPLVSLGS RAATSGGCCGELEMG\TG\LDIKSKR ANKVYHAGEVLSGVVVISSKDSVQ HQQVSLTMEGTVNLQLSAKSVGVF EAFYNSVKPIQIINSTIEMVKPGKFPS GKTEIPFEFPLHLKGKNKVLYETYHG VFV\NIQYTLRC\DMKRSLAKDLT KTCEFIVHSAPQKGKFTSPSPVDFTIT PETLQNVKERALLPKFLLRRTS\QLN KLCHHAATNGRAGGGELGSR\HQK

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						RGAAAGARGDVRVCR\SYARDAPE IQNI\QIADGDVCRGLSVPIYMVFP LFTCPTLETTNFKVEFEVNIVLLHP DHLITENFPLKLCRI
1818	7315	A	1954	2	236	DRCLMLKQGSEAWLTSISIEPPAPPV YQAPCQSCPEPPGAHEPSDSPHHTP VHPPPE\TRTPVLPQPRAVPPRSSM S
1819	7316	A	1955	760	925	HLEYLPTYANSSYS\WPSSVAHTCN PSTLGGRGGRITGGQEFKTSVANIT KPCLY
1820	7317	A	1956	32	487	SRRHGSSLWGKVNVEDAGGETLGR LLVVYPWTQRFFDSFGNLSSASAIM GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG
1821	7318	A	1957	41	638	APSPRRPWGHFTEEDQGLLSTSLWG KV\NVEK CWKEKTPGKGLSVVYPA WT\QRFFD\SFGNLSSAFAHHGQTP KVKAHGK\KVLTLGRCQQSTLDD LKGTFACL\SELHCDKLHVDPENFK LLG\NVLVTVL\AIHF\GKDFTPGGC RASW\QKMGD\*SGQCPVLQ\IPLSS L\PMMQSFSRIRLLFLQAITNNKSISA KRSP
1822	7319	A	1958	3	227	
1823	7320	C	1959	171	366	MHTPSVEKPSCGSQLFVYIRKFWKK RNLVKVLNMTTSSVTEVDVPLYPEW CMLWRYPASRPNVRKP*
1824	7321	C	1960	332	421	MEEKIFSQPGMVAPT CNPSTLGGQG RWIT*
1825	7322	A	1961	322	1145	RFSKSPDPSGAQLVSPSGSRTRQQV ELAATPTQCSTLLSPWASDGTGCHG AAGRSSGRLRPTGALRWVPLHFPS PARGDSQARSLPTRAASADSSLPG CGRREVCGRAPAGG/PPLAPAPPA APVPASAAAQPPAPAWAYEQVWA GRGALRSPSASSGEAADD SYGVVA GRWGRPVQDSRLGTAGEGIAGRES WGSVTSWVLGSHMVKFLVAELGI CETQDWRRGSEGGAGEFGAVAIHC IGTWVADNAVTCPLLNTTQLEIPFG VQFWML
1826	7323	A	1962	30	2814	LPRAKVEGAPRAPSPQDPGVPPRAP SPRSPSPALRALPAPLSPRSPLDEPM ARPRRAREPLL VALLPLAWLAQAG LARAAGSVRLAGGLTLGGLFPVHA RGAAGRACGPLKKEQGVHRLEAM LYALDRVNADPELLPGVRLGARLL DTCSRDTYALEQALS FVQALIRGRG DGDEVGVRCPPGGVPPLRPAPPERV VAVVGASASSVSIMVANVLRIFAIP QISYASTAPELSDS\TRYDFFSRVVP DSYQAQA\MVDIVRALGWNVYSTL ASEGNYGESGVEAFVQISREAGGVC

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						IAQSIKIPREPKPGEFSKVIRRLMETP NARGIIIFANEDDIRRVLEAARQANL TGHFLWVGSDSWGAKTSPILSLEDV AVGAITILPKRASIDGFDQYFMTRSL ENNRNRNIWFAEFWEENFNCKLTSSG TQSDDSTRKCTGEERIGRDSTYEQE GKVQFVIDAVYAIHAHALHSMHQAL CPGHTGLCPAMEPTDGRMLLQYIR AVRFNGSAGTPVMFNENGDAPEGRY DIFQYQATNGSASSGGYQAVGQWA ETLRLDVEALQWSGDPHEVPSSLCS LPCGPGERKKMVKGVPCCWHCEA CDGYRFQVDEFTCEACPGDMRPTP NHTGCRPTPVVRLSWSSPWAAPPLL LAVLGIVATTTVVATFVRYNNTPIV RASGRELSYVLLTGIFLIYAITFLMV AEPGAAVCAARRLFLGLGTTLSYSA LLTKTNRIYRIFEQGKRSVTPPPFISP TSQLVITFSLTSLQVVGMIAWLGAR PPHSVIDYEEQRTVDPEQARGVLKC DMSDSLIGCLGYSLLMVTCTVY AIKARGVPETFNEAKPIGFTMYTTCI IWLAFVPIFFGTAQSAEKIYIQTTLT VSLSLASVSLGMLYVPKTYVILFH PEQNVQKRKRSKATSTVAAPPKG EDAEAHK
1827	7324	C	1963	334	387	MKCYIYIYMTLVLLIV*
1828	7325	A	1964	1	489	
1829	7326	A	1965	152	717	VESIEDVGNHRTDHGADMISIHVEE ENAFILDTLAKKQWKGPDILLGMV YDTDASFKWVDNSNMTFDKWT QDDEVEDLVDTCAFLHIKTGEWKK GNCEVSSVEGTLCKTAIPYKRKYLS DNHILISALVIASVILTVLGAIWFL YKKHSDSRFTTVFLTGPQLPYMEN CVLVVGEENEYPVQFD
1830	7327	A	1966	3	614	LLFFPSAKMALETGPKDLRHLRACL LCSLV/KGTIDQFEYDGCDCIYAYL QMKGNR\EM\VYDCTSSSFDGIAM MSPED\SWVSK\WQAKSSNFKP\GV YA\VSVTGRLAPK\GIR/VRELKSR\G VALQIPGDTANKDLAKMQGCQHLC SPPPCLCHSCSWNLNEQNQFQLPTLQ FRLSSTVERAAHHFIILSSLDYRWG GRDLGWVD
1831	7328	A	1967	66	407	
1832	7329	A	1968	2	1272	CPWPESTGQSGVTSSKARPSLAERW AGPAKKKRKGVEHGPAAREAGLM KRLSS/LGDLTSPSEIYVFTDIKVR THCPKSLPGTETVQIELSSFFLNILG GKKKKQSWEQEGCHLKDFGDLST PVPKDDLYNNLIVNPRSVGLANQEL AEVVSRAVSDGYSCVTLGGDHSLAI GTISGHARHCPDL CVVWVDAHADI NTPLTTSSGNLHGQPVSFLLRELQD KVPQLPGFSWIKPCISSASIVYIGLR DVPPEHFILKNYDIQYFSMRDIDR LGIQKVMERTFDLLIGKRQRPIHLSF

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						DIDAFDPTLAPATGTPVVGGLTYRE GMYIAEEIHNTGQRNTTENFDTSQ TLTEGLLSALDLVEVNPQLATSEEE AKTTANLAVDVIASSFGQTREGGHI VYDQLPTPSSPDESENQARVRI
1833	7330	A	1969	212	460	
1834	7331	A	1970	1	1223	TVVECLSPA WHEESSGGRWRS LPA SNRAEPLPWRFSVL RIMSLRGSLSR LLAQTRVRSILKKS VHSVHVIGAPFS QGQKRKGVEHGPA AIREAGLMKRL SSLGCHLKDF/GQDLSFTPVPKDDL YNNLIVNPRSVGL ANQELAEVVSR AV/SQDGYSCVTLGGDHSLAIGTISG HARHCPDLCVWVDAHADINTPLT TSSGNLHGQPVSFLLRELQDKVPQ LPGFSWD/IKPCISSARIVYIGLRDVY PPEHFILKGTMDIQYFISMEEILDR L GIQEGHNGTFDL LIGKRQRPIHLS YDIDAFDPT HAPAHRTPVVGDITYR EAMYIAEKIHNTG LLSALDLVEVN PQLATSEEEAKTTANLAVDVIGLPS LWVQTRREGGAYWSYDPTFTP\SSP DESENQARVRI
1835	7332	C	1971	162	425	MVGPSLHAGXXXVYIPRFLYIRSWL PCIFFSGGVTVGNIGRQLAMGVPEK PIVIESSKPXILESXGRFLEENLXLVD YXKGLSFFLK*
1836	7333	A	1972	89	308	
1837	7334	A	1973	2	454	
1838	7335	A	1974	570	1418	PMPRLHDHFWSCSCAHSARRRGPP RAIAAGLAAKVGEMHIVFVSGPSLM AVLSASDADPAPRGRSAVKSGPYP GSPYPNTWHHSLMQKSLVLFVGE VLALVLNLLQIQRNVTLPPEVIATI FSSAWWVPP\CCGTAPADVGLLYPC IDSHLGEPHKFKERMGQVSMRCIAV FVGINHASAKLDFANNVQLSLTLAA LSLGLWWTFDRSRSGLGLGITIAFL ATLITQFLVYNGVYQYTSPDFLYIR SWLPCIFFSGSVTVGNIGRQLGYG VFLEKPHSD
1839	7336	A	1975	1	287	KFQERGIIQIKYPP/RAFTLSHTHTRH AHIQAPTVTNQTP/DFP/RPRR*ESSS SSEGANSFLKIMT*RQSSSPKEKDV RPATSTTSCSMLLSILFIG
1840	7337	A	1976	1	166	
1841	7338	A	1977	37	448	GGCTCPCSRWQGSPPQAPAGLPPPL ASGPAPSASASPQSGGPIPLH/VR*E SSSSSEGANSVCSSRSCSLAETFS*S AHCLE*NLTPSPSFYETPLSVVSLA LVVSSGGRPVLGPCAESPGRHWV ASPWSSGWSP
1842	7339	A	1978	45	249	
1843	7340	A	1979	77	3801	KGGVFAHDLVPLPFQGTDSPPRAP PGRGVPLPPGALTMNTRD\TPRVAE TSHHLKIFLPKKLLECLPRCPLLPE RLRWNTNEEIASYLITFEKHDEWLS

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						CAPKTRPQNGSIILYNRKKVKYRKD GYLWKKRKDGKTTREDHMKLVQ GMECLYGCVHSSIVPTFHRRCYW LLQNPDIVLVHYLNVPALDCGKG CSPIFCSISSDRREWLKWSREELLGQ LKPMFHGIKWSCGNGTEEFVSEHL VQQILDTHPTKPAPTHACLCSSGGL GSGSLTHKCSSTKHRIISPKVEPRAL TLTSIPHPHPPEPPPLIAPLPPELPA HTSPSSSSSSSSGFAEPLIRPSPTS RGGSSRGGTAILLTGLEQRAGGLT PTRHLAPQADPRPSMSLAVVVGTEP SAPPAPPSPAFDPRFLNSPQRGQTY GGGQGVSPDFPEAEAAHTPCSALP AAALEPQAAAARGPPQSVAGGRRG NCFIQDDDSGEELKGHGAAPPISP PPSPPPSPAPLEPSSRVGRGEALFGG PVGASELEPFLSSFPDLMGELISDE APSIPAPTPQLSPALSTITDFPEWSY PEGGVKVLITGPWTEAAEHYSCVF DHIAVPASLVQPGVLRCPAHEV GLVSLQVAGREGPLSASVLFYRAR RFLSLPSTQLDWLSLDDNQFRMSIL ERLEQMEKRMAEIAAAGQVPCQGP DAPPVQDEGQPGFEARVVVLVES MIPRSTWKGPERLAHGSPFRGMSLL HLAAAQGYARLIETLSQWRSVETG SLDLEQEVDPLNVDFHSCPTLMWA CALGHLEAAVLLFRWNRQALSIPDS LGRPLSVAHSRGHVRLARCLEELQ RQEPSVEPPFALSPPSSSPDTGLSSVS SPSELSDGTFSVTSAISSAPDGSPPP APLPASEMTMEDMAPGQLSSGVPE APLLLMDYEATNPKGPLSSLPALPP ASDDGAAPEDADSPQAVDVIPVDM ISLAKQIIEATPERIKREDFVGLPEAG ASMRERTGAVGLSETMSWLASYLE NVDHFPSSTPPSELPFERGRLAVPSA PSWAEFLSASTSGKMESDFALLTSL DHEQRELYEAARVIQTAFRKYKGR RLKEQQEVA AAVIQRCYRKYKQLT WIALKFALYKKMTQAAILIQSKFRS YYEQKRFQQRRAAVLIQHYRSY RRRPGPPHRTSATLPARNKGSFLT KQDQAARKIMRFLRRCRHRMRELK QNQELEGLPQPLAT
1844	7341	A	1980	1	4333	MQVQDDGVNLIPFAKCSRVSRSPP PRLPSQSLRPMPPQRYGDVFWKLN QRPTPTWLEEQHIPMLRATGCSQL GLYPPEQLPPPEMLWRRKKRRPCLE GMQQQGLGGVPAVRAVITYHLED LRRRQSIINDTSPSPRPLRPGVTLPP GALTMNTKDTTEVAENTRPLKIFLP KKLLECLPRCPLPPERLRWNTNEEI ASYLITFEKHDEWLSCAPKTRPONG SIILYNRKKVKYRKDGYLWKKRKD GKTTREDHMKLVQGMCECLYGCY VHSSIVPTFHRRCYWLLQNPDIVLV

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						HYLNVPALEDCGKGCSPIFCSISSDR REWLKWSREELLGQLKPMFHGIKW SCGNGTEEFVSVEHLVQQILDTHPTK PAPRTHACLCSGGLGSGSLTHKCSS TKHRIISPKVEPRALTLTSIPHAHPPE PPPLIAPLPPELPAHTSPSSSSSSSS GFAEPLEIRPSPPTSRGGSSRGGTAIL LLTGLEQRAGGLTPTRHLAPQADPR PSMSLAVVVGTEPSAPPAPPSPAFDP DRFLNSPQRGQTYGGGQGVSPDFPE AEAAHTPCSALEPAAALEPQAAAR GPPQSVAGGRRGNCFFIQDDDSGE ELKGHGAAPPISPPSPPPSPAPLEP SSRVGRGEALFGGPVGASELEPFSL SSFPDLMGELISDEAPSIPAPTPQLSP ALSTITDFPEWSYPEGGVKVLITGP WTEAAEHYSCVFDHIAVPASLVQP GVLRCYCPALPLPYTQKSALLGDLK DHQSDRLAALLSTSVFSPSLYSSIQH VSHEVGLVSLQVAGREGPLSASVLF EYRARRFLSLPSTQLDWLSLDDNQF RMSILERLEQMEKRMAEIAAAGQV PCQGPDAPPVQDEGQGPGEARVV VLVESMIPRSTWKGERLAHGPSFR GMSLLHLAAAQGYARLIETLSQWR SVETGSLDLEQVDPNLVDHFSCTP LMWACALGHLEAAVLLFRWNRQ ALSNDPSLGRPLSVAHSRGHVRLA RCLEELQRQEPSVEPPFALSPPSSSP DTGLSSVSSPELTDGTFVTAAYS SAPDGSPPPAPLPASEMTMEDMAPG QLSSGGPEAPLLLMDYEATNSKGPL SSLPALPPASDDGGGPEDADSPQAV DVIPADMISLAKQIIEATPERIKREDF VGLPEAGASMRERTGAVGLSETMS WLASYLAENVDFHPSSTPPSELPPFER GRLGLSLTAPSWAEFLSCIPPVGKI GKLIFALLTLSD\QEQRLEYAARVI QTAFRKYKGRRLKEQQEVAAAVIQ RCYRKYKQFALYKKMTQAAILIQS KFRSYYEQKRFQQRRAAVLIQGH YRSYRRRPGPPHRTSATLPARNKGS FLTKKQDQAARKIMRFLRRCRHRH SALPFKTHRPLSVTPKMADLLGSILS SMEKPPSLGDQETRRKAREQAARL KETTRARETTESGVS
1845	7342	A	1982	1	145	
1846	7343	A	1983	1	419	
1847	7344	A	1984	3	532	PRASRSRPTGLREAAGSGPREAPRR SGCKSPGLGTVAMLRPKALTQVLS QANTGGVQSTLLLNNEGSLLA\YS GLRGTTDAPGSPAIA\SNIA\AYG PETGTQAFNEDNLQ\IILHGTCMGG AVLGHSPELANLSCLLYCIAKEDRG AFGNCFKAKGPGLLGGSYLEEPLTQ VAAS
1848	7345	A	1985	2	555	
1849	7346	A	1986	90	323	



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1850	7347	A	1987	1	4695	
1851	7348	A	1988	81	523	SCLCRDRACLTSLPVSFQVQGVGSK GWRDVTTFFSGKAEGPLDSPSEGH YQNSGLDHFQNSNIDQSFWETFGSA EPTKTRKSPSSDS\WTCADTSTER\R SSDSWEVWGLASTNR\NSNSDGV GGEGTKKAVPPAVPTDDGWDNQ W
1852	7349	A	1989	1187	1720	QNQSRDKMRDLREGQMEPPKSELI GWGGGETSRWVRGGASPPPALSP LFLITWSGHKDLK\DLKVRGLRGL APRVNVWETEANQAGLQPLGPPAT IGLRPRRPGPGRVREGGPAWPLG EFGSGPGVGLRARHQHELRRWRPGR ASPRPERKAAWKGQPGQPAGPADG RAARSRG
1853	7350	A	1990	738	1086	GTASENLGCKILKHRQOMLRKVYP VVLHILSYRGSHSRKKNWGRLLKNI LKTFFFLGGGGDGCWQRPGWELQ WALFSGSLQSPPGF\KQFSCSLLS SWEYRCTPPCLANFCIFQ
1854	7351	A	1991	1	340	LGEGGRTAVEALPGPSLDHWYRSA GEEKDGP/VYCAAQHLRGRSLPKA WPPPPSSLPVLTDEQKSR/YPGHEAH DQGG\WDARQSIIRKVVDPETGRTR WGAFGLTYTTGSGSVG
1855	7352	A	1992	1	142	
1856	7353	A	1993	58	328	LKKKGKEKAEAAQQVEALPGPSLDQ WHRSAEEEEEDGPVLTDEQKSR/YPG HEAHDQGG\WDARQSIIRKCGGPLR RGAPGLLKGDGEGPKRKS
1857	7354	A	1994	120	416	LFFGESSRLTVLEDLKNVFPQVAV FEPKAEIFHTQKAPLVLATGFYPD HVELSWWVNGKEVHSGVSTDPQP LMEQAALNDSRYCLSSRLRVSATF
1858	7355	A	1995	1	977	VKLPCPDPMGTSLLCWMALCLL GADHADTGVSQNPRLNITKRGQNV TFRCDPISEHNRLYWYRQTLGQGPE FLTYFQNEAQLEKSRLSDRFSER PKGSFSTLEIQRTEQGDSAMYLCAS SIGAGLPSSNQPHFGDGTSLILE LNKVPPEVAVFEPSEAEISHTQKAT LVCLATGIFPDHVELSWWVNGKEV HSGVSTDPQPLKEQPALNDSRYCLS SRLRVSATFWQNPRLNHFRCQVQFY GLSENDEWTQDRAKPVTQIVSAEA WGRADCGFTSVASYQQGVLSATIL YEILLGKATLYAVLVSAVLMMAMV KRKDF
1859	7356	A	1996	2	883	FVSQLSPEKVVCGHHLKMLSLLLLL LGLGSVFSAVISQKPSRDICQRGTSV KIECRSLDFQATTMFYRQFPKKS MLMATSNEGSKATYEQGVEKDKFL INHASLTSLTVTSAHPEDSSFYICS ARESTDPKNEQYFGP\GTRLTVLE DLKNVFPPEVAVFEPSEAEISHTQK ATLVCLATG\FFPDHVELSWWVNG

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						KEAHSGVSTDPQPLKEQPALNDSRY CLSSRLRVSA TFWQNP RNHFRCQV QFYGLSENDEWTQDRAKPVTQIVS AEAWGRAGEWGLGRCLEIR
1860	7357	A	1997	195	1133	PQHGGHFPRKIKSCSWQARPLEDEA TLGQCGVEALTTLEVTRPACLEVKS MVPWPVLEKVRGQTPKVAKHGEK KKKKTGRAKRRMQYNRRFVNVVP TFGKKKGTTFTKIFVGGLPYHTTDA SLRKYFEGFGDIEEA VVITDRQTGK SRGYGFVTMADRAAAERACKDPNP IIDGRKANVNLA YLGAKPWCLQTG FAIGVQQLHPTLIQRTYGLTPNYMY PPAIVQATVVIPAAPVPSLSSPYIEYT PASPAYAQYPPATYDQYPYAASPA TVRSFVGYSYPAAVPQALSAAAPA GTTFLQYQAPHVQPD RMH
1861	7358	B	1998	60	378	NAVLEADFAKRGYKLPKVRKTGTT IAGVVYKDGIVLGADTRATEGMVV ADKNCSKIH FISPNIYCCGAGTAAD TDMTTQLISSLAAMAVFEDKFRPD MEEEEAKNLX*
1862	7359	A	1999	1	437	DPRATEGMVVADKTCQKSTGRLPE LVTAIRMLKQMLFRYQGYIGAALV LGGVDVTGP/HLYSIYPHGSTDIAAG IFNDLGSGSNIDLCVISK NKLDLFRP YTVPNKKGTRLGRYRCEKGTTAVL TEKITPLEIEVLEETVQTMDS
1863	7360	A	2000	2290	2481	
1864	7361	A	2001	3	860	FLGKMAAVSVYAPPVGGFSFDNCR RNAVLEADFAKRGYKLPRPRKTGT TIAGVVYKDGIVLGADTRATEGMV VADKNCSKIH FISPNIYCCGAGTAA DTAMT\TQLISS\NLKLHSLSTGR/LP RV\VTANRMLKQMLFRYQGYIGAA LVLGGVDVTGPHLYS IYPHGSTDK VPYVTHGFLAPLA\AMAVFEDKFR PD\MEEEEAKNLVSEDSPPQFPPPS WRIFNDLGSGSNIDLCVISK NKLDF LRPYTVPNKKGTRLGWRYRCEKG VTTAVLTEKIPLLWST
1865	7362	A	2002	1	340	RQGTIVAISIQGKMSIPFRSAYAAS KHATQAFFDCLRAEME QYEIEVTVI SPGRSC/VEVAQDVLAAAGKKKKD VILADLLPSLAVYLRTLAPGLFFSL MASRAR*ERKSKNS
1866	7363	A	2003	56	385	RPWTSSPPQSPCCSAAWASSASS GCCSGCAGRPTCGMLWW*SQAPA QGRSPVEVAQDVLAAVGKKKKDVI LADLLPSLAVYLRTLAPGLFFSLMA SRARKERKSKNS
1867	7364	A	2004	2	409	
1868	7365	A	2005	1	1092	
1869	7366	A	2006	50	1101	LTMVSPATMKSLPKVKAMDFITST AIL\PLLFGCLGV\FGL\FRLQWVR GKAYLRNAV VVITGATSGLGKECA KV FYAAGAKLVLCGRNGGALEEL\

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						RELTAS\HATKVQTHKPLLGGPSDL TDSGAIVAAAAEESFSCF\GYGRHY FVNNAGISYRGTVTMDTVTDVVKR VMETNYFGPV\ALKALLPSMIKRR QGHIVA\SSIQGKM\SIPFRSGICQPS KHATQA\FFDCLAVPEMEQY\IEIV TVISPG\YIHTNLS\VNAITADGSRYG V\MDTVT\SPGPESPVEGGPRMFLAC LWGKKK\KDV\TLADLPALPLAVY\ LRTLPA\GLLPSSLPCLPRAQKRAGN PKNSLV
1870	7367	A	2007	75	461	
1871	7368	A	2008	3	426	DAWVCLSPAFILLELCAARV*EGLP NRVHRTEEVNHVDFYAFSYYYDLA GGAGPIDAEKGGSLVVGDFEIAATKY VCRTLETQSQSPFSCMDLTYVSL LQEVGFPRSKVLKLTRKIDNVYTT WAPGAIFHYIDSLNRQKS
1872	7369	A	2009	3	421	QALGNRGVVSRGWRRPGRG SPKDRLPAPRKRALVSVGVAERA VHETPTLTHETFKALPGLSAYADD VEKSAQGIRELLDVAKQDIPDF*K ATPLILK/ATAGLRLPEKKAQR*LA K\GKEVFKA\WLFEGNDW
1873	7370	A	2010	337	769	PLALCLAPAASLHELCAAKVSEVLH NRVHRTEEVKHVDFHAFSYYYDLA AGVGLIDAEKGGSLVVGDFEIAAK Y\VGVTWSVKGRVSSPVCRTLETQP QSSPFSCMDLTYVSLLLQEFGFPRS KVLKLTRKIDNVETSWALGAIF
1874	7371	A	2011	2	486	
1875	7372	A	2012	176	1643	MKKGIRYETSRKTNYIFQQPQHGP WQTRMRKISNHGSLRVAKVAYPLG LCVGVIYVAYIKWHRANATQAFF SITRAAPGARWGQQAHSPLGTAAD GHEVFYIMFDAGSTGTRVHVQF TRPPRETPTL/TAHETFKALPGLSA YADDVEKSAQGIRELLDVAKQDIPF DFWKATPLVLKATAGLRLPGEKA QKLLQKVKEVFKA\SPFLVGGDCVSI MNGTNE\GVSAWITINFLTGSLKTPR RSNVGMLDLGGGSTQIVFLTHVEG TLQASPPRYLTALRMFNRTYKLYC YSYLGLGLMSARLAILGGVEGQPA KDGKELVSPCLSPSFKGEWEHAEVT YRVSGQKAAASLHELCAARVSEVL QNRVHRTEEVKHV\DFYAFSYY\YD LAAGVGLIDA\KGGSLVVGDFEIA AAKYV/CVRTLGETQP/QSSPFSCMD LTYVSLLLQEFGFPRSKVLKLTRKID NVETSWALGAIFHYIDSLNRQKSPA S
1876	7373	A	2013	21	119	PGWPQTPDFKRS/PPLWPPKVLGLQ V*ATAPGPK
1877	7374	A	2014	1420	1627	IGLNPSSVPSTFFSYSPQFTEGVPP/P GMERP/PFPWEQRPTGWSFFSPCPQ TP\SPPTSEHGTPPNWPKC

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1878	7375	A	2015	447	775	QIPKEHLHHP/PQTSHSNRPLR/P/GN RPNPESPTGSPPECCSCLAPRGSA WGDPNPLQRTPGAGKVAGGPFPPP TQQSPPGKALCINLKKGKFAAIKLLD NVLQPSSALGFL
1879	7376	C	2016	49	519	MYGKGKSNSSAVPSDXQAREKLAL YVYEYLLHVGAQKSAQTFLSEIRW EKNITLGEPPGFLHSWWCVFWDLY CAAPERRETCEHSSEAKAFHDYPPFM SPRYPGGPRPPLRIPNQUALGGVPGS QPLLPSGMDPTRQQGHPNMGGPMQ RMTPPRGMVP*
1880	7377	A	2017	1	1155	
1881	7378	A	2018	56	1416	WVDRCVTVGAAALGTSMYGKG\KS NSSAVPSDSQAREKLALYVYEYLL HVGAQKSAQTFLSEIRWEK\NITLG EPPG\FLHSWWCVFWDLYCAAPER RETCEH\SSEAKAFHDYSAAAA\PS VLG\NIPPGRWACQLGPVTTRGSFQ PFMFTFGYPG\GPRSPLR\VPNQUALG G\VPGGQPLLPSGMDSTRQQ\GHPN MGGAMQR\MTPPRGM\VPGLPQFLT PWL\SLQNYGGA\MRPPL\NALGGPG MPGMEQGSRCGRPW\PNPTNA\NSL PFSSAFSWNLLGPPG\GGGPPG\TPI MPSSSRFQPTSGDNMYTLMNAVPP GP\NRPNF\PMGP\GSDGPMGGLGG MESHMHMNGSLG\GDMAISISKNSPN NMSLSIQP\GIPK\DDGAMGANFLN PFQSESYSKPYKCVFPFGLFMKP TVSQPFPELRTEENYSSTSVPVKQR NLSHTKPTFLFPALSPLL
1882	7379	B	2019	162	349	LEEEEEEELDLVLLRAFCLLLSW DVEAEQFLEVSLFFFLFSDPRPRD RLRLRLRLREPT*
1883	7380	A	2020	2	353	SSSDGRKKRGKYKDKRRKKKKKR KKLKKKGKEKAEAAQVEALPGPSL DQWHRSAEEEEEDGPVLTDEQKSR/ YPGHEAHDQGG\WDARQSIIRKVV DPETGRTRWGAFGLTYTTGSGSVG
1884	7381	A	2021	1	142	
1885	7382	A	2022	404	946	PVCACPRPEQGTKVYLFPSWLSSLT FSLHHREKQAEGRGEEEDASSASS SSSSSSSSSSSSSSSDGRKKRGK YKDKRRKKKKKKRKKLKKKGKEKA EAQQVEALPGPSLDQWHRSAEEEE DGPVLTDEQKSR/YPGHE\THDQGG\ WDARQSIIRKCGGPLRRGAPGLLKG DGEKPKRKS
1886	7383	A	2023	3	634	
1887	7384	A	2024	131	546	VAGTPGRHPHTRLIFPVFCRGGVFL CFPGWSFFFFKPSDLDSFHLEMIHPR CESWKMPGALPM/YCSP/CCLLVLL KDQGGGASTGVRRRKESWLPAPHS STVQVTQEGWREQSRELKTECQL GWFLFLLQPYSRFRFY
1888	7385	A	2025	363	578	RPYPCLSPPRSSSTNPLSS**LNKIPS

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						LPSSWEKW*IPPKNNCLSLNPSPPS LAPSLDDIKEGLSWKKKKK
1889	7386	A	2026	166	191	KNVIHQSKNCVFKLLDQIHNFPLS TLLHVIVDLFLGLFGVPE/CSDP*RLP GTPPYQPAPARQPAPADHRQWPVPQ RGPEASG
1890	7387	C	2027	358	405	MSSREGARDGGEGLRS*
1891	7388	C	2028	306	347	MSPGRGPGMEGRG*
1892	7389	A	2029	2	358	QCGGIRFWRAPVFLVLSWSPQDGIT GEEPDTSHDPRLHQASSCPPAHPLP PTQSCSSCQGWLCPPQGCGPPGPRRT A/CIVPWPSFVASAATQERGQCPL DLPSPNQTRALHLSGTSGK
1893	7390	B	2030	1043	1146	MPSSVSWGILLAGLCCLPVSLAE DPQGDAAQKTDTSHTDQDHPTFNK ITPNLAFAFSLYRQLAHQSNSTNIF FSPVSIATAFAMLSLGTADTHDEIL EGLNFNLTEIPEAQIHEGFQELLRTL NQPDSQLQLTTGNGLFLSEGLKLVD KFLEDVKKLYHSEASPVISGASKRA KKQINGKMGETLLKSKDPRKEDFT LDQVTTVKGAYDEAFRACTSSHX *
1894	7391	A	2031	2	402	SQTQREPTMVLSPADKTNVKA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKLKRVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR
1895	7392	A	2032	9	509	NSARATDSERTHHGARLLPDKTNV KA\AWGKVG\AHAGEYGAEALERM FLSFPT\TKTYFPHFDL\SHGF\AQVK GATAKKVA\DA\TKAVA\HVDGHA QTALSALSGPATAHKL\RVGPSTF KLL\SHLPCW\TLGRPPSPA\EFQPLA VARLPWNKVPGLLVEAPLLEPSK
1896	7393	A	2035	413	674	CRSDRWAKEHRGKRGQDSSKDVM ARLMEAPKQTAQYFFIFYFFETKSY SVTQAGVQWLDLGS\LRPPPG\SD SPASASRAWPQTAH
1897	7394	A	2036	2525	2734	LTNGTESTPPRPTPSRCSRQRCPE VGPPF\CSPPFCVPAHF\KLLPWTFQG TVISSPQI\SSSSVCAFF
1898	7395	A	2037	168	392	NKSFFPPSSSFDLSILNTFSFPLTLSSL RSGPTHHTHTHAN/THHTHTHTHT HTPSSDPQAHPHTLTDNWVSTL
1899	7396	A	2038	216	528	AGEKLGLGAGDTSWRVWVPAACT PGRVERVGWCRV\GPADPSGGLTPG \ACGASWQGPFSWAKDLQGGPSW WPVWPPTRPFLDLGSSGLLIWVHK WPWGVCVYV
1900	7397	A	2039	37	424	RWNFLATTPSAVFRVWEAQMLTCE RWPTLSGRRQTYLLLPFAP*PQTGC WSPDGSRLLFTVLGEPLIYSLSPER CGEGKGALEVQSQRLWQICLRQ QYRHQMVRRLGERLTPWSGTPVG NVWLCL

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1901	7398	A	2040	1	442	PEFRVDDFVLRYPAYESSPGTELRECL/WPFRPGVCRLQTSCEPWNLPLQLTKDPLKTPGRLDHGTRTAFIHREQVWKRCINIWRDVGLFGVLNEIANSEKEVFEWVKTASGWALALCRWASSLHGSLFPHLSLRNEDLIAEF
1902	7399	A	2041	722	1395	CLCLGLWACQSCILIWTL\DPSTLFTRPSSG\CAQVLSHPGHTPVTS LAWAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLWSPDGSKI LATTPSAVFRVWEAQMWDLWRRWPTLSGRCQTGCWSPDGSRL\FTVLGEPLIYSLSPERC GEGKGALEVQSQ QRLW\QICLRQQ/YTRHQMVRRLGLERLTPWSGTPVGNVWLCFMKGKAQGLPGW
1903	7400	A	2042	1	418	MPEQEPTAEQLS*IAAENEDEHSVNYKPRAQKSIQEIQLDKDDESLRKYKRALGRVAVSADPNVPNVVAPGRVLLPQALSATTGPRPSLTQPGTNKGPSAHIAESRLCLPRPIGLRVVSARLRQRRLSLLF
1904	7401	A	2043	1	525	LSQQASLESF*KHFFCLKEVVEYRIKISFRVNREIVSGMKYIQHTYRKGVKID\KTDYIVGSYWPRAEEYEFLTPKSPRWASPTPSVLQSGAPLGHQYLLPSPVPSSGHWPVCSPRLVPPLGRPSLTLPGTNKGPSAHIAESRLCLPRPIGLRVVSARLRQRRLSLLF
1905	7402	A	2044	354	487	
1906	7403	B	2045	61	516	KSIQEIQLDKDDESLRKYKEALLGRVAVSADPNVPNVVVTGLTLVCSSAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYMGVSYGPRAEEYEFLPRPIGLRVVSARLRQRRLSLLF*
1907	7404	A	2046	11	328	
1908	7405	A	2047	1	507	LTFVCSFRPVPLYDLRSN\LD SKNQSFLFKEAVDYRIKISFRFHPKYISL\*YIQHTYSK/GVKIDKTDYMLGSY/GPRAEEYEFLTPVEEAPKGMLARGSYSIKSRFTDDDKTDHLSWEWNLTISIYCLRPCRPWATGLAPVPPGSGCHHPRQAFDPARNKQGTKCTHC
1909	7406	A	2048	1	327	TAEQLAQIAAENEDEHSVNYK/PPAQKSIQEIQLDKDDESLRKYKEALLAPLAVSADPNVPNVVVTGLTLVCSS/APGPLELDLTGDLESFKKQSFVLKEGVECTVGPH
1910	7407	A	2049	1	452	
1911	7408	A	2050	3	868	SHFVLDVIPGVGH\LTLPQRMPLSRNRGGGEERRCPPWSPFGAPLQPTLLRSAPPLGIQVQGLSPSRPQVSRPRLSLMAEQEPTAEQLAQIAAENEDEHSVNYKPPAQKSIQEIQLDKDDESLRKYKEALLGRRWPFSADPNVPNVV

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						VTGLTLVCS\SAPGPLELDLTGDLAE SFKKQFVLCLKEGVYRIKISFRFNP RDNCPGMKYIQHTYRKGVKIDKTD YMGVSYG\PRAEGSFELTPVEEAP\ KGMLA\RGSYSIKSRFTDDDKTDHL SWEWNLTIKKDWKD
1912	7409	A	2051	1	618	TLLVPQDSERTHPWLLSPADK\TNV KGPPGGKVGAAHVRSMCAEALER MFLSFPTTKTYFPFHLHGSAQV\ KGHG\KKVADALTNAVAVH\DDMP NALSAL\SDLHAHKLRVDPVNF\KL LKPLACLVDPGPAHLPAEFQPLAV ATSSLGQSFLGFLWANLKFEQIPV KLGSLGWAMLSLPLWAFPPAPPPLS CTRTPVVFEIKS
1913	7410	A	2052	3	398	
1914	7411	A	2053	1773	3913	FEQNTKLDQAQQAPEDHYPISLLLP SHMAIGLLMAQEGHCKDSSAMGEE AHHPLTPATPPFPPLSPDWGHMQPD FFVPVAVPAVFRGPPQLQCHGRRLF LNSPCAQKSSSGLVVEPGLSRTLE MVKLTSMRGQFLEAQIPTGISLTQ YQLYQKQTNKNMSYSFVLFKWW ALGQGRRAGYPSLEDADSRFRNGS RSFLITVIGITLTVEIVTSGMMKGTR VRWSGAGNEGMMGLEEGRNERSV KEAPPRRAVEAQPKDRTWDVGKG QGTEGEGRGLEVEGQQHQGSEPGTI PFSVSWGVLLLAGLCCLVPSSLVED PQEDAAQKTDTSHHDQGDWEDLA CQKISYNVTDLAFDLYK\SWLIYHN QHVLVTPTSVAMAFAMLSLGTKA DTRTEILEGLNVNLTETPEAKIHECF QQVLQALSRPDTRLQLTTGSSLFVN KSMKLVDTFLEDTKKLYHSEASSIN FRDTEEAKEQINNYVEKRTGRKVV DLVKHLKKDTSALVDYISFHGKW KDKFKAERIMVEGFHVDDKTIRVP MINHLGRFDIHRDRELSSVLAQH YVGNATAFFILPDPKKMWQLEEKL TYSHLENIQRAFDIRSINLHFPKLSIS GTYKLKRVPRNLGITKIFSNEADLS GVSQEAPLKLSKAVHVAVLTIK GTEATGAPHLEEKAWSKYQTMFVN RPFLVIIKEYITNPLFIGKVVNPTQK
1915	7412	A	2054	3	409	PGPVVVSNNSSAHGSQRTSGPESSM K\YCCPEMVEYQKKGKSLDSEPSVP SAAKPPSPEKTAPVASTPSSTIPALS PPTKVPEPNENVGDAVQTKLIMLV DDFYGRDGGKVAQLTNFPKVATS FRCPHCKRLY
1916	7413	C	2055	235	366	MRIPETKPLTRNGSEVKELAHSSPQ DNQNDQMSFFIVLLPRNG*
1917	7414	A	2056	3	484	STIPTATQPTSLWQLAVQSPGQSNQ TTNPKLGKASEEEMAEPGLGWVVE NR*LSLGHRA\PSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIP SLGQSPGPVVVSNNSSAHGSQRTSG

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						PESSMKGTTIT*KTLSQSFKNINKVF VVSELYTQK
1918	7415	A	2057	2	4256	FVHGSMADTDLFMECEEELEPWQ KISDVIEDSVVEDYNSVDKTTTTSV SQQPVSAPVPIAAHASVAGHLSTST TVSSSGAQNSDSTKKTTLVTLIANN AGNPLVQQGGQPLILTQNPAPGLGT MVTQPVLRPVQVMQNaNHVTSSPV ASQPIFITQGFVRNVRPVQNAMN QVGIVLNVQQGQTVRPITLVPAGT QFVKPTVGVPQVFSQMTVPVRPGST MPVRPTTNTFTTTPATLTIRSTVPQ SQSQQTKSTPSTSTPTATQPTSLGQ LAVQSPGQSNQTTNPKLAPSFPSPP AVSIASFVTVKRPGVTGENSNEVAK LVNTLNTIPSLGQSPGPVVVSNNSS AHGSQRTSGPESSMKVTSSIPVFDL QDGGKICPRCNAQFVRVTEALRGH MCYCCPEMVEYQKKGKSLDSEPSV PSAAKPPSPEKTAPVASTPSSTIPAL SPPTKVPEPNENVGDAVQTKLIMLV DDFYGRDGGKVAQLTNFPKVATS FRCPHCTKRLKNNIRFMNHHKHHV ELDQQNGEVDGHTICQHCYRQFSTP FQLQCHLENVHSPYESTTKCKICEW AFESEPLFLQHKMDTHKPGEMPYV CQVCQYRSSLYSEVDVHFRMIHED TRHLLCPYCLKVFKNNGNAFQQHYM RHQKRNVYHCNKCRLQFLFAKDKI EHLQHHKTRFKPKQLEGLKPGTK VTIRASRGQPRTPVSSNDTPPSALQ EAAPLTSSMDPLPVFLYPPVQRSIQK RAVRKMSVMGRQTCLECSFEIPDFP NHFTYVHCSLCRYSTCCSRAYAN HMINNHVPRKSPKYLALFKNSVSGI KLACTSCTFVTSVGDAMAKHLVFN PSHRSSSILPRGLTWIAHSRHGQTRD RVHDRNVKNMYPSPSFTNKAATV KSAGATPAEPEELLTPLAPALPSPAS TATPPPTPTHPQALALPLATEGAEC LNVDDQDEGSPVTQEPELASGGGG SGGVGKKEQLSVKKLRVVLFAACC NTEQAAEHFRNPQRRIRRWLRRFQ ASQGENLEGKYLSEAEKLAEWV LTQREQQLPVNEETLFQKATKIGRS LEGGFKISYEWAVRFMLRHHLTPH ARRAVAHTL\PKDVAENAGLFIDFV QRQIHNDLPLSMIVAIDEISLFLDT EVLSSDDRKENALQTVGTGEPWCD VVLAILADGTVLPTLVFYRGQMDQ PANMPDSNLEAKESGYSDDEIME LWSTRVWQKHTACQRSKGMVMD CHRTHLSEEVLAMLSASSTLPAVVP AGCSSKIQPLDVCIKRTVKNFLHKK WKEQAREMADTACDSVLLQLVL VWLGEVLGVIGDCPKLVQRSFLVA SVLPDPGNINSPTRNADMQKELIA SLEEQLKLSGEHFESSTPRSSPEE



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						TIEPESLHQLFEGESENE\SFYGFEEA DLDLMEI
1919	7416	A	2058	3	824	
1920	7417	A	2059	1	1077	MLSGVGGFVLGLLFLGAGLFIYFRN QKAEESFVSALSIDLSGGGNMALLS MVCLKFPGG\SCMAALT\VTLMVLS SPLALAG\DTR\PPVRLRKTEDEPLG CVLSGLRVGPDSVFPGGRFCNRIVL VPPARFLEQVKHECHFFNGTERVRF LDTRYFYHQEEYVRFDSDVGEYRAV TELGRPDAEYWNSQKDLLEQKRAA VDTYCRHNYGVGESFTVQRRVYPE VTVYPAKTQPLQHHNLLVCSVNGF YPGSIEVRWFRNGQEEKTG\VVSTGL IQNGDWTFTQLVMLETVPRSGEVY TCQVEHPSLT\TSPLTVEWRARSESAQ SKMLSGVGGFVLGLLFLGAGLFIYF RNQKGHSGLQPTGFLS
1921	7418	A	2060	2	867	GRVGLPAALAPGPVLFSSMVCLRLP GGSCMAVLT\VTLMVLS\PLALAGD TRPRFLEYSTSECHFFNGTERVRYL DRYFHNQENVRFDSDVGEFRAVT ELGRPDAEYWNSQKDLLEQKRAA VDNYCRHNYGVVESFTVQRRVHPK VTVYPAKTQPLQHHNLLVCSVSGF YPGSIEVRWFRNGQEEKTG\VVSTGL LIHNGDWTFT\HTL\VMLETVPRSGEV YTC\QVEAPRA*QAPLTVE\WRARS ESAQSKMLSGVGGFVLGLLFLGAG LFIYFRNQKGHSGLQPTGFLS
1922	7419	A	2061	3	940	RNFRVDPVRREEGFIVLPERDLPA SLAPGPVLVSSMVSLKLPGGSCMTA RTVSLMVLS\PLALAGDTRPFLW QPKRECHFFNGTERVRFDRYFYN QEEVVRFDSDVGEYRAVTELGRPD AEY\WNSQKDLLE\QRRAA\VDTYC RHNYGVGESFPVQRR\VEPKVTY PSKTQPLQHHNLL/VFCSVSGFYPGS IEVRWFLNGQEEKAG\VPQALIQN GDWTFQTW\VMLETVPRSGEGLHC QSE\HPGVTSLLTVEWRARSESAQS KMLSGVGGFVLG\LLLPLGPGLFYIY FRNQKGHSGLQPTGFPELKCR
1923	7420	A	2062	25	384	EFHRLRENPPMVAVSCPTKTNVKG PPGGKVGAAHVRSMCAEALERMFL SFPT\TKTYFP\HFDL\SHG\SAQVKGP RQRRWPNALTKRRGAPLDDMP\NT ALSALSDLHAHKLVRDPVQLSSS
1924	7421	A	2065	47	353	AGRVRILWDCVEVDLT\ELGAGQSV EASRHAWEVVRNRCHWAPQLFLS FAPGWGG\GEGRVGDGGA\VGWFPS PQPPSSPPGVMP\CPHDDRGT\EPGRD LVPAQ
1925	7422	A	2066	3	692	KRLPKMAEVQVLVL\DGRAHSSLG\ RLAGHRGLNQVLLGRK\VVVV\RC GI\NISGNFYRNEVKVPWLFPSKR\I NTNPSRRPLTTSGAPSR\FWRTVRG MLP\HKTQAEAKAA\LDRL\KVFDGI

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						PAPPYGQEKSGMVVPAALKVVRLLK PTRKFCLIFFFSGGGALAHQVGWK YQAVTAPLEEKRKREKPRFHRYRK KENSIMRLARKQAREETWRKKIDKY TEVLKTHGLLV
1926	7423	A	2067	1	2091	
1927	7424	A	2068	384	4189	ERTSPAMITSELPVLQDSTNEATAH SDAGSELEETE VKGKRIRGRPRPP STNKKPRKSPCEKSKIEAGIRGAGR GRANGHPQQNGEGEPVTLFEVVKL GKSAMQSVVDDWIESYKQDRDIAL LDLINFQICSGCRGTVRIEMFRNM QNAEIIRKMTTEEFDESDGYPLTMP GPQWKKFRSNCFEFIGVLIRQCQYSI IYDEYMMDTVISLLTGLSDSQVRAF RHTSTLAAMKLM TALVNVALNLSI HQDNTQRQYEAERNKMIGKRANER LELLQKRKELQENQDEIENMMNSI FKGIFVHRYRDAIAEIRAICIEIGV WMKMYSDAFLNDSYLKYVGWTLH DRQGEVRLKCLKALQSLYTNRELF KLELFTNRFKDRIVSMTLDKEYDVA VEAIRLVTLILHGSEALSNEDECENV YHLVYSAHRPVAVAAGEFLHKKLF SRHDPQAEALAKRRGRNSPNGNLI RMLVLFFLESELHEHAAYLVDSLW ESSQELLKDWECEMTELLLEEPVQGE EAMSDRQESALIELMVCTIRQAAEA HPPVGRGTGKRVLTAKERKTQIDD RNKLTEHFIITLPMLLSKYSADA EK VANLLQIPQYFDLEIYSTGRMEKHL DALLKQIKFVVEKHVESDVLEACS KTYSILCSEETYIQNRVDIARSQID EFVDRFNHSDVLLQEGEEADDDDI YNVLSTLKR L TSFQNAHDLTKWDL FGNCYRLLKTGIEHGAMPEQIVVQA LQCSHYSILWQLVKITDGSPSKEDL LVLRKTVKSFLAVCQQCLSNVNT VKEQAFMLLCDLLMIFSHQLMTGG REGLOPLVFNPDTGLQSELLSFVMD HVFIDQDEENQSMEGDEEDEANKIE ALHKRRNLLAAFSKLIHYDIVDMHA AADIFKHMYKYNDYGDIIKETLSK TRQIDKIQCAKTLILSLQQLFNELVQ EQGPNLDRTSAHVSGIKELARRFAL TFGLDQIKTREAVATLHKDGIEFAF KYQNQKGQYPPPNLAFLEVLSEFS SKLLRQDKKT VHSYLEKFLTEQMM ERREDVWLPLISYRNSLV TGGEDDR MSVNSGSSSKTSSVRNKKGRPPLH KKRVEDES LDNTWLNRTDTMIQTP GPLPAPQLTYTVLRENSRPMGDQI QEPSEHGSEPYFLHNPQM QISWLG HPKLEHLNPKDITGMNYMKVITGA RHAALCLMEEDAEPFEDVMMSSR SQLEDMNNEEFEDTMVIDLPPSRN RRERAELRPDFVDSAAIIEDDSGFG MPMF

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1928	7425	A	2069	1	2661	
1929	7426	A	2070	1	1454	
1930	7427	A	2071	1	2364	
1931	7428	A	2072	1	1368	
1932	7429	A	2073	114	1473	VKGDRFGALRFNDPCPAGIKLPMTFF TELEKTTLKFIWNQKRARIKSIQS KNKAGGSTLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTGPSEITPHT YNYLIFDKPEKNKQWGNDSL FNKW CWENWLAICRKLKLDPFLTPYTRIN SRWIKDLNVRPKTIKTLEENLGITIQ DIGMGKDFMSKTPKAMATKDKIDK WDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKQIY KKKTNNPIKKWAKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIKTT MRYHLTPVRMAIKKSGNNRCWRG CGEIGTLLHCWWDWKL VQPLWKS VWRFLRDLELEIPFDPAPLLGIYPN DYKSCCYKDTCTRMFIVALFTIAKT WNQPKCPTMIDWIKMWHIYTME YYAAIKNDEFM/SFVG TWKLEIIIL SKLLQE QKTK
1933	7430	B	2074	1	1890	MDKFLDTYTLPRNLNQEVEESLNRPI TGSEIVAINSLPTKKSPGPDGFTAEF YQRYKEELVPFLLKLFQSIEKEGILP NSFYEASIIIPKPGRD TTKIENFRPIS LMNIDAKILNKILANRIQQHIKKLIH HDQVGFTPGMQGWFNICKSINIIQHI NRTKDKNHMIIISIDAEKAFDKIQQH FMLKTLNKLGDGTYLKMIRTIYDK PTANIILNGQKLEAFPLKTGTROGCP LSPLLFNIVMELLARAIRQEKEIKGI QLGKEEVKLSLFADDMIRIKYLGIG LIRDMKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTLNFI WNQKRARTAKSILSQKNKARGIML PDFKLYYKATVTKTAWCWYQNRD IDQWNRTPESEITPHIYNYLIFDKPD KNKQWGKDSL FNKWCWENWLAIC RKLKLHPFLTPYTTINSRWIKDLN RPKTIKTLEENLGNTIQDIGMGKDF MSKTPKAMATKAKIDKWDLIKLS FCTAKETTISVNRQPTKWEKIFATY SSDTGLISRIYNELKQIYKKKTNNPI NKWAKDMNRHFSKEDIYAAQKHM KNAHHHWPSEKCKSKHNEIPSHTS*
1934	7431	A	2075	1	2676	MKAEIKMFFEINENKDTTYQNLWD AFKAVCRGKFIALNAHN RKQERP KI DTLTSQKLEKEKQE QTHSKASRRQE MTKIRAE LKEIEIQKTLQKINESRSW FFERINKIDRPLARLIKKKREKNQID AIKNDKGDITTDPTIEIQT TIREYYKH LYANKLENLEEMDKFLDTYTLPRNL NQEEVESLNRPI TGPEIVAINSLPTK RSPGPDGFTAEFYQRYKEELVPFLL KLFQSIEKEGILPNSFYEASIIIPKPG

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						RDTTKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIQGMQG WFNIRKSINVVQHINRTKHKNHMII SIDA EKAFDKIQPFMLKTLNKL SID GTYLKIIIRATYDKPTANIILNGQNLE AFPLKTGTRQGHPLSPLLFNIVLEVL ARAIRQEKEIKAQNLLKLISNFRKVS VYKINVQKSQAFLYTNNRQTESQIM RELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNIPCS WIGRINIVKMAILPKVIYRFNAIPIKL PTTFFTELEKTILKFIWNQKRAHIAK TILSQKNKAGGIMLPDFKLYYKATV TKTAWYWYQKRDIQWNRIELSEII PHIYNHLIFDKPDKNKKWGKDSVF NKRCWENWLAICRKLKLDFTLTPY TKINSRWIKDLHVRPKAIKTLEENL GITIQDIGMGKDFTSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRVNR QPTKWEKIFAIYSSDKGLISRIYKEL KQIYKKKTNNPIKKWAKDMNRHFS KEDIYAANRHMKKCSSSLAIREMQI KTTMRYHLTPVRKAIKKSGNNRC WRGCGEIGTLLHCWWDCCLVQPL WKTWVQFLRDLELEIPFYPAIPLLGI YPKDY
1935	7432	A	2076	1	3045	MDKFLNTYTLPRLKQEEVESLNRPI TGSDIEAIINSLPTKK/SPGPDGFTAE FCQRYKEE/LEKEGILPNSFYEASII PKPASDTTKKENFRPISLMNINAKIL NKILAKQIRQHIKKLIHHDQVGFIQ MHGLFNICKSVNIIQHINRTNDKNH MIISIDA EKPFDKIQHFMLKTLNKL AQNLLKLIGNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMNEFPFTIASKR IKYLGIQLTRDVKDLFKENYKALLN EIKEDTNKWKNIPCS/WEKTTLKFI W/NQKRAHIAKSII SQNKAGGITLP DFKLYCKATVTKTAWYWYQNRDI DQWNRTESEIMPHIYNHLIFDKPD KKKKWGKDSL FNKWCWENWLAIC RKLKLDPFLTPDTKINSRRIKDLNVR PEMIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLSF CTAKETTIRVNRQPTWEKIFAIYSS DKGLISRIYNELKQIYKKKTNNPIEK WAKDMNRHFSKEDIYA AKKHKMCK CSSSLVIREIQIKTTMRYHLTPVRMA IIKKSGNNRCWRGCGEIGTLLHCW WDCKLVQPLWKS VWRFLRDLELEI PFDPAIPLLAAPSLPSGLRSPSKSSPS PPSRCTLVII LLHVFWDIVFFDGCEK KRWYILLIVLLTRLLVSACTFTEGY TVGFSTFEALRLGLSRYWLPSSAC RRPVGLQLVMINSNGNFQVIAMEGT VASECCHGNGKLTWHRPVLSVCSF SRCTVQAAGGSAILEDGDP LLTAPL GSTPQAAVCRGPRGRELRAAPADS

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						HLFQRDLWPFNKVIVHGEKGSNQT SQGLLNTGSEMTIVLENPKYHSGPP VRVSPDGGQVIEVLADPSYTGPTA LNNVFFAFQCNFYFDHIPENCGFSD PSDPQNLQKGEGCPSLVRASTAPPQ EKATEQPLLCKTTESPFGMTVGPCT DETLDHGAPSKHVPGTAHNELALL DLRVKSAGSAAVHHKLKVLHWRS SLSNNKGTGRLYEQVA
1936	7433	A	2077	1	2142	
1937	7434	A	2078	1	1551	MRFKEKIHLHNIKEPSEAASADGGA VASYPDLAKIVDEGRYKAEVMQLR CGWRAPASDCVHSVAVVGVDVSL EVLARAIRQEKEIKGIQLGKEEVKLS LFADDMIVYLENPTVSAQNLLKLIS NFSRVSGYKINVQKSQAFLYTNNK QTESQIMSELPFTIASKTIKYLGQLT RDVKDLFKENYKPLLNIKEDTNK WKNIPCSWIGRINIVKMAILPKVIYR FNAIHIKLPMTFFTELEKTTLKFIWN QKGVHIAKSILSKKNKAGGIMLPHF KLYYKATVTKTAWYQYQNRYPDQ CNRTEPSEIIPHIYNHLMFDKPDKNK KWGKDSL FNKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNVRPK PIKTLEENLGITIQDIGMGKDFMSKT PKAIATKAKIDKWDLIKLSFCTAK ETTIGVNRQPTELEKIFAIYSSDKGLI SRIYKELKQYKKKNNPIKKWVKD MNRHFSKEDIYAVNRHMKKCSSSL VIREMQIKTTMRYLTPV
1938	7435	A	2079	1	1458	GLSGDLLGAHQLPDVLGCVQPLPD LLLPPQNLLALQSLQDDLLWALDP AAAAPWAMDRGAATQWAVGPVV SDPWVMEAVASLPSAMDLDAAQP TWLLGAASLLVTDQPMQPSADQL AEFPDLLSKVSQSLRIKYLGIKLTRN VKDLFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIYRFN APIKLPMTFFTELENTTLKFIWNQK RACIAKSILSQKNKAGSIMLPDFKL YHKATVTKTAWYQYQNRDIDQWN GTEPSEIMSHIYNLIFDKPEKNQR GKDSLFSKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKIIT LEENLVNTIQDIGMGKDFMSKTPKA MATKAKIDKWDLIKQKSFCTAKET TIRVNRQPTEWEKIFAIYSSDKGLIS RIYKELQQIYRKKTNNPIKKWAKD MNRHFSKEDIYAANRHMKKCSSSL AIREMQIKTTMRYHLTPV
1939	7436	A	2080	1	2028	
1940	7437	A	2081	2	1547	
1941	7438	A	2082	3	1945	
1942	7439	A	2083	1	2124	
1943	7440	A	2084	1	2250	
1944	7441	A	2085	2	2483	GKYYKLSSGTAPTCVSLGWGLARG

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						DSAAPALGSRTSACAPCSHGTWKL SLEPSDRLSPCDRSSEEAHTHAPHRL LALVASLPWSRLPLLAPQSHSEAEA TSQPTGVENHHQKTRYVKAGGPVI CRSLPESRGFLWASEGRKCMIGSW AAMGRLRKSTISSRFGPQTLGTGR PQAIPVLKKHSDAVLLGVCFLKLLH QHHQELGENADSQTLPQTHWEFILS EDYNKMTPVKNYQVLEVLARAMR QEKQIKSIQLGKEEVKLSVFADDMI VYLENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTNRRQTESQIISEL PFTIPSKRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNIPCSWV GRINIMKMAILPRVIYIFNAISIKLPM TFFTELEKTTLKFIWNQKRARIAKTI LSQKNKAGGITLPDFKLYYKATVT KTAWYWYQNRGVDQWNRIEPSEII PHIHNHLIFDKPDKNKKWGKDSLFT KWCWENWLAICRKLKLPFLTPYT KINSTWIKDLNVRPKTIKTLEENLGI TIQDIGMGKDFMSKTPKAMATKAK IDKWDLIKLSFCTAKETTIRVNRQ PTEWEKIFTIYPSDKGLIPRIYKELK QIYKKKSNNPIKKWAKDINRHFSK EDIYAANRHMKKCSSSLVIREMQN KITIR/YHLTPVRMAIKKSGNNRDM DEAGNNHSEQTIARTENQAPYLLTH RWELNNENTWTQVEEHHTLGPIVG VICRKVFPNGSGPSKPSGLHFSQPLP QVTSVVAKITIVPWEMKLIAMGVQ DELNIAFHKNHLLMNDTTIHMTPIYI QPAPKS
1945	7442	A	2086	1	2622	
1946	7443	A	2087	853	2831	YPESTMNSNKFTRKKQTTPSKSG*R I*TDTSQKKTFMQPKDT*KNAQHH WSLEKCKSKPQ*DTISHQLEWRSLK SQDRKD*QSTLLAILIKKGQKNQI DT/IKNDKEGITTDPREIQTIREYYK HLYTNKVENLEEMDKFLDTYTLPT LKQKKEVKTLNRPITGSEIEAIINSLP T/KKSPGPDRAFTAEFYR/DIRSSGQG NQARERNKGYSIRKRGSIQIVPVC* HHCIFRKPHHLSPKSS*ADKQLQOS LRIONQSAKITSIPHQ*QTNREPNE *TPIHNCFKENKMPRNPYTKGCEGS LQGELQTTAQ*NKRGHKRMEEHSM LMDRKNQYRENGHTAQGNL*IQCH PHQATNDFFRIGKNYFKVHMEPK KSPHRQVNPKEQSWRHHTT*LQ TILQGYNSQNSMVLVPKQRHRPME QNRAPGNNTIHLQLSDL*QI*QKQE MGKGFPI**MVLGKLANHM*KAET GSLPHILYKN*FKMD*RLKC*T*NH KNPRRKPRQYHSGHRHGQGLHD*N TKSNGNKSQN*QMGSN*TKELLHST RNYHQSEQATYRMGENFCNLLI*Q RANIQNLQRT*TNLQDKNKQPHQK

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						VGKGYEQTLKRRHLCSQKTHEKM LIITGHQRNANQNHNEIPSHTS*NGD H/SNQVRKQQVLERMWRN
1947	7444	A	2088	1	4954	MVFSIDAQKAFDKIQHRFMLKTLN KLGIDGTYLKIIRAIYNKPTGNIILNG QKLEAFPLKTGTRQGCPLSPLLFNIV LEVLAIRAIQEKEIKGIQLGKEEVK LSLFADDIIVYLENPIVSAQNLLKLI GNFSKVSGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYLGIQL TRDVKNLFKENYKPLLNEIKEDTDK WKNIPCSWIGRIHIVKMATLPKVIY RLHAIHIKLPMTFFTELEKTTLKFIW NKKRARIASILSQKNKGGGITPPDF KLYYKATVTKTARYWYQNRDIDQ WKTREPSEIIPHIYNHLIFDKPDKNK KWGKDSL FNKWCWENWLAICRKL KLNPF LTPYTKINSRWIKDLNIRPKT IKTLEENLGNTIQDKGVGKDFMSQT PKAMATKAKIDKWDLIKLSFCTA KETTIRVNRQPTWEKIFAIYSSDKG LISRIYKELKQIDKKANNPINKWA KDMNRHFSKEDIYAANRHMKKSSS SLAIREMQIKTTMRYHLTPVRMVII KKSGNNSEGLNPGYKGFPTIWAFL PVAQSKDSGLASLNSDPDIPSMLEC SLKAPQLYRSKNVGQVFISSASQAF TKKARIYARLRVSQALKTLCKSSCH DGWSFERLARIQEVSLPISPDILCSE AYHYGTPQWLVAATGTAQTFLEL NQSQYQKQEQTHSKASRMQEIT KIRAELEIETRKTLQKIDESRSWFF ERINKTDRPLARLTKQKREKNQIDA IKNGKGDITDPTGIQITIREYYKHL YAKKLENLEEMDKFLDTYTLPRLN QEEVDSLNRPITGAEIVAIINSLPTKK SPGPDGFTAIFYQRHKEELVPFLK LFQSIEKEGILPNSFYEASILPKPGR DTTKENLRPISLMNIDAKILSKILA NRIQQHIKKLIHHDQVCFIPGMQGW FNIRKSINVIQHINRAKDKNHMISID AEKAFDKIQQTFLKTLNKLIGIDGT YFKIIRAIYEKPTANIILNGQKLEAFP LKTGTRQGCPLSPLLFNIVLEVLAIR AIQEKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFSKVS GYKIYKIDVQKSQAFLYTNNTDKQ ESQIMSELPFTTASRIKYLGIQLTR DVKDLFKVENHKPLLNEIKEDTNKW KNIFIPCLWVGRINIVKMAILPKGIY RFNAIPIKLPMTFFTELEKTTLKFIW NQKRARITKSILSQKNKAGGITLPDF KLYYKATLTKTAWYWYQHRDINQ WNRTEPSEIIPHIYNHLIFDKPDKNK KWGKHSLFNKWCWESWLDICRKL KLDPYTKFTPYTKINSRWIKGLNVR PKTIKTLEDKPIQVFNTIQDIGMGKD FMSKTPKAMATKAKIDKWDLIKLK

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						SFCTGKETTIRVNRQPTWEKIFAIIY SSDKELISRIYKELKQIYKKK\TNNPI KKWAKDMNRHFSKEDIYAANKHM KK\CSSSLAIREMQIQTMMRYHLTPV RMA\IKKSGNNRCWRGCGEVGTL HCWWDCNLVQPLWKS VWRFLRDL ELEIPFDPAPILLGIYPKDYKSCCYK DTCTRMFIVALFTIAKTWNQPKCPT MMDWIKKMWHIYTMEYYAAIKND EFMSFVGTWMKLEIILSKLSQEQT KHRIFSLIGGN
1948	7445	A	2089	93	225	
1949	7446	A	2090	133	849	PVWPKWSGWPLLMRSFAPARIATV VIGGVVAMAAVPMVLSAMGFTSV GIAASSIAAKMMSTAAIANGGGVA AGSLVAILQSVAWLYSSSHQEPLRK STPDPKATELTRAGMEASALTSSAV TSVAKVVRVAS/GSCVVLPLARIAT VVIGGVVAMAAVPMVLSAMGFTS VGIAASSIAAKMMSTAAIANGGGV AAGSLVAILQSVAWLYSSSHQEPLR KSTPDPKATELTRAGMEASALTSSA VTSVAKVVRVASGS AVVPLAALS PNISLLRPLLGALEASSFMLGSLTGT LFCNLEMGNRLRKWRGSQCGSTHR MFFWFPARIATSCDWRSCGPMAGC ANGCSSAMGLQLRAGIALVLP
1950	7447	A	2091	161	1344	TCPVLR YHSTMSSHKGSAVAQNG APASNREADTVLAEGLPLEEKGK RVIANPPK\AEEEQTCPVPQ\EEEE VRVL\TLPLQAHAMEKMEEFVYK VWEGRWVIPYDVLPL\WLKGNL YLLHGHPPMPSPFRACFKSIFR\HTE TGN\WTHLA/LGFVLFLLGILTML RPNMYFMAPLQ/EKKVVFGMFFLG AVLCLSFSWLFHTAYCHFGGVFSTF PQRELFKGLLLNMGELWSPGLYY SFYCSP\QPARLIYLSIVCVLG\ISANV AQWDRFATPKHRQTRAGVFLG\LG LSG\VVPTMHFTNRWRALSKATT GQ\MGWFFLMAVMYITGKLAFNAA RIPERFFPGK\FDIWFQSHQ\FHVL VV\AAAFVHFYGS/VSNLQEFPLTGL EGGL
1951	7448	A	2092	2	1419	RLRDPYRSSRLCRRGASRTSSAARS RSRSPAVEGCNRSPPGAPQAPRARR RPSRGAPGRAMVKVA\FNSALAQK EAKKDEPKSGEEALIIPDAVAVDC KDPDDVVLVGQRRACGWRMCFGL AFMLAGVILGGAYLYKYFALQPDD VYYCGIKYIK\DDVILN/ESPSADAP AA\LYQTIE\ENIK\FEERRSLNFISVP VPEFADSDPAKIVQDFNRKLTAYL DFNL\DKCYVIPLNTSMCYATPKTL LELLINIKAGNLFALSPYLD SMRHM GYLLDR\ENIDHLGF\FIYRLCHDK\ ETYKLATRRKLFKGIQ\KREGQQLF SAISGIFENKFAVETLICSW



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1952	7449	A	2093	1	669	
1953	7450	A	2094	267	550	GRITMMFGAKRRQEEWEKVRKPED PEECPEEVYDPRSLYERLQEQKDRK QQLRGTVSNCKNMVRGLDEDET TFLDEVSRQELIEKQPKRRRT
1954	7451	A	2095	1	418	
1955	7452	A	2096	272	383	
1956	7453	A	2097	118	379	RSGGGRGRRGPEVLHLKHPMLKRP DFLYRKPFSSRGWEHGPPSRKSHLL/ GAPPPFPKFFCHLC*APSPFRVLSPY QKRIHLVPPTQLH
1957	7454	A	2098	1	276	
1958	7455	A	2099	1	341	
1959	7456	A	2100	1	450	ACPYLALNSSMFCPDLILPTCLISST GFVGEGKFLQGFKSLSPGSLWLSEG LDYFLSVPGDQYDVCAICLDEYED GDKLRVLPCHAHYHSRCVDPWLTQ TRKTCPIK\QPVHRGPGDEDQEE\ ETQGQEEGYEGE\PRDQPAASERTPF LG
1960	7457	A	2101	238	525	
1961	7458	B	2102	178	373	XLPQPLRGPLAHS DPERPAPFASSLF IGVLGKTKRKKLKGKEEGDERGS KGTNPALRKDPTFGF*
1962	7459	A	2103	634	1940	SGVDISFFELVFLPRRPHVAGKWDL GGGWDPGIPKGGAGRAQNSASAPC YQDARPPQPLSSRCHAPLQPFPLPV VVA AVLWGSGPDPGASFRATS DH NCQH GIFADLPALF\GATLSLEG PQG L\LGEPHPDNACSPIAPPPAPVNGS VFIALLRRFDCNFDLKV LNAQKAG YGAAVIHNVNSNELLKMVWNSEEI QQQIWIPSVFIGERSSEYL RALFVYE KGARVLLVPDNTFPLGYLLIPFTGIV GLLV LAMGAVMIARCIQHR\KR\ LQ RNRLTK\EQLNQIPTQT NQKRDQY DVCAICLIEYEDGDK\LR\VFPGAHA YHNRCVDPWLTQTR\KT\CPICK\Q PVHR\GPGDEDQEEETQGQK\EGDE GE\PRDHPASERTPLL G\SSPTLPTS\ FGFLRPKFPLVFS LGP\STD PPLSPPS SPCYPGLITPHTYTFG
1963	7460	A	2104	25	527	EFHRLRENPPMVA VSCPTKTNVKA\ AWG\KVG AHA VRSMCAEALERMF LSFPT\TKTYFPHFDL\SHG\SAQVKG ATGKKVADALTN A VANVDDMPN VAVRPEATLHAHKL RVDPVNF\KL LKPLACLVDPGPAHLRPSFTPGGA TSSLGQSFLGFL LKHRCNLNPNYR
1964	7461	A	2105	262	364	
1965	7462	A	2106	3	1265	PRPGLRAPDAPGSAPRERAQPRDPR AGQVRRLD LGDKARPRAQLRRESG GAESVTRPLRAASPAPPRAARAA MSEKPKLGRRAPSASLSARCRA PR CCSCRARRPRI PPQQCRSVFACSSP ESLLVGVALSPGIALGAGSCVECTE SAREQASGVTPKGRALRGLAPVSST

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						AVLPGRPSRPRYSPTSPHRVPAIASP SVRPPLSFVSPQSCPQCAPTPTHRAP CAPTASIAPGVRPPLPIAPPGVRPR LPITPPMEGVKTENDHINKVAGQD GSVVQFKIKRHTPLSKLMKAYCER QGLSMRQIRFARFDGQPNQWKLDDL STAGDWKDEDTIDVFPSSKTGRCA GEQPWQGTVSRGPVPKPGPSILALL LNGEHGDHADHKGVCGNSRTFTT MIFLSLMYFKLQLKTISAGMNL
1966	7463	A	2107	4	408	
1967	7464	A	2108	1	465	PACGYVPALSSASKSRSALGFPLPR CPRGRVDPELAALWPLLQCCCQLL QMGCFLPLGLGPAI*SPHPHQSHSLGI DRS*FQNAQSPPGFCVSCGPLREVS VCLP*PG*ARCCLGCSFGSGHSRLG NTAQ TANQCILPQASSTLCC*LHPQ NLVCP
1968	7465	A	2109	126	488	
1969	7466	A	2110	1	5586	
1970	7467	A	2111	68	310	TDLPTQNMVFTFSSNWG/TVRQVLS /YSCTRETLQHRELDKTRARGPE*GS VVLTSPLWSPCRKCATGTYHGSPH CQSSGGGR
1971	7468	A	2112	2	630	FFFFSDLLNFISSESLGSQQGCKAK WQ*LKGPEQSWCWEGPAWTGRRG GDLNIQG*KPVNSSPSSVFVFCVASP AYRRSSSSFSRISFSVSGICPWWDSP DGEVGTTFPSQFAKGRKGLIRRGGP QHPLRLSPGPIEEQK*GLVSPKARLG ISPCQLCPGFWSYL\DSVSPPPGGSC SGCTVPGSSHNVSVPVSHSPGPACGV RTALSSA
1972	7469	A	2113	331	754	NFLKTNNVWSKWTHVLSQFWYQG FJLFLGSIKCTEIDSSICTEAPSHTK QHMLGGKNQTLNS/DPQGVKCSG* EAM*PRGGISQKDNMGEMNGTT TTKTFCFIFMPGEDQGCSSCVSTRIT RKSQVQKSRGTISRYFHK
1973	7470	B	2114	110	225	XLGRPQLAGSLRSRFPISGMRGEFFT QDCQRNAGREELQGRLSIQSFSPILA LGPDDSCETKTGMDKLS*
1974	7471	A	2115	83	287	SLLKCSGVIVLRRPLGYGQVMK* PGAAY*GRTG*SHPFSTDWSTDTG VRKSIWCHRNCRWESPS
1975	7472	A	2116	167	397	EPLLALLKSGEVAPARQEATGLGEA KCSCAMGLSGPKTQPQEGCEERRL QSKR*SSGDPGWDEGHWPPTNRS CLL
1976	7473	A	2117	1	540	FCHLQIYYFISSESLGSQQGCKAK WQ*LKGPEQSWCWEGPAWTGRRG GDLNIQG*NTSNSSPSSVFVICVTSP AIRRKLLNLSLGLSLKFLGSPGGT AGMGKSVPLSPSQVCCGFRSFNHQ AGHAPGCTVPGSSP*CVSRVQHPSG PCMWWVTYPALSLSFNKSQCPWVFP LPTMPPG

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1977	7474	A	2118	1	3121	RQEAELARMGFDLQNVWIVSHINS NYKLCPSYPQKLLVPVWITDKELEN VASFRSWKRIPVVVYRHLRNGAAI ARCSQPEISWWGWRNADDEYL VTS IAKACALDPGTRATGGSSTGNNDT SEACDADFSSLTACSGVESTAAPQ KLLILDARSYTA AVANRAKGGGCE CEEYYPNCEVVFMGMANIHAIRNSF QYLRAVCSQMPDPSNWLSALESTK WLQHLSVMLKAAVLVANTVDREG RPVLVHCSDGWDRTQIVALAKILL DPYYRTLEGFQVLVESDWLDFGHK FGDRCGHQENVEDQNEQCPVFLQW LDSVHQLLKQFPCLFEFNEAFLVKL VQHTYSCLYGTFLANNPCEREKRN YKRTCSVWALLRAGNKNFHNFLYT PSSDMVLHPVCHVRALHLWTA VYL PASSPCTLGEENMDLYLSPVAQSQE FSGRSLDRLPKTRSMDDL SACTS SPLTRTSSDPNLNNHCQEV RVGLEP WHSNPEGSETSFVDSGVGGPQQT GEVGLPPPLPSSQKDYL SNKPKSH KSCSPSYKLLNTAVPREMKSN TSDP EIKVLEETKGPAPDPSAQDELGRTL DGIGEPPEHCPETEA VSALSKVISNK CDGVCNFPESQNSPTGTPQQAQPD SMLGVPSKCVLDHSLSTVCNPPSAA CQTPLDPSTDFLNQDSSGSVASISH QEQLSSVPDLTHGEEDIGKRGNNRN GQLLENPRFGKMPLELVKRPISQSI SEFSFLGSNWDSFQGMVTSFPSGEA TPRRLLSYGCCSKRPNSKQMRATGP CFGGQWAQREGVKSPVCSSHSNGH CTGPGGKNQMWLSSH PKQVSSTKP VPLNCPSVPPLYLDDDG LFPPTDVI QHRLRQIEAGYKQEVEQLRRQVRE FQMRLDIRHWCAPPAEPPMDYEDD FTCLKESDGS DTEDFGSDHSEDCLS EASWEPVDKKETE VTRWVPDHMA SHCYNCDCFWLAKRRHHCRNCG NVFCAGCCHLKLPIPDQQLYDPVLV CNSCYEHIQVSRARELMSQQLKKPI ATASS
1978	7475	A	2123	3	259	FPHRAGPILSSFQVPQRWL VGGFGR NCIAGGESVWDR TNKYTRN* AQE WGMFWSLDGHLGESIIRGRSNTG ALSCPWPLGHL P
1979	7476	A	2124	1171	1784	KLYSLSVLYKGEAKV VLLKPA YDV SSFSFFQRP TVQEFMTFTSQLIVER S/SRKGTASVKEQDYLCHVYVRN DSL AG/VVVIADNEYPSRGGPFTLLA EKVLDEFSQAKSHRIDW PVGIPWL TIHYPALDGHL SRYQNPREADPMT KVQAELDETKIILHNTPWESLLERG EKLD DLVSKSEVLGTQSKAFYKTA RKQNSCCAIM
1980	7477	A	2125	2	262	RGNWVFLHTTEFSL TRSLISFN SCFI TRLECSGAITAHCSLDLLGSS/QSPTS

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						PSRVAGTTGVCHHTQLIYLKQFFLE MRSPFVAQLV
1981	7478	A	2126	36	376	PFDPAVLAKAAVRALVASRLAAA SAFTSLSPGGRTSPQRAALHLSVPRP AARVALVLVHLSRGGAEVQIFAPD VPQMHVIDHTKGQPSGESRCGGGI GTCFLSTSHGAAFF
1982	7479	A	2127	3	724	LAAASFTPLCPVCRTSPQRAALHL CVPRPAGRVSLVLSGCGVYNGTDIH EASAILVHLSRGGAEVQIFAPDVPH MHVNDHTKGQPSGESMNVLTES ERIRRGKITDLANLSAANHDAIIFP GGFGAAKNLSTFAVDGKDCKVNKE VERVLKEFHQAGKPIGHSKLDLPGH CPGRPLKWSLRKRCRLRAPEGGPC CSRVTAGVKVSPMVSTSGSRPCQRS VPWMSAQREPMALSSVTD
1983	7480	A	2128	172	1020	PSDPAVLAKAAVRALVASRLAAA SAFTSLSPGGRTSPQRAALHLSVPRP AARVALVLSGCGVYDGTIEHEASA ILEHLSRGRAEDHIFAPDVPHMHVI DHTKGQPSGESRNVLTESARIARG KITDLANLSAANHDAIIFP/GEFG AAKNLSTFCRWTKICKVNKEVER VLKEFHQAGKPIGLCCIAPVLA VLKGVEVTVGHEQEEGGWVYAG TAEAILALGAKHCVKVEVVEAHVD QKNKVVTTPAFMCETALHYIHDG GAMVRKVLELTGK
1984	7481	A	2129	1	416	IQYRSDELHSITMKKGGVLFLLGII LLVLIAAHGTPVVRKGRCSIIITNQ GTIHLQSLKDLKPFGPSQCKIDIIA TLKNGIQTCLNPDSADVKELIKKW EKQVSQKKKQKNGKKHQKKVLK VRKSQRSRQKKT
1985	7482	A	2130	2	81	
1986	7483	A	2131	2	130	
1987	7484	A	2132	1	524	RPRIRHEPQTQREPTMVLSPAIDKTK AQRPPRLKLGA TPGEYGGEPLE VLFPPPTPKPYFPHFDLSHGSAQVK GATAKKVA/DALTKAVAHVDGHA QTALSALSDLHGAQAFGWDPVNF QASLSHLPCLGEPWAGPPSPAEPHP LAVARLPWQSFGLGFLKHKRCLNL PNYR
1988	7485	A	2133	388	654	GLFFVLQFFFLFCFVFLRSHSVSQAG VHWCRHGSAAST/SPGSSDPPTLAS KVLGVTDMSHCTWAESYFFTKMGS SPVVACACSSSYLGG
1989	7486	A	2134	384	622	INAPPRCPQLCTSEVCAME/CPQRV PAGPCPGCPRGNLLIHAPSNRPGTTS QINDPQPFLRICFWGSPKTPSHRHS FFF
1990	7487	C	2135	44	340	MKCSQPXRCHFQSDFOKCAPCPRA QTHWLEPPGRVQTISSMRNAQKGF ADSIRLWRLPASGVGVVVSPEGAG DPSHLLDPPGHSAPYSPAPRQLSRV

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						P*
1991	7488	C	2136	2413	2829	MFPRRACATCPNLKRACVCAPLRP RFGTSRVWCACLLPSPEPTGSVNVI FYVPLPSGLLSTAPGSRASGVGV LEGARGSFSSPWTLPGHFWSLFPSS LGSLSRCPLGKGDQEALVQGALGW GQRAWTPAQCSVDNG*
1992	7489	A	2137	69	332	YQVLKTDKNMSRISFFPFLRKGLAL SPRMECSGAIHAHCSLRISQSQ/DDP/ AHVSLSSWGLQGTCHHTQLIFLFF VGDEGLCCPGVRS
1993	7490	B	2144	73	358	XVPGSRGPETKLWDDFMSQATKR KHVVKEVLGEHIVPSDQQIVRVLR TPGNLHEVETAQGQRFVSMPSK YRKNIWIKRGDFLIVDPIEEGEK*
1994	7491	A	2145	80	201	
1995	7492	A	2146	498	748	FLPRRGDNDSSYPQ/WTACACRRRRRT CW*T*TWIRSGQRKMWSCGRRSL TTCMPRTRTAARLMACGSGSWRR SGPSCGCRLSP
1996	7493	A	2147	1	1764	MTTSQKHRDFVAEPMGEKPVGSLA GIGEVLGKKLEERGFDKAYVVLGQ FLVLKKDEDLFREWLDTCGANAK QSRDCFGCLRE/WCAKSRPAEVS LKADSKEGPQAQGPEQERTGL
1997	7494	A	2148	842	1186	FLPRRGDNDSSYPQ/WTACACRRRRRT CW*T*TWIRSGQRKMWSCGRRSL TTCMPRTRA WTTWRSKNLALSCP SMTKSLKSGHIPSAWSRAARLMA CGSGSWRRSGPSCGCRLSP
1998	7495	A	2149	526	1158	SCGLSLIKMTTSQKHRDFVAEPMGE KPVGSLAGIGEVLGKKLEERGFDKG L/YVVLGQFLADIEKMKTSFREWLD DTCGANAK\QSRDCFRMPFEK WCE ALLVDALLGKFSIPPAPQSRSLASRS RDSSPCPSYEGKD\CYCRTHL\RRYF RGSFGEFSPLNHFQLFFGILRSWHAF PRPFFPWVPSWVTYQLFLEWDFP GPIPHPHPHFQSV
1999	7496	A	2150	150	446	HEGLLLKLRLSDVYFLFFETRSCF VAHAGVQWHHYNLSL/T/PPGTPMF PLLASQVAGSTGMNHQAQIIKKT FGENMILLCCSGWLSGIFFVLYSLY
2000	7497	C	2151	203	427	MNFVRSIWMAQSTILLTARGXATLI IAISFLAPXLAQSVHAVSSFQSQAD LLNGQCGFQSSSEPQPHVHTTSS*
2001	7498	A	2152	1	1065	
2002	7499	A	2153	597	1292	QTFSENTIFLLTRHKQHSMLVPMNT PGVKIIRPLSVFGYTDNFHGGHFEIH FNQVRVPATNLILGEGRGFEISQG RLGPGRIHHCMTVGWAERLLQI MCERATQRIAFKKKLYAHEVVAH WIAESRIAIEKIRLLTLKAAHSMDTL GSAGAKKEIAMIKVAAPRAVSKIVD WAIQVCGGAGVSQDYPLANMYAI TRVRLADGPDEVHLSAIATMELRD QAKRLTAKI

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2003	7500	A	2154	1694	1886	ASDSRVPAPGIS/PSAPFPTQLSPRRS PPSPPPPPQSPGLGIFSPKASPVGILHL FKTLFCILNV
2004	7501	A	2155	1002	1480	MLLLKTTERFEVSVCMACTYV\SNL GKKQRSVSFLASGLMRVSTGPELRL HHSFVLTDVGRRICRLLVGLFTKG DTSSKR\HPPSPGP\CFLLCDLAR\V GSSPKINRVPHFTRTQTSTQRSCTVF VWQRCSLVGPFQVTFTM\YFHHS RSISRFS
2005	7502	A	2156	1	1623	RLPFVDVDARVYADAPAKLLLPL AFWELAVRLRGAEASERQVYSVA VKLLLLHPAFQSCLLLTLLGLWRTT PEAHASSLGAPISAASFLQDLHRY GEGDSLTLQQLKALLNHLVDVGVR GNVTQHVQGHRNLSTCFSSGDLFT AHNFSEQLRIGSSELHEFCPTILQQL DSRACTSENQENEENEQTEGRPSA VEVWGYGLLCVTVISLCSLLGASV VPFMKKTLYKRLLLYFRALAIGTLL LKRLFQLIPGAVWFQPLEDYVVS AVVFGGFYLFFFTEKILKILLKQKNE HHHGHSHYASESLPSKKDQEEGVM EKLQNGDLDHMPQHCSSELDGKA PMVDEKVIVGSLSVQDLQASQSAC YWLKGVRYSDIGTLAWMITLASDGL HNFIDGLAIGASFTVSVFQGSTVAI LCEEFPHELGDVIL\NAGMSIQQA LFFNFLSACCCYLGLAFGLAGSHFS ANWIFALAGGMFLYISLADMFP NEVCQEDERKGSILIPFIQNLGLLTG FTIMVVLTMYSGQIQIG
2006	7503	A	2157	1	604	MGTRWEPGWRAPLAPAAQARSS GRAAPAGSERARERERDGGSVGG GGSSAIPSERAAAHGEDSGAYR WERANRPFSNNCCCLAFYLGMEEA RWLYAGLFCVYGASLIAIAITHVPLF GSQIKAE/DPSGDSAPAAHLPPQPAQ /PHLPQAQLMLTGSQLAGHPLGMR WSMATQHAGCVSQRCLFPMTVG CSQGNILWSL
2007	7504	A	2158	22	1358	VHFSMGAPEIRMSKPLEAEKQGLDS PSEHTDTERNGPDTNHQNPQNKTSP FSVSPTGPSTKIKAEPSGDSAPAAP LPPQPAQPHLPQAQLMLTGSQLAG DIQQLLQQLVLVPSHHLQPPAQF LLPQAQSQPGLLPTPNLFQLPQQT QGALLTSQPRAGLPTQPPKCLEPPS HPEEPSDLEELQFARTFKQRIKLG FTQGDVGLAMGKLYGNDFSQTTIF RFEALNLSFKNMCKLKPLLEKWL DAETMSVDSSLPSIQLSSPSLGF LPGRRRKKRTSIETNVRFALEKSFL ANQKPTSEEILLIAEQLHMEKEVIRV WFCNRRQKEKRINPCSAAPMLPSPG KPASYSPPHMTVPQGGAGTLPLSQAS SSLSTTVTTYILSCGDAPPQDSWR GWGRGRGCAPPQFHPLCHSPTPGH

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						HQQHKPQPLKAATRLSACQA
2008	7505	A	2159	3	452	
2009	7506	A	2160	9	633	NSARATDSERTHHGARLLPDKTNV KAAWGVGAHAGEYGAEALERMF LSFPT\TKTYFPHFDLSQRSQVKG ATGKKVADALTNAVAHVDDMPQ TALSGPEATLHGAQSFGVDPVQLSS SLSHWPAWLTGPAHLPRPSFNPW RLQRLPWGQSFLGFLVEEPLLEPSKI PVKAWKPSGWPCFLCPFGASPGQGP SLSWNPYPYRWSFE
2010	7507	B	2161	55	372	MERFLMDGFQPPQLSTYALTLYKH TATVDGKTILVADINVTQKSFNFAK KFSLPLYFVSAADGTNVVKLFNDAI RLAVSYKQNSQDFMDEIFQELENFS LEQEEEN*
2011	7508	A	2162	552	1809	QLRGRGASRKWSALRRELGRRAWF ESAQSPDWRQGPKGPTSRVPLSSP HSEPHPEMAEDKTKPSELQDQGYD ADDNVKIIICLGDSAVGKSKLMERFL MDGLYPSRFEVLLVPVGLPTLMYQ CPTAHPFVPAAQEGGLDFWDTAGQ DTLSSPPTPHPSMELVPVCSQPQQLS TYALTLYKHTATVDGKTILVDFWD TAGQERFQSMHASYYHKAHACIMV FDIQRKVTYRNLSTWYTELREFRPEI PCIVVANKIDDRPMSYLLSTADINV TQKSFNFAKKFSLPLYFVSAADGTN VVKVWLTAEVASKLFNDAILAVS YKQNSQDFMDEIFQELVGVQVHISG GMEETAPLQG*GLQPSRVTLA*VCP TKCIRAAVEQMGGQASPATLFTNF SLEQEEEDVPDQEQSSSIETPSEEA
2012	7509	A	2163	807	1389	EPMAENKTKPSELQDQGYDADDNV KIIICLGDSAVGQSKLMERFLMDGFQ PQQLSTYALTLYKHTATVDGKTILV DFWDTAGQERFQSMHASYYHKAH ACIM/LDINVTQKSFNFAKKFSLPLY FVSAADGTNVVKLFNDAILAVSY KQNSQDFMDEIFQELENFSLEQEEE DVPDQEQSSSIETPSEEVASPHS
2013	7510	A	2164	3	923	RAARTRAEPEVECAARAGPAGVV RERAESRHGGRARGADPQRPWSLQ PSLGTARDNTLPSLGPGLSTARS QWAKNKTTPSELQDQGYDADDNV KIIICLGDSAVGKFKLMERFLMDG\ FQPQQLSTYALTLYKHTATVDGRTI LVDF\FHTAGQERFQSMHASYYHK AHAICIMVFDVQRKVTYRNLSTWY TELSGSFRPEIACIVVANKIDADINV TQKSFNFAKKFSLPLYFVSAAIDGT NVVKLFNDAILAVSYKQNSQDFM DEIFQELENFSLEQEEEDVPDQEQSS SIETPSEEAASPHS
2014	7511	A	2165	1	2715	
2015	7512	A	2166	1	2256	
2016	7513	A	2167	339	1086	IQMNRFLLLMSLYLLGSARGTSSQ

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						PNELSGSIDHQTSVQQLPGEFFSLEN PSDAEALYETSSGLNTLSEHGSSEH GSSKHTVAEHTSGEHAESEHASGEP AATEHAEGEHTVGEQPSGEQPSGE HLSGEQPLSELESGEQPSDEQPSGEH GSGEQPSGEQASGEQPSGTILNCYT CAYMNDQGGKCLRGEGTCITQNSQQ CMLKKIFEGGKLQFMVQGCENMCP SMNLFSHGTRMQICCRNQSFNCNI
2017	7514	A	2168	2	425	
2018	7515	A	2169	2	169	GRVGDTLKAGINAVERRSNRCNGN SGFEGQSRYPSSGMSAKELCEND DLSTSLVDPYLGFTHKMNT*FG S
2019	7516	A	2170	2	227	
2020	7517	A	2171	177	1400	LNAPGSQLSVGMKGLGESKNMVV NGRRNGGPLSNDHQQNQSKLQHTG \KDTLKAGKNAV\ERRSNRCNGNSG FEGQSS/RYPVSYGMTAKELCENDD LATSLVDPYLGFTHKMNTSAFPS RSSRHF\SQSDSLSHNNPVRFRPIKG RQEELKEV\ERFKKDEHLEKAFKCL TSGEWARHYFLNKNKMQEKLKE HVFIYLRMFATDSGFEILPCNRYSE QNGAKIVATKEWKRNDKIELLVGCI AELSEIEENMLLRHGENDFSVMYST RKNCAQLWLGPAAFINHDCRPNCK FVSTGRDTACVKAL\RDIEPGEEISC YYGDGFFGENNEFCYTCERRGT GAFKSRVGLPAPAPVINSKYGLRET DKRLNRLKKLGDSSKNSDSQSV/SA LNTDADTTQEKNIASK
2021	7518	A	2172	3	114	
2022	7519	A	2173	328	471	
2023	7520	A	2174	1	190	
2024	7521	A	2175	2	132	SGLGRLPGPWQEAGSSRGPSGDM AGVKALVALSFSGAIGLTF/LHMLG CALEDYGVYWPLFVLIF/HAISPIPHF IAKRVTYDSDATSSACRELAYFFT GIVVSCLWISPILARVALIK\WGAC GLCV/VAGNAVIFLTIQG\FFPIFGRG DDFSWE\QWGYWTDfs
2025	7522	A	2176	191	479	NTSLPNPSEVSHSSLRLDSSGAEAF VGGGTGVLKKPEGAGPAAPS/LGW RPRG*APHRTGSAQPPTAVPCR/PGA LGEDSSPGPPGALGGLGVIPQPSM
2026	7523	A	2177	1920	2524	TQYPPAEQRSQTLMDVFALPLNSL CAQSSKTLNCKTQCHPCSILCKNLL KNKCLILHSRFTPTQTAPFEGGQLRI PLFPKPKVRSSQFQASVLELRRSQK PFVGGGTGVLKKPEGAGPAAPTS WRPRGEAPHRTGTAQPPTAVP/SGG RIWGKIPLPGPPGALEGVGFPSASPR FQLQPRKLKLDAGRRLRSGSKPHVK HL
2027	7524	A	2178	239	380	
2028	7525	A	2179	34	202	EPTTRQTLYMLITFTPHNHLVRETSS



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						VPFEQMKN*GSERFNTLSKALQTISAKTRI
2029	7526	A	2180	1	1566	KSKCRFPEGLSEGFGPMRKEALSSG SVQAEAEAMLDEPQEQAEGSLTVYVI SEHSSLLPQDMMSYIGPKRTAVVRG IMHREAFNIIGRRIVQVAQAMSLTE DVLAAALADHLPEDKWSAEKRRPL KSSLGYEITFSLNPDPKSHDVYWD IEGAVRRYVQPFLNALGAAGNFSV DSQILYYAMLGVNPRVYSASSSYIF GHAQLPHVINPVESRLGSSAASLYP VLNFLLYVPELAHSPLYIQDKDGAP VATNAFHSRWGGIMVYNVDSKTY NASVLPVRVEVDMVRVMEVFLAQ LRLFLGIAQPHLPPKCLLSGPTSEGL MTWELDRLLWARSVENLG\QATTT LTSLGAASWARSATLFIKGRRGHLE VLQRLAPVQKSAEELASGHL\DLF LSPAREAVTSSELAFFDPSLLHLLYF PDDQKFAYIPLFLPMAVPILLSLVKI FLETRKSWEKA
2030	7527	A	2181	574	1949	
2031	7528	A	2182	76	419	AFIPAMAELIQKKLQGEVEKYQQQL KDLSKSMSGRQKLEAQLTENNIVK EKRYESQLRDLERQSEQQRETLAQ LQQEFQRAQAAGAPGKA
2032	7529	A	2183	71	350	
2033	7530	A	2184	175	1032	GLLPHLGPRVQRLPRLSLSTLPCSLT RCPHPFLLPQIHIHLTRIVGIGGTFDV SKLPFLSSPDLSKSMSGRQKLEAQL TEYNIAKEVRDWDLWGEEGPVLA MVLITYVPSLHQELALLDGSNVVFK LLGPVLVKQELGEARATVGKRLDY ITAEM*VFIPPPCAAPCDASEPLE*R C*TIAEQLSIVAPSPVPPTLSFPF*PP FFSLPWISRFSTYLFLAFSTLHSESY* FLPFCLSPSLLSKRYESQLRDLERQ SEQQRETLAQLQQEFQRAQAAGAPGKA
2034	7531	A	2185	112	520	AFIPAMAELIQKKLQGEVEKYQQQL QKDLSKSMSGRQKLEAQLTENNIV KEELALLDGSNVVFKLLGPVLVK QELGEARATVGKRLDYITAEIKRYE SQLRDLERQSEQQRETLAQLQQEFQ RAQAAGAPGKA
2035	7532	A	2186	635	1015	GGQKHPTGLLKPPANTAATMPKRK AKGDAKGDKAKVKDEPQRRSARLS AKPAPPKPEPGLKKASAKKGEKLP KGRKGGKADAGKGLGNPAKNPR LPLHFQFQKAE\GTGGLPSEMFIFES SGTYW
2036	7533	A	2187	302	471	TLSHRVLVEAQSREQLAALKKHHE EEIVHHK\KEIERLQKRNL SRHK\QK DSKLLKH
2037	7534	A	2188	3	399	LARNERLLAGGRDARGAAPASQWP VTAVGRRGTWLGRV/WGVRTM\QA RGFGSDQSENFTGPRAPHP/RKAG

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						GALGKREQAEEERYFRAQSREQLA ALKKHHEEEIVHHKKEIERLAEKK FERHKQKIKMLKH
2038	7535	A	2193	2	406	ARAEMSRVALAVLALLSLSGLEAI QRTPKIQVYSRHPAENGKSIFLKCY VSGFHPSDIEVDLLKNGKE/RLKK VEPSDLS/FSKDWSEFYLA/LPYTEFH PQLKKGVC PARVN\HVTLSAPARL VK\WDRRHVKQH
2039	7536	A	2197	319	393	WL/TPVIPTLWEAEVGGSFHEHRSSR
2040	7537	C	2198	84	290	MLPSKGLSFFSLQHLRDSRSLFPM SMITMLELECCRASSNHEVRWLKX HXVSQICSLICFPXMLTIRA*
2041	7538	A	2199	2	743	PRVRSESVYRSLADPEPTGRDGMT YADLFKYIIIGDTGVGKTCFLLQFTD KRFQPVHDLSLGVEFGGSLCSTLME NQFKLHIWD\TAGQESFRSITRSY/Y RGAAG\ALLVYDITRALKPFNHLAS WLGGLPGQHFSFPTWVIHCFIGNKS DLESRRDVKREEGEAFARE\HGRIFR GTSAKTACN\VEEAFINTAKR\YRKI HQGLFDVHNEANGIKIGPQQSISTSV GPSASQRNSRDIGSNSGCC
2042	7539	A	2202	20	222	
2043	7540	A	2203	1	458	RSSLTSLSNSAAAMAPVKKPCGEG GAKKKKQVLKFTLDCT\HPVEDGI MDAAQF*ASFCKERIKVKRKKLGT LSGGG/V*PIERSK\SKITVTSEVPFS KRV/YLKYLTKKY\LKKNLRLDLV CRVVAYQPKRELRYSYFQINQ\DE GRREED
2044	7541	A	2204	2	321	FIFFSFSSFFSFFSETGSCSVAQAG VQCHDHGSPQS/PNLPGSSDLPTSAS \KVLGITGVRHSLPPLGFQMGIFLL FSMLKFCFWVCSALLCTVLEFLRTN YFLS
2045	7542	C	2205	46	234	MTLRXWITWPFLFLSPSSKCLHLI ASILLDLQLGSTHSSLSTIFFVVLAF RKIGLVCPP*
2046	7543	A	2206	1	243	
2047	7544	A	2207	144	479	RPLKPRRTF\CKK\CGKAPNPHKSDH STKKGKDSLYAPGKAAMVTRKQS GYGGQ\TKPIFRKKAKTTKIVLKA LSALSPTCRSKRMLAF\KRWQAFNL LGDKKRKGPSASS
2048	7545	A	2208	75	540	GGSGSVRVLRSSESPREEAVEEEVAA VAVVVAVAEEAGTNQLRAETMANI AVQR\IKREFKEVLKSEETSKNQIKV DLVDENFTELGEIAGPPDTPFERG RFPLELKIP\ETYPFNPPK/VFRFYAL KLWHPNISSV\TGAICLDILKDQWG SWQWT
2049	7546	A	2211	1	2640	MYSGNRSGGHGYWDGGAAGAE GPAPAGTLPAPLFPSTYERLALLL GSI GLLGVGNLLVLVLYKFQRLR TPTHLLL VNISLSDLLVSLFGVTFTF VSCLRNGWVWDTVGCVWDGFGSGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LFARPAPLPARPRAPRPTPPRSPLAS STLPDPSRMAGAFLLRPLPPHAVQ DSIPVVSHLPPTCHQTL LLPK MADN LPTEFDVVIIGTGLPESILAAACSRSG QRVLHIDSRSYGGNWASFSGLL SWLKEYQQNNDIGEESTVVWQDLI HETEEAITLRKKDETIQHTFAFCYAS QDMEDNVEEIGALQKNPSLGVSN FTEVLDSALPEESQLSYFNSDEMPA KHTQKSDTEISLEVT DVEESVEKEK YCGDKTCMHTVSDKDGDKDESKST VEDKADEPIRNRITYSQIVKEGRRFN IDLVS KLLYSQGLLIDLLIKSDVSR VEFKNVTRILAFREGKVEQVPCSR DVFNSKELTMVEKRMLMKFLTCL EYEQHPDEYQAFRQCSFSEYLYTKK LTPNLQH FVLHSIAMTSESSCTTIDG LNATKNFLQCLGRFGNTPFLFLYG QGEIPQGFRCMCAVFGGIYCLRHKV QCFVVDKESGRCKAIDHFGQRINA KYFIVEDSYLSEETCSNVQYKQISR AVLITDQSILKTDLDQQT SILIVPPAE PGACAVRVTELCSTMTCKMDTYL VHLTCSSSKTAREDES VVKLFT YTETEINEEELTKPRLLWALYFNMR DSSGISRSSYNGLP SNVYVCSGPD GLGNEHAVKQAETLFQEIPTEEFC PPPPNPEDIIFDGD DKQPER/PLGTNN VVMAKLESSE\ESKNL\ESPEKHPSK LEKSNLEMLFWTSFMASEFSLKD RFPI
2050	7547	A	2212	328	583	
2051	7548	A	2213	1	416	PSSGDMAGVKALVALSFSGAIGLTF LMLGCALEDYGVYWPLFVLIFHAI SPIPHIAKRVTYDS DATSSACRELA YFFTGTGIVVSC LWISPVILARVALIK\ WGACGLVLAGNAVIFLTIQGFFLIF GRGDDFSWAEQW
2052	7549	A	2214	1	180	AAATGAVGAATYPCAPNWK*RND EKTAADYKILGGSVLHLVLALRGG GGLRQ
2053	7550	A	2215	162	557	VASEHSPKIGASQGLDYEPLLVAK VWYLTRPTGTKAGSVFSQYLPFLEP GILGPASLPWLRQTLTGKEIEIDIEP\ TDKVERNQRSVWEEKGNPPPQQQ RLHLQVAKQMNDKDS SLIYKILR WVQSFT
2054	7551	A	2216	684	1496	LETSGLSENPLGQAVGFGQDEFFLE QTKKKGVKRPARLHTKPSQAPAVE EAPSGA\SYNPSFEDHQTL SAAHE VELQRQKEAEKLERQLRPCATEQ ARHPRSSTFQELCEGLLESDGE PGQGE GPEAGDAEVCSTPARLATT EK\KTEQQRRREKAVHRLRV TARA ALRAARLRATQELVFRVRGIQRPQ VALRLA\ELARRRRRRQ\ARREAEA DKPRRLGT/RFKYQAPDIDVQL\ SSE LTD SLRTLKPEGQHPSRPVQELPRG

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						GI
2055	7552	A	2217	116	285	KLRNQRIQERHTDGGPEPLKSL* CSP KTRVESRSASRRGPLFLNKGHARAR SSLTLA
2056	7553	A	2218	3421	3698	AGRGPLRLQSHRFGRPSQVDCLSPA APDQPGQHKGKTPSPQK\QKLAGHG GAHLQSQPLGRLRREDPLSPGGGGC SEPRSHHCTPAWAREYGD
2057	7554	A	2219	381	1772	KMAESENRLQELSES\SQEEAGNQIM VEGLGEHLERGEDAAAGLGDDGKC GEEAAAGLGEEGENGEDTAAGSGE DGKKGGDTDEDSEADRPKGLIGYV LDTDFVESLPVKVKYRVLALKKLQ TRAANLESKFREFHDIERKFAEMY QPLEKRRQIINAIYEPTEECEYKS DSEDCADDEEMCHEEMYGNEEGMV HEYVDEDDGYEDYYYDYAVEEEEE EEEEDDIEATGEENKEEEDPARGIPD FWLTVLKNVDLTLPLIKKYDEPILK LLTDIKVKLSDPGEPLSFTLEFHKP NEYFKNELLTKTYVLKSKLAYYDP HPYRGTAIEYSTGCEIDWNEGKNVT LTKIKKKQKHRDLWGTIRTVTEDF PKDSFFNFFSPHGITSNGRDGNDLFL LGHNLRTYIIPRSVLFFSGDALESQQ EGVVREVNDAIYDKIYDNWMAAI EEVKACCKNLEALVEDIDR
2058	7555	A	2220	17	250	
2059	7556	A	2221	2	899	GFSKKCVSSRSPELRVTRLRYLRIQ AFRGSCLATADLLLVSPLRHPEPA KVLVLFLLSFASCWAGPGRAGPPG RSLTMA SLFKKKTVDDVIKEQNR ELRGTRQANRDRAALEKQEKQLEL EIKKMAKIGNKEA\CKVLAKQLVH LR\KQKT\RTFAVSSKVTSMSTQTKV MDS\QMKMAGAMSTTAKTMQAVN K\KMDPQKTLQTMQEFPGRENMK M\EMTEEMINDTLDDIFDGSDD\EEE SQ\DIVNQVLDEIGIEISGKMAKAPS A\ARSLPSA\STSKATISDEEIERQLK ALGVD
2060	7557	A	2222	3	586	ARAMGISRDNLHKRRKTGCKRKP HKKRKYELGRPAANTKIGPRRIHT VRVRGGNKKYRALRLDVGNFWSG SECCTRKTRIIVYNASNNELVRTK TLVKNCIVLIDSTPYRQ/WTPEEEEL NKKRSKKIQKKYDERKKNAKISSLL EEQFQOGKLLACIASRPGQCGRAD GYVLEGKELEFYLRKIKARKGK
2061	7558	A	2223	2	727	LFPASAEQMGISRDNWHKPRKTG GPRESYPQQEAKSMSLGRPAANTK ILAPRRIQHSPVCRGG*QVNTVPLRF D\VGNFWSG/SKECCTRKTRMIDVV YNAI**PSWVRYRPLVERICI\VID EQHPY\RWVRSPTYAL\PLGPQRK GAKLDSLKKEEIFKPKTDLK*IQKK YD*/ERKKNCQNSASLPGRSSFQQG KASLRCIAFK/RPGQC\GRA\DGMYT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ERLQQKTGIPFS\QMIL\FDDERRNIV DVSKLGTE
2071	7568	A	2233	79	564	SPTSAARSLRLRVMARLPKLA VFDL DYTLWPFWVDTHVDPPFHKSSDGT VRDRRGQDVRLYPEVPEVLK\DLQS LGVARCGCFQGQVRLGRGQPATGA LLTFFRYFVHR\EIYPGSKITHFERVA AE\TGISF\SQMIFDDERREYCRRSA NWCVTCTSHPEW
2072	7569	B	2234	48	209	XKNQCETRTMQENGYSSHAVDGT GPAGGAGRPAGSTGAQVSVQPNFQ QDKFLGRX*
2073	7570	A	2235	2	353	
2074	7571	A	2236	3	676	SAVEFPPLSHTTGTRPRTPIILQOE NGYFIHTLWMGLALLGVLGDLGSGQ HRRPRSPCQPNFQQDKFLGRWFKR G\LASNSSWLREKKAALSMCKSVV APATDGG\FNLSTFLQEKTSVETR TML\LQPRGVPSASLQLTGVPHWGQ A/HYSVSVVETDYDQYALLYTRAS KGPGEFRMATLYSRTQTPRAELK EKFTAFCKAQGFTEDTIVFLPQTDK CMTEQ
2075	7572	A	2237	1	1165	MGVTEVFLKDVITLLNLEELVQCRQ TWGEARTRGKRVLGSLADEIVVRT QQPPSLEHKAWNATCKHWLAEEA ALEKYYLSIFYGIEFVVGVLGNTIVV YGYIFSLKNWNSSNIYLFNLSVSDL AFLCTPLMLIRSYANGNWIYGDVLC ISNRYVLHANLYTSILFLTFISIDRYL IHKYPFREHLLQKKEFAILISLAIWVL VTLELLPILPLINPVITDNGTTCNDF ASSGDPNYNLIYSMCLTLGFS\PLF VMCLFYKIALFLKQRNRQVATAL PLEKPLNLVIMAVVIFSVLFTPYHV MRNVRIASRLGSWKQYQCTQVVIN SFYIVTRPLAFLNSVINPVFYFLLGD HFRDMLMNQLRHNFKSLTSFSRWA HELLLSFREK
2076	7573	A	2238	1	567	
2077	7574	A	2239	58	544	GKKMGSKAKKRVLLPTRPAPPTVE QILEDVRGAPADPVFTILAPEDPP VFRMMEDAEAPGEQLYQQSRAVY AANQRLQQAGNVLRQRCCELLQRA GEDLEREVAQMKQAALPGGEGWL LGLTLWGLGALGRAQGW SATQAL PGGPSAPDWH SRGPSRGC
2078	7575	B	2240	1	1551	MCELDILHDSLYQFCPELHLKRLNS LTLACHALLDCKTLTLTELGRNLPT KARTKHNIKRIDRLGNRHLHKERL AVYRWHASFICSGNTMPIVLVDWS DIREQRLMVLASVALHGRSVTL YEKAFPLSEQCSKKAHDQFLADLAS ILPSNTTPLIVSDAGFKVPWYKSVE KLGWYWLSRVRGKVQYADLGAEN WKPISNLHDMSSSHSKTLGYKRLTK SNPISCQILLYKSRSKGRKNQRSTR HCHHPSPKIYSASAKEPVV LATNLP

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						VEIRTPKQLVNIYSKRMQIEETFRDL KSPAYGLGLRHSRTSSSERFDIMLLI ALMLQLTCWLAGVHAQKQAFPCD DSSAVHRLRYCKGRDYNRVRSSCV QRHAPVLNRKIGTGSQDHANEFGLS WILLGARTPTCKADLSRPYSCPH QPQQRFLGDSGITTKSVPYRGQEH CLHPKLQSTKRFIKCTTAWNENRRK YQVMPIEAQRPKCQLLPNRSPTWQ ISIDKGPRQDTFMLFPPIKI*
2079	7576	A	2241	2	456	GTRSTRTARRRWLSSPPRACPGTEV RSTACTPSCAPPVSMRLAAALLL LLALYTARVDGSKCKCSRKEPKIR YSDVKKL\EMKPK\YPHCEEKMMVIIT TKSVSRYRGQEHCPHPKLQSTKRFI KWYNA\WNEKAQRRVYEEAQGLR RRIG
2080	7577	A	2242	308	615	ETRVAVSGTGAAEV*GMVRLDISE GRAAVAAVGGVVAVGTVLVALS AMGFTSVGIAASSIAAKMMSTAAIA NGGGVAAGSLVAILQSVGAAGLSV TSKVIG
2081	7578	A	2243	332	484	
2082	7579	A	2244	240	610	LWVEVQSEWRLTEAKGPTMGKES GWDSGRAAVAAVGGVVAVGTV\ PWRSSAMGFTSVGIAASSIAAKMM STAAIANGGGVAAGSLVAILQSVGA AGLSVTSKVIGGFAGTALGAWLGS PPSS
2083	7580	B	2245	158	2382	MARGKAKEEGSWKKFIWNSEKKEF LGRTGGSWFKILLFYVIFYGCLAGIF IGTIQVMLLTISEFKPTYQDRVAPPG LTQIPQIQKTEISFSSMAIRDAGFEIS AMQMFMNMDRVNVEQFYEVYKGV VTEYHDMVTEMYSGPCVAMEIQQ NNATKTFREFCGPADPEIARHLRPG TLRAIFGKTKIQNAVHCTDLPENGL LEVQYFFKILNN*
2084	7581	A	2246	753	1007	LAQGCSPGPSQDTALPGPPPCTEP/ CPVPYVLRSTPEPPQHGTCHSPCLLP IPLCSSPSLGGGGNSEGEKALTFHV CGDHPVKN
2085	7582	A	2254	188	833	ALIMSFIFEWYINGFSSVLQFLGLYK KSGKLVL\GLDNAGKTTLLHLWLK DDQIGPTLFPPLPTSEE\LTIAGMT\ FTTFD\LGGHGAKHVAVWKNYLP QLMGFVFLVDCA\DHFSWNPKE LNALMT\DETILMCPIL\ILGNKIDR TDAISEEKLREIFGLYGQTTGKGNV TL\KELNARPM\EVFHVAVLLKEGK VYGRGFSAGLLPVLF
2086	7583	A	2256	333	621	CRKNSCYQAQNFNLRIPFSTTKLINL FHF*NDSQKST*/SDSHLARSSQFCS LN*NY*I*TAKSHDVVCTRQHFP ESYIWHVKEKKYNPTAAAI
2087	7584	A	2257	29	659	LSVASFSFLSNASAEDTMSRLSRLL WAATCLGVLCVLSADKNTTQHPNV

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						TTLPPIVRETSAPVTPLPLVTTTPAPET CEGRNSCVSCFNVSVVNT\CFWIE CK\DESYCSHNST\VSD\CQVGNTTD FCSVST\ATPVPTANS\TAKTHSSSP LLQLPRQLLHQGTNNNTVNS\TSQP VRKSTFDAASFIGGIVLVLEIRCHTR NYIPDLKK
2088	7585	C	2258	101	411	MEMKMQSERLSKEYDQLLKEHSEL QKQREILPHRRGESTVTTXXXXXX XEPQQRNADXXXXXXXXXXXXXXXX XXSSSRSMALQIPIKXXXXXXXXXX XXXXXLF*
2089	7586	A	2259	2	575	
2090	7587	A	2260	1	265	SDALSKAQNDVMEMKMQSERLSK EYDQL\KEHSELQHSSFGFLSKRS HKNGSIGKQTGSRKGSFRKRQKEK TVNFIKDTLQYTVSK
2091	7588	A	2261	47	906	RKKLPLQWPAVPPFLYAEIGLILIFC LPFIPPQRWQKIFSFNWVGKIATFW NKAFLTIILLIVLFLDAVREVRKYSS VHTIEKSSTSRPDAYEHT\QMKLFRS QKNLYIPGISLFFWLVRRLVTLITQ LAKEPVTQRCALYLQAENTNKA K\FMEENEKLRILKSHGKDEECVL EAENKKLVEDQEKLKTELRTSDA L\SKAQNDVMEMKMQSERLSKEYD QLL\KEHSELQVPLGSFYILAFAPGL HNPHPSPPRSGGFSADNPRGALPP CLVCVLFHHL
2092	7589	A	2262	669	995	KVFFCFYRIYVCICVCVCVCVC/TLQ TL/CYSIANMLTSSQCLQSCGSQSW CQMHKSSKAIMTIPCKFISRKPWEG DCSSLEPHGVSAFDIWPQLCIKKV LNHFSPRKN
2093	7590	A	2263	3	379	WPFLKLRLGTCGTCCSHEGRAAA WSAESSLQHSVVTMSLPLNPKPFL NGLTGKPMVKLKWGMEYKGYL VSD\GYMNMQLANTEEYIDGALS GHLGEVLIRCNVLY\RGVEEEED GEMRE
2094	7591	A	2264	68	268	QYLSLLLQYSLVFICWLFICLALYV YFLCMLLCKYGLQLFLCGILSFRIS CKLLESRIHVIPLFL
2095	7592	A	2266	190	554	HGVRSDLGRWPDHLCAVCRHYHH LLHLLLLLPLQDVPPTTSWLSPPHP PLWCM/PPYPQPPSVPPSYGPSLPG LPHHAASARECQQHPYPIAVPHTLT HAHAHGPTTRPLAGRSSRD
2096	7593	A	2267	2	445	
2097	7594	A	2268	200	894	TSPRARPHCSLCLPNLPPVTYMHY ETDGFSLGVFLKSGTSLPHDHPG MHGMLKVLYGTVRISCMKLDAG GGQRPRALPPEQQFEPPLQPRREA VRPGVLRSAEYTEASGPCILTPHR DNLHQIDAVEGPAAFLDILAPPYDP DDGRDCHYYRVLEPVVRPEASSA CDLPREVWLL\ETPQADDFWCEGEP



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						YPGPKGLPLKPLAHQERWAEDVPP PTTRAVSLPP
2098	7595	A	2269	257	781	QELLSGLVNYFSLSWFLYVAQESIP SLPQSPMRETPSKAFHQYSNNISTLD VHCLPQLPEKASPPASPIAFPPAFE AAQVEAKPDELKVTVKLKPRLRAV HGGFEDWRPLNKKWTGMKWKKG KIYIGTPNGTLKTPLADEID/EFSE MGHFLKPDGPKIIGKVWVHEKGM NDK
2099	7596	A	2270	271	404	
2100	7597	A	2271	2	5684	PTSPCGEGYGISLNLTFIISNMRVLR AHFIELQFPFMGQVVTGTQNSEQN LGPQAIPQDGSITHQISRPNPPNFGP GFVNDSSQRKQYE\WPQETQQLLQ MQQKYLEEQIGAHRKSKKALSAKQ RTAKKAGREFPEEDA\QLKHVTEQ QSMVQKQLEQIRKQKQKEHAELIED YRIKQQQQCAMAPPTMMPVQPP PLIPGATPPTMSQPTFPMPVQQLQH QQHTTVISGHTSPVRMPSLPGWQPN SAPAHPLPLNPPRIQPPIAQLPIKTCTP APGTVSNANPQSGPPPRVEFDDNNP FSESFQERERKERLREQQERQRIQL MQEVDQRALQQRMEMEQHGM VGSEISSRTSVSQIPFYSSRLYLCDF MQPLGPLQQSPQHQQQMGQVLQ QQNIQQGSINSPSTQTFMQTNERRQ VGPPSFVPDPSIPVGSFNFSVVKQG HGNLSGTSFQQSPVRPSFTPALPAAP PVANSSLPCGQDSTITHGHSYPGST QSLIQLYSDIPEEKGKKRTRKKKR DDDAESTKAPSTPHSDITAPPTPGIS ETTSTPAVSTPSELQQADQESVEPV GPSTPNMAAGQLCTELNKLPSNDF SQATPNQQTYANSEVDKLSMETPA KTEIKLEKAETESCPGQEEPKLEEQ NGSKVEGNAVACPVSSAQSPPHSA GAPAAKGDSGNELLKHLKLNKSS SLLNQKPEGSCSEDDCTKDNKLVE KQNPAGLQTLGAQMGGFGCGN QLPKTDGGSETKKQRSKRTQRTGE KAAPRSKKRKKDEEEKQAMYSSTD TFTHLKQVRQLSLLPLMEPIIGVNFA HFLPYGSGQFNSGNRLLGTFGSATL EGVSDYYSQLIYKQNNLSNPPTPPA SLPPTPPMACQKMANGFATTEELA GKAGVLVSHEVTKTLGPKPFQLPFR PQDDLLARALAQQPKTVDPASLP TPPHNNQEELRIQDHCGDRDTPDSF VPSSSPESVVGVEVSRYPDLSLVKE EPPEVPSPHPILPSTAGKSSESRRND IKTEPGTLYFASFGPSPNGPRSGLIS VAITLHPTAAENISSVVAAFSDLLH VRIPNSYEVSSAPDVPSMGLVSSHRI NPGLEYRQHLLLRGPPPGSANPPRL VSSYRLKQPNVPFPPTSNGLSGYKD SSHGIAESAALRPQWCCHCKVVILG

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						SGVRKSFKDLTLLNKDSRESTKRVE KDIVFCSNNCFILYSSTAQAKNSEN KESIPSLPQSPMRETPSKAFHQYSNN ISTLDVHCLPQLPEKASPPASPIAFP PAFEAAQVEAKPDELKVTVKLKPR LRAVHGGFEDCRPLNKKWRGMKW KKWSIHIVIPKGTFFKPPCEDEIDFL KKLGTSLKPDVPVKDYRKCFCHEE GDGLTDGPARLLNLDLWVHLNC ALWSTEYETQAGALINVELALRR GLQMKCVFCHKTGATSGCHFRCT NIYHFTCAIKAQCMFFKDKTMLCP MHKPKGIHEQELSYFAVFRVYVQ RDEVQRASIVQRGERDHTFRVGS LI FHTIGQLLPQQMQAFHSPKALFPV GYEA\SRLLGGTRYANRRCRYLC SIEGGRDGRPVFVIRIVGNKGHGR TGV LKVDISPKGVWDKILEPVACV RKKSEMLQLFPAYLKGEDLFGLTVS AVARIAESLPGVEACENYTFYGRN PLMEPPLAVNPTGCARSEPMSAH VKRFVLRPHLTNSTSTSKSFQSTVT GELNAPYSKQFVHSKSSQYRKMKT EWKSNVYLARSRVSGGWGLLWL VRRLEETHHGSFEYIGTNHFETKL GQQGKEKLYESQNRGVYMFMDN DHVIDATLTGGPARYINHSCAPNCV AEVVTFERGHKIISSSRRIQKGEELC YDYKDFEDDQHKIPCHCGAVNCR KWMN
2101	7598	A	2272	1	2806	
2102	7599	A	2273	288	843	AGSGVLQGLFICPKAPGPRPTGAEG KR\KLQIGVKKR\VD\HCPIKSRK\GD VLHMHYTG\KLEDGT\EFDSKPAPR TSPFVFSL\GTGQVIK\WDQG/LCL GMCEGE\KRKLVIPS\ELGYGE/RGE LPPKIPRPVQPLVFEVELLKIRADEL SCNQTGEGQGEKAPHQGPDCSKKK NKKQKPIKTLKSPK
2103	7600	A	2274	80	308	VLTHLGNWILGSTEGPMGGP*FCTN LSEGLRFGISPSWREALYGWHA
2104	7601	A	2275	2	456	RSFFFFFCEVGSWVGS MRVVMARL LSEGEQGIPTACAAFAQQPGRPRR GLAGVGEGGPQCSWVNYRCTLEFL VSL LGTDLARGRGNASGP\TAPAD SKQLSCKTFIAVLSLSKEAGFCHVV QGWVSTSWGSSSPVPQFFPKLLEF TGK
2105	7602	A	2276	2	81	
2106	7603	A	2277	325	485	ELRVDPVNF\KL\LSHCLLVTLAAHL PAEF\TPAVHASLDKFLASVSTVLTS KYR
2107	7604	A	2278	291	529	LFL LCKVGTWHQGP NHQKAPKAPG TPPTPSYPGTPSRQLLWQWVQRPRA LPA\PLPAVGTSSSTSPGRQC PFSAQ HHLFP
2108	7605	A	2279	52	109	TVRLPR\HPGSRKNMASYCRIPACIA AERRYGT C MYQGR I WAFSS

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2109	7606	A	2280	3	452	
2110	7607	A	2281	26	526	NSTDSE RTHPWLLSPADKTTVK/AP AWGKVG AHAGEYG\SEALERMFLS FPTTKTYFPHFDLSHGFCPLRATG KKVADALTKRRGAPLDDMPNALV RPL\SDLHAHKL\RVGPGSTFKLLKP LACL\LTLP AHLPRPSFTPGGCKAS LGQSFLGFLKKHRCNLNPNYR
2111	7608	A	2282	447	539	
2112	7609	B	2283	8	694	MQYNRRFVNVPVTFGKKKGTTFTK IFVGGPYHTTDASLRKYFEGFGDIE EAVVITDRQTGKSRGYGFVTMADR AAAERACKDPNPIIDGRKANVNLA YLGAKPWCLQTGFAIGVQQLHPTLI QRTYGLTPHYIYPPAIVQPSVVI PVPSSLSPYIEYTPASPVYAQYPPAT YDQYPYAASPATADSFVGYSYPAA VHQALSAAAPAGTTFTVQYQAPQLQ PDRMQ*
2113	7610	A	2284	3	191	
2114	7611	A	2285	101	444	CSLFVPRPRSLQPLRRVTGQETGRP RSKAHVASTWRAFPEDQVVLLAG AP\LEDEATLGQCGVEALTTLEVTG \RMLGGKSPWFPWPVLGKVMKVRL LKVAKQGERRKKKTGSG
2115	7612	A	2286	2622	2881	KKSKDNKTFFFFFETESCSALQAGV QWCNLGSLQTLPGSND SHASAR VAGTKGMCHHARLIFVFLVETGLH HVGQACLGT PDLK
2116	7613	A	2287	41	655	TKLVMMQKLLKCSRLVLALALILV LESSVQGYPTRKPRHQWVPCNPDS NSANCLEEKGPMFELLPAE\STKIPR L\RTDLFPKTRIQ\DLNRIFPLSEDYS GSGFGSGSGSG\SG\GSWFPNGKW EQDYQLVDE\SDAFHDNLR\SLARI LASASRDWGQHGLAEFNVIKEDL PTLTTRQM VVKQYFNVPVMNMIN WDKEFYRNF
2117	7614	A	2291	163	703	READMGTMKTQRDGHSLGRWSLV LLLLG\VMPLAIIAQVLSYKEAVLR AIDGINQRSSDANLYRLDLDPRPT MDGGP\DTTK\PVSF TVKETVCPRP TQQ\SPKDGD FKR DGLLRGMGTV\ TLN\QARGSF DISCDKNKR FALLG DFFRKSKEKIGKEFKRIVQRIKDFLR NLVPRTES
2118	7615	A	2292	100	546	PPRTGQRQPLHSARRHGPSV\ELAC I\YSALISARTDEVTVTEDKINAL\IK A\AGVNVE\PFWPWLCLQRPLA\NV NIGSL\CNVRGPVEPAPSSLVAAP\ AGRSLPPPLACCSKLKEERKLEAKK RKNPKEVLNDDIGLLVLFELKPLL
2119	7616	A	2293	33	494	
2120	7617	A	2294	1	609	PLKRS DGCNDGRPTRPPTRPDTTVF TSNLKQTRMVHLTPEEKSAVTALW GKVNVD EVGGEALGRLLVVPWT QRFFESFGDLSTPD AVMGNPKVKA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HSVKKGLRGAFSDGLAHLADNLKGT FATLSELHCDKAAPWIPEELQAPW ATCLVCVAWPITFGKRISTPPVAGL PNQENWLAWCWLNALGPTSNHLS LAFLAGPISN
2121	7618	A	2295	1	338	AALAWAVSRLHFSRLSFPFWAFRG AFAAVPTTAAMISLTDQKIGMGLT GFGVFFLFFGMILFFDKALLAIGNG FFPVVDGFIRRVPLGSLNLPGIRS FVDKVGESNNMV
2122	7619	A	2296	67	283	LPFPGCFFLF*VLFVAGLAFVIGLER TFRFFQKHMKATGFFLGGVFVV LIGWPLIGMIFEIYGFFLLFR
2123	7620	A	2297	3	209	
2124	7621	A	2298	3	544	TRAALAVAVSRLHFSRLSFPFWAFR GAVAAVPTTAAMISLTDQKIGMG LTGFGVFFLFFGMILFFDKALLAIGN VLFVAGLAFVIGLERTFRFFQKH KMKATGFFLGWVYLVVLIGL/WPLI GMIFEIYGFFLLFRGFFPCRCWTFI RKECPVLGIPSPNLPGIRSFVDKVG ESNNMV
2125	7622	B	2299	54	1731	XKLSRECEIKYTGFRDRPHEERQAR FQNACRDGRSEIAFVATGTNLSLQF FPASWQGEQRQTPSREYVDLERA GKVYLKAPMILNGVCVIWKGWIDL QRLDGMGCLEFDEERAQQEDALAQ QAFEEARRRTREFEDRDRSHREEME VHELEKSKRALETQMEEMKTQLEE LEDELQASEDAKLRLVNMQALKG QFERDLQARDEQNEEKRRQLQRQL HEYETELEDERNERLAAAANKKL EGDLKDLELQADSAIKGREEAIKQL RKLQAQMKDFQRELEDARASRDEI FATAKENEKAKSLEADLMQLQED LAAAERARKQADLEKEELAEELAS SLSGRNALQDEKRRLEARIAQLEEE LEEEQGNMEAMSDRVKATQQAE QLSNELATERSTAQKNESARQQLER QNKELRSKLHEMEGAVKSKFKSTIA ALEAKIAQLEEQVEQAREKQAAT KSLKQKDKKLKEILLQVEDERKMA EQYKEQAEKGNARVKQLKRQLEEA EEESQRINANRRKLQRELDEATESN EAMGREVNALKSKLRGPPQETSQ*
2126	7623	A	2300	1	2448	
2127	7624	A	2301	1	2655	
2128	7625	A	2302	5	605	VDPDSGQIQVPCTPRGLKWSPNMN PARKTDACGEDTHPSLLGVFSPRPP LGILRFALQNPRSPGKESEMLPPPA WVYLKAPMILNGV/CVIWKGWIDL QRLDG/MGCLEFDEERAQSWPW*A HPQC*EGRRPSCRELGNVALGADG DSPGSIYTRRWKLSQRVPAPPPQE PKMPSLCCRNTSTTFSGRPSQSPRTK KQRP
2129	7626	A	2303	1	588	MGFCHVDQTGLELLTQPLALIGAA

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						LEGGRAGGAADLAPDFGRLALQIK YTGFRDRPH/EERQARFQACRDGR SE/IFFPASWQGEQRQ/TPSREYVDL EREAGKLNIPKGPAGDETPSSLSSM MIVLSSDSGPAVLAIPLNLTTPRYTP MVPCGGHHQAQRKRPLCTPPSSIQ QGSMSVKSMPTPVAAHKSFTSALC
2130	7627	A	2304	1	615	GLKGGKMPRVVPDQRSKFENEFF RKLSRECEIKYTGFRDRPHEERQAR FQACRDGRSEIAFVATGTNLSLQF FPASWQG\DQRQTPIREYVDLAREA GTVYLKAPMILNGVCAIWKGWIDL QRLHGMGCLEFDEERAQQEDALTO QAFEEARRMTREFEDRDRSHRQEM EARVSQLLAVTGKK\QLDPRPGSNL GGGDDLKLR
2131	7628	A	2305	73	168	
2132	7629	A	2306	322	671	RLWASPAAPGKKKEMGNSMKSTP APAERPLNPEGLDSDFLAVLSDYP SPDINPPIFRRGEKLRVISDERGWW KAISLSTGRESYIPAIICVARSYHGW LLRGP\KNMAEELLQLPD
2133	7630	A	2307	624	1581	KAATSENKIICCEWRTSQAALMLHR LWASPAAPGKKKEMGNSMKSTPAP AERPLNPEGLDSDFLAVLSDYSP DISPPIFRRGEKLRVISDEGGWWKAI SL\STGRESYIPGICVARVYHGL/W LFEGLRDKA EELLQLPDTKVGSF MIRESETKKGFYSLSVRHRQVKTY RIFRLPNNWYIISPLTFQCL\EDLAV NHYSEVADGLCCVLTTPCL\TQSTA\ APAVRACSSPVTLRQKTVDWRRVS RLQEDPEGTENPLGVVESLFSYGLR ESIASYLSLTSEDISSFDRKKKSISLM YGGSKRKSSFFSPPYFED
2134	7631	A	2308	52	454	SQTQREPTMVLSPADKTNVKA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHLKLRVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR
2135	7632	A	2309	3	452	
2136	7633	A	2310	26	502	NSTDSETHHGARLLPDKTKAQRPP RLKLGANA\GEYFGGPWKG MFLS FPNPPKTYFRQFRP*ANGFAQG*RG HGQRKVA\DALQSPCRNVD\DMPPQ TALSAPEATLHG\HKL\RVDPVNFKL LSH\CLLG*PWPAHLPRPSFTPCGCT PSLEQSSWAF
2137	7634	A	2313	43	595	LRNMWQLERNVET\INTFHQYSVK LGHPADTL\NQGEFKELVRKDLGQN FLKKENKNEK\IEH\IEDLDTNAA Q\LSFEFIMLMARAKPGALPTRR MHEGDKGPWPPPHKPGLGEGTPPR PQWPRSPVATAHGKSWWPRPQA TNHGGQATLPLPKPGRGLLCQTVL AVGLGGWGQIKSLP

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2138	7635	A	2314	3	419	SLYHNSSQKRHWTFSSSEQLARLRA DANRKFRCKAVANGKVLNDPVFL EPHEMTLCKYYEKRLLEFCSVFKP AMPRSVVLTCAFLACKVDEFNVSN PQFVGNLRESPLGQEKALEQILEYE LLLIQQLNFHLIVHN
2139	7636	B	2315	324	487	MQRVRAGRIVVTTARQRRLPDALG FREIFSSEQLARLRADANPNSDAK PWPTGS*
2140	7637	A	2316	1	1050	
2141	7638	A	2317	191	229	
2142	7639	A	2318	186	1232	CVWVLVCRPSGPGHDSIMYHNSSQ KRHWTFSSSEQLARLRADANRK\FR CKTRAH\GKVFPNDPVFLEPHEMT LCKYYEKRVIE\FCSVFKPAMPRSV VG\SRACMYFKRFYLNNSVMEYHP RL\IML\TCAFLACKVDEFNVSSPQF VG\NL\RESPLGQEKALEQILEYELL PYTSNFNHFL\VNHPY\RFEGFLND LRTR\YPILNPEILRK\TA\DDFLNRI ALTDAYFLYTPSQ\ALTAILSSASRA GITMESYLSLSMLKENRTCLSQLL DIMKSVRN\LVKKYEP\PRSEVAVL KQKLERCHSAELALNVITKKRKG YEDDDYVSKKSKHEEEWTDD\DLV ESL
2143	7640	A	2319	152	371	DVLLATSSSEPSLFCPLCLTASTPKP LPPPG\PLPCPVWAMWGTGGFPLPG PPGQPRVRGPTAARGTPCCRPS
2144	7641	A	2320	4	474	PQYPAWHEGERAEWLCCRVSSETGS ACSMADQL\TLKEQIAEFKEAFSL\F DKDGDGTITTK\ENLGTVNEILLGSN PTEAELQDMINEVDADGNGTIDFP EFLTMMARKMK\DTDSEGRKLAEEA F\RVFGLRVGNGLYL\ACRNFRHV DGQTLGGGSLPD
2145	7642	A	2321	291	648	LTQLKTHCPLIKSKTMNKKRAIREP AQEPGPQKEENPKKHRSPSTSTSF GLEVPASYSPTKAEQPGQVRKAV QPAVRLEPRASHPAGPPVPPSGVLV SRRRPEPGQGKPPESDFDH
2146	7643	C	2322	155	316	MTGPVSGSFIHWVLFSGFSSMSNA SNVFLVRPSC TTGLSRMAADSAG CCSL*
2147	7644	A	2323	28	1323	PSGARVAGAGPCGGGMFVQEEKI FAGKVLRLHICASDGAEWLEEATE DTSVEKLKERCLKHCAHGS�KDPK SITHHKLIHAASERVLS DARTILEENI QDQDVLLLIK\RAP\SPLPKMADV AEEKKK\QDQKAPDKEGILG\ATAN LPSNKLDRAAVQTNMRDFQTELK ILVSLIEVA\QKLLAL\NPDAV\ELFK EGECNCWDEDGGMSVWDEACPA AFOREMGLFRENRTKALQLNHMS\ VPQAIGSWL\NEHA\EDPTIDTPLPG\ QAPPEAQG\ATAAASEAAAGASAT DEEARDELTEIFKKIRRKREFRADA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						RAVISLMEMGFDEKEVIDALRVNN NQQNAACEWLLGDRKP\SPEELDK GIDPD\SPL\FQAIWDTRWVQLGLTN PKTLAFEDMLENPLNSTQWMNDP ETGVPVMLQISRIFQTLNRT
2148	7645	A	2326	307	412	SVQTIVFQPQLASRTPTGQS*SSCPY PLFATINAE
2149	7646	A	2327	50	247	
2150	7647	B	2328	276	779	MRTLAILAAILLVALQAQAEPLQAR ADEVAAAPEQIAADIPEVVDSFAW DERAPLQVSGKSSPVCARLLLLQET RDRGLLFALPLHSAYLEDLLRQSHF RQELMKLQPRSSLEQMIRKWLMP HGMKVPLFRFQPDKIIVLSTLIPTGD YSPHNLKNLFMRMVTTPSP*
2151	7648	A	2329	3	333	
2152	7649	A	2330	35	717	RRSSPSLLPLAERGGRARGRPERA PHPSTPATRTAPPPWARRMMKLKS NQTRTYDGDGYKKRAACLCFRSES EE\EVLLVSSSR\HPDRWIVPWKEG MEARRKEAKCGKQVREVCEGRLG VKGT\LGRLVGIFENQERKH\RTYV\ YVLIVTE\VLEDWEDSVNIGRKREW FKIEDAIKVLQYHKPVQASYFETLR QGYSANNGTP\VV\ATTYSVSGFRA SMFRAFRWT
2153	7650	A	2331	104	381	IQGGSMTSSFSSTICQKILNKEKQS CCSN*SKWSRNVSSNGKPNWTGTS LPALTEMARTTIWKKHIFTKKFSSV SIFQVFKSF*I*GSVLS
2154	7651	B	2332	228	445	METSSRELQAAEYLEKHQIKEVVSY LTSALLFLRPALKTLGLCTEDEDLQ DDGHKITLDKFKEEVNKRMEIX*
2155	7652	A	2333	3	1459	GSKQVSEGTDNGDLPSYVSFAFIEKE VGNDLKSLLKLDKLEQRTVSKMQ LEEQVLTISSEIPKRIRSALKNAEESK QFLNQFLEQETHLFSAINSHLLTAQP WMDDLGTMISQIEIERHLAYLKWI SQIEELSDNIQQYLMTNNVPEAAST LVSMALDIKLQESSCTHLLGFMRA TVKFWHKILKDKLTSDFEEILAQH WPFIAAPPQSQTVGLSRPASAPEIYSY LETLCQLLKLQTSHELLTEPKQLPE KYSLPASPSVILPIQVMLTPLQKRFR YHFRGNRQTNVLSKPEWYLAQVL MWIGNHTEFLDEKIQPILDKVGLSV NARLEFSRGLMMLVLEKLATDIPW LLYDDNLFCHLVDEVLLFERELHSV HGYPGTFASCMHILSEETCFQRWLT VERKFALQK\MDSMLSSEAAWVSQ YKDITDVDEMKNVPCDAETFMTHLL VITDRYKNLPTASRKLQFLELQKDL VDDFRILINTK
2156	7653	A	2335	46	1146	
2157	7654	C	2336	17	196	MTTLVTTTTMDMVIATSRVVMGR YPGEVVIKIATNHTKLFHLQLIPNSG NFIAGPVSR*

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2158	7655	A	2337	208	1504	FRFAAGGCSLGGSGGDTSTMSEEQF GGDGAATAA VGG SAGEQEGA MVAATQGA AAGSGAGTGGGTA SGGTEGGSAESEGAKIDASKNEEDE GHSNSSPRHSEAATAQREEWK MFI GGLSWDTTKDLKDYFSKFGEVVD CTLKLD PITGRSRGFGFVLFKESES DKVMDQKEHKLNGKVIDPKRAKA MKTKEPVKKIFVGG LSPDTPEEKIR EYFGGFGEVESIELPMDNKTNRKG FCFITFKEEPPVKKIMEKKYHNVL SKCEIKVAMSKEQYQQQWGS GGFAGRARGGGGPSQNW NQGY NYWNQGYGNYGYSSPRLRWLWRI *LHWLPTTTYGYGDYSNSQSGYGK VSRRGGHQNSYKPHLNYSICNL\S PTGGEAVFS\NLKIQFESGS/CH*LLI AVQTKFLYQVPEWKYD\VGSL
2159	7656	A	2338	208	1466	FRFAAGGCSLGGSGGDTSTMSEEQF GGDGAATAA VGG SAGEQEGA MVAATQGA AAGSGAGTGGGTA SGGTEGGSAESEGAKIDASKNEEDE GHSNSSPRHSEAATAQREEWK MFI GGLSWDTTKDLKDYFSKFGEVVD CTLKLD PITGRSRGFGFVLFKESES DKVMDQKEHKLNGKVIDPKRAKA MKTKEPVKKIFVGG LSPDTPEEKIR EYFGGFGEWDPIELPHGQTRPNKRR GFCFITF*GEEPVKKIMEKKYHNVL LSKCELK\VA\MSKEQYQQ\Q\QW DSRGGCAGRA\RGRGGDQ\QSGYG K\VSRRGG\HQNSYKPYLNYSICNL SPTAGTSLQALCRADFRFSQARSMR TG*RDAPRSRMLPFGGEAVFSNLKI HL\NGGSCHLLIAVQTKFLYQVPE WKYDVGSL
2160	7657	A	2339	1070	1238	PQRDFQFFLLWPPGGEA\VFSNLK\IP FERGSCHLLIAVQTKFLYQVPEWK YDVGSL
2161	7658	A	2342	1	456	RPRRPQREPTMVLSPADKTNV KAA WGKVG AHAGEYGAEAL/RMFL/SF PTTKTYFP HFDLSHGSSQVKGHGKK VADALTNA VGHVDDMPNALSALS DLHAHKL RVDPVNFKLLSHCLLV LAAHLPAEFTPAVHAFLDKFLASVS TVLTSKYR
2162	7659	A	2343	2	512	GLEFGTSHRLRENPPWCLSPA\DKT NVKA\AWGKVG AHAGEYGAEAL RMFLSFPTTKTYFP HFDLSHGFAQ VKGATAKKVA\DA LTKAVAHGRGT CPNALSALSGPATAHKL RVGPST FKLLKPLACLVDPGPAHLPRPSFNP WRLQGFLG TKFLGFLVEAPLLEPSK
2163	7660	A	2344	265	426	SFSISVFAACLALPMAQPQ*PCSQK V*QHCRVYMH AHTWPLCLQDVLV ECCSQS
2164	7661	A	2345	56	341	IVTLDWSRNLKYNRCWSKCYILSSS DSSSSFRDSFTNPAEF*FKSFILNFV



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						MYVYVNYFCNFFNDITAGHFFHLKL LYFRLCSLPGFADGTAPITV
2165	7662	A	2346	333	534	LMEDMKLFQKI*EKKQRNMLRNL* RKKMNQMM/YNM*HLLQHLLYFK FLLVHPM*LFSPGLYILSNFH
2166	7663	C	2347	117	386	MDILICTDFGSVNYFNWRLPKSYL SLFYRIYIVHDEVKDKAFELELSW VGELTNGRHEIVPKDIREEAKEYAK ESLKEEDSDDDNM*
2167	7664	A	2348	2	359	FEDGVLLCHPRLEGSGT\ISAHCNLS LPGFKRSSCLRLPASSWDYRNMPY PGYFCIFGFTNNTETGFHQASFKLL NSRDLPTLAPVKCWDYRHEHCTR PKYIFYQRYSHCMLEQHLLN
2168	7665	A	2349	648	887	SWKLLLLLCLLKNEHLPTKPATGHS NIADQTLKKSFCLEPFFHKV*KGLIF LTPRTTSLHLPIAVLLFSTAFIAYS T
2169	7666	A	2350	306	449	EIKKKYLLPGVVAHACKPSTLGGR GGQIISGQEFET\SLTNMAKPCFF
2170	7667	A	2351	1	625	NFALEAKNSARAISYVQTPMGHFT RGGPRLTITSLWGK\VNVEDAGGE TPGKGSLLVYP\WTQRFDSFGNLS SAFCPSWPTPKVKAHGK\KVLTSLG DAHKSTWDDLKGHLLPKPEVNLHC \DKPAMWDPENFKAPGEMCLVTRF GQSLFRQKNFTPEGCRASLGKKDG ELQLASCPGPSQITTEASWPMNSEA FKDKAFILASNYK
2171	7668	A	2352	1324	1671	IVQTLSTLSKSSCRSTEPCTSCLPDLP QVGTTCPHGTCC/NRCHVGGLMN PLKPNC/GCRKCNCGYLYIYKQGR LHPRGKFQPGNNHRFSCQTQSVHMDI THGSGMFSLCFPGSTMF
2172	7669	A	2356	8	564	SAQMAVTTADPRVRPRVRTQLCSL ASLIQTLLVHLTPEEKSAVTALWGK VNVDEVGGKALGRLLVVPWTQR FL\ESVFGDLSTPNVMANPKVKAHS \KK\LGALLVVGLAHL\DNLKGTF HTEVSLHCDKLHV\DPENFQAPGAT CLVLCWANHFVQKNFTPPV\QAC LFRKL VAGIVANALAHK
2173	7670	A	2357	23	679	GLLTSGGAHLSPSRVTQGIYMSAL SEMPKPPDYSELSDSLTLAVGTGRF SGPLHRAWRMNFRQRMGWIGV GLYLLASAAFYVFEISETYNRLA L\EHQQHPPEPLEGTTWTHSLKAQ LLSLPFW\WDSYFFWVPYLQMF VSLYSCYKELDPQNSGGYCYPSPIW LWAVYFGNRHHAF/VVKASNSDSA DLQLIDTVKSVTRFFPLRITKTGQS
2174	7671	A	2358	17	392	SFKMADQDPAGMSPLQQMVASGT GAVVTSLFMTPLDVVKVRLQSQR SMAS\DAFVKIVRHEGTRTLWSGLP ATLVMTVPATAIYFTAYDQLKAFL CGRALTSPLYAPMVAGALARREHR LGPLTS

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2175	7672	A	2359	1	725	RFTGTMDAFVKIVRHEGTRTLWSG LPATLVMTVPATAIYFTAYDQLKAF LCGRALTSPLYAPMVAGALARLSI VLGL*PPSVPTSAQTQSVAPSPNLC QPRDRGVF*VPRPGTAGR*CHVRPV ISLLPIVTPNPHTVGTVTVISPLEMR TKLQAQHVSYRELGACVRTAVAQG GWRSLWLGWGPTALRDVPFSALD WFNYELVKS/WLNGLRPKDHTSVG M/SFVAGGISRTVAELTLPY
2176	7673	A	2360	102	1573	SFKMADQDPAGISPLQQMVASGTG AVVTSLFMTPLDVGKVRLQSQRPS MAELMPSSRLW\SLSYTKLPSSLQS TGKCLLYCNGVL\EPYLA\CPNGAR CATWF\QDPTFRFTGTMD\AFVKIGE ARGAPRTLWSGLPATLVMTVPATA IYFTAYDQLKAFLCGRALTSPLYAP MVAGALARLGPVELWISPLGALCS NKACRVQHVVNRNRELG\ACVRTAV AQGGWRSLWLGWGPTALRDVPFS VHPPQAL\YWF\NYEL\VRSW\NG LRPK\DQTSVG\MSFV\AGGISRTVA AVLTLPF\DVVKTRQ\VALGAL\EA VKSEPPCNVDST\WLL\LRRI\AESG TKGTLLQASFPRI\KGCPSCA\IMIQ HLIEFRQKAFFPRGLNPGTGFLLGL EKGPKGKDPVSSQREWGRGQGGD PSQSAFSSALREGGLFSLPLPATKLP GQGCPSGRPSTSSRHNFLLLPVGI ITYPPPKFKTKSSELPPFVFPCLL
2177	7674	A	2361	1	215	QVPMSEESDQYLAVLTFPRCVLV MIHTHAQVLNHVCIYVCVHMSVAV Y/ISACRATDPDTHTCVYMYIQT
2178	7675	A	2362	3	543	TRNTLGWEVSSFSPLLSSCLNMVRT KADSVPGTQEKVVAARAPRKGL\G SSTSAHLIRPSVSIEESLKNKYARRE PPFCVRP/TLPKWAKREIGEFFR\LSP KDSEKENQ\PEE\AGSSGL\GKRQRR KSMFLLQPGFTQLMEKGLGTFLHFI FGLTSPLFYPGYSRKVKFTINGVWF QLGFG
2179	7676	C	2363	69	290	MCLWNCCRKTQLAADILWLTAPAS PRDLRLGCVAEVFLARWELFGEDSF REKFFGFFFRDGWQPFLLSAGER*
2180	7677	A	2364	663	793	DGDSVMVLPTIP\EEEEAKKLFPGGVF \TKELPFGKKYLRYTPQP
2181	7678	A	2365	1	726	MPGGLLLDVAPNFEANTTVGRIRF HDFLGDSWGHFSQ/RGGFTPWCA PRSFARAAKLAPDFAKR\NVKLIALS IAVFEDHLC/AESKDIHVYHCE/ESPT EKLFP\PIIDRNRELANPVGACWIP AEKDEKG/LCPVTASVWCVFVGP** RKLKAVYPSYPSYPLAGNFE*RFLR VVHLLSQLTA/EKKRVAHPQLIWKD GD\SVMLPNPSPEEEA\KKLFPEKE SFTQKELPNLAKKYLRYTPQP
2182	7679	A	2366	3	452	
2183	7680	A	2367	1	627	TLLVPQDSERTHPWLLSPADK\TNV

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						KAAWGVKVGAAHVRSMCAEALER MFLSFPTTKTYFPHF\DLSHG\SAQV KGATGKKVADALTKRRGAPLDDM PNAL/SSALEATLHAHKL\RVGPGST SKLLKPLACLVDPGPAHLPRPSSTP GGCNVFPGTKFPGLFVEAPLLEPSK LPLKLGSLRLAIVFLPLWGFPPAPP LSCTRTPVVFEIKS
2184	7681	A	2369	1	467	GTSACGVASLSVVDCVPAPFSQQQP LPEGERTLGGRHRLRTRARALHPAP ACFCHASLCVCM/CA/CVLVCGLLC EHQSDSIHCLCHLCLCKCNLYLCIRA ASSQHLKCHWVGGNKTCFGPDDL GGRSEPTFETLSGEPATPADGKTGS CTGPERYQM
2185	7682	A	2370	131	406	EAMGILKLQVFLIVLSVALNHLKAT PIESHQVEKRKCNTATCATQRLANF L\HSSNNLGGILSSTNVGSNTYK RNAVEVLKREPLNYLPL
2186	7683	C	2371	257	422	MQVCFRQGF\LPKGHHGLIATLGA POLYMFLVLRASLFLWLSXF\RSX KLXXXRN*
2187	7684	A	2372	621	1202	GVPEPRARPSTSGMNGDRIRLPCWR NDRQK\THML\DVMDHFSRASSIH RRALSRDRFTREPQ\DTYHYL\PFQ PCPHRRP\HFFPKSRNRPA*\CPFSS \TKPLNFHAMFQPFLEMIHEGSAGP WDIHFHSPAFOHPPTFEIREGD\DDR DCCAGE\RHNSTGLPCGLKDQVVT K\CREDLVLWDCFHQQLPG
2188	7685	A	2375	154	1702	IGHRDPARGRSCRCSGYYSRMVCE KLAPQSEMASAG\VSLRATILCLLA WAGLAAGDRVYIHPFHLVIHNESTC EQLAEANAGKPKDPTFIPAPIAKTS PVDEKALQDQLVLVAAKLDTEK RAAMV\GMLANFLGFPYMGMH ELWGV\VHG\ATVLSPTAVFGTLAS LYLGALDHTADRLQAILGVPWKDK NCTSR\DAH\KVL\SA\QAVTGLLVA PGRADKQ\A\QL\ALSTVGVFTAPG LHLKQPFVQGLALYTPVVLPRSLDF TELDVAAETID\RLMQAVTGWKTG CSLTGAKADSTLAFNTYVHFQGKM KGFSLLAEPQ\EFWVDNSTSVSVP LSG\MGT\FQH\WSDI\Q\DNFSVTQVPF TD\SAFLLLIQPHYASDL\DKVEGLT FQQN\SFNWMRKL\FPRTIHLTMPQL VLQGSY\DLQDLLRPGSSCPPFLHTE LNLGRISGN\DRIRVGEVLNSIFFEL EADEREPTTESTQQLNKP\EVLEVPL TRPFLFAVY\DQGATALALSWGRV GKPA
2189	7686	A	2376	181	353	VGDRCEGNGNEARGHWKREVCCP GARSGASV*GSSGRLGLCL*VG TREAG*PGYPASLVPT
2190	7687	A	2377	1550	1823	GRLLDEPQAAHKFLRGEMGGQSPG VRGTELLGAFSLPGES/GSPGRASPL PFPNLEKTVTFQSLGLPLKIPKEG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LKEIKLTNVKKSCTLTP
2191	7688	A	2378	134	321	GCF*KGRDLFADKMQEHSIQ*FTAL FQPTNQKISSWVCGPKVNFKAIKTG SRSGKAIQNVES
2192	7689	A	2379	1	602	RTRASTRPSRDYGNVVLWTRTSHP RPLTEPEPRATMSHGKGTDMLEPIA APVVGFLSSLLRTRGCVSEQRKLVFS GALQEA\TEHYNNHHWFPEKP\SRG SG\YRCIR\NHK\MTPIISRVASQ\VG LSQAQL\HQLP\SELTLWVDP\YEV S\YRIGEDGSICVLYE\EAPLAASCGA SFT\CARNQVACWGRSSPSKINYVM AVSS
2193	7690	A	2380	28	423	SKPLKMADDLDFETGDAGASATFP MQCSALRKNGFVVLKGRPCKIV*M STSKTGKHGHAKVHLVGIDFTGKK YEDICPSTHNMDVPNIKRNDFQLIGI QDGYLSLPQESGGGIRDPLNLQRPP PRAWPGSG
2194	7691	A	2381	1	930	
2195	7692	A	2382	171	695	NRQDDLDFETGDA\GASATFPM\QC SALRKNGFVVLKGRPCKIVEMSTSK TG\KHGHAK\VHLVGIDFTGKK\YE\ DICPSTHD\MDVP\NIKRN\DFQLIGI QGWGTL\SL\Q\DSGEVREDL\RVSP EGDL\GKEIEQKYDCGEEILIP\VLSA\ MTEEEA\VAIKAHGKITGSPGVAVV ASK
2196	7693	A	2383	789	1380	IPYFLMVYGLQTLMCKHITRRIRDH LHEAMNYFLIPSSPFLEANPPPTPG TICPAC/YPPPPRAGQQLACFLSIPPL FPNLPIPPQKKDYWVLLSLGAPKFK GYLVLCMLQEPCKQPGKSTGWI RNYPSWMHLATSTPQLRRGSKEVH NYKTMGSRPQKRYETGPGTQGGAE RILLSKPGRWRGSPGQEQVLGLQ
2197	7694	C	2384	248	433	MSGILVLNLFLTGLSGVGPSSSVTLTV LSVHQLPACAKLEKGNLHPCPNSS FPPRDFCVHPP*
2198	7695	A	2385	1	1108	
2199	7696	A	2386	1	1528	MGTRAARPAGLPCGAENPARRRLA LGARQQIHSWSRTPSTRLTAPAGP ARGVARPAMAPDPVAAETAQAQGP PRYFTWDEVAQRSGCEERWLVID\R KVYN\INEFTRRHPPGSRVISHYAG QDATDPFVAFHINKGLVKKYMNSL LIGELSPEQSFEPKKNKELTDEFRE LRATVERMGLMKANHVFFLLYLLH ILLLDGAAWTLWVFGTSFLPFLLC AVLLSAVQAQ\AGWLQHDGHL VFSTSK\WNHLLAHFVIGHLKGA SWRNHMHFQHHAKPNCFRKDPDIN MHPFFALGKILSVELGK\RKKKFM PYNHQBKYFFLIGPPALLPLYFQWY IFYFVIQRKKWVDLAWMITFYVRF LTYVPLLGLKAFGLFIVRFLASN WVFWVTQMNHHPMHIDHNRNMD

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						WVSTQLQVATCNVHKSC/AFNDWV SVG\HFNQIEHHLFPTMPRHNYHK VA\PLVQSLCAKHGIEYQSKPLLSAF A\DIHSLKESG\QLWLDAYLHQ
2200	7697	A	2387	45	949	APWWWYHPERLLGYPIAATLPSRL VLPGEVEPSTQWCSPLRLEPQFHLL PLQHLRRDSSSLSPPLPALGRTRGRR SSAPAHGDESCSLLPRPLSLAHGEP GRRRAEACSRLSRSRGRHSMTEPR STSASAAHAAAFCCFCCCRPPRPRP LAPPPP*PCR*SRRGCAGIDGAAAD VALGHPPE/HCPVPDVQMTSRRLMF IQLSQSPGVHCTSPHFSAPPTWCRR GPGSPATSPPLHTLPAVVAAPRAL RRAADRGRGRGLDRGVACAAERL QRQQLSRQSQSRSEAQPDAMEQ PRKRW
2201	7698	A	2388	804	985	VGGDSQDLRDPVPPQTAPPPNSLS PPALSPRCASPSYPQKCLP/PPVTHR SACLSSAHRTHKKGQELVTG
2202	7699	C	2389	258	461	MSVTFIAVARGKLFFENLGHSELPL SLEWQTSDEGEVEARGSRGGEALPR PGSMQPCPADVTRRPTRP*
2203	7700	A	2390	1	370	GTRVTSGGGSRRPGMAAWSPAAA APLLRGIRGLPLHHRMFATQTEGEL RVTQILKRKVSPRLQLIKVTDISGG CGA\MYEIKIESEEFKEKRTVQQHQ MA\NQALKEEIKEMHGLRIFTSVPK R
2204	7701	A	2391	1	1107	
2205	7702	A	2392	1	1230	
2206	7703	A	2393	1	908	
2207	7704	A	2394	177	934	PGLSQEPSGSMETVVIVAIGVLATIF LASFAALVLVCRQRYCR\PRDLAQ RYDSKPIVDLIGAMETQSEPSLE L\DDVVITNPHIEAIL\EN\EDWIEDAS GLMSH\CIAIL\KICHTLTEKLVCHD NGALGAKMKTSASVSDIIVAKRIS PRVDDVVKSMYPPLDPKLL\DART TALLLSV\SHLVLVTRNACHL\TGIG LDW\NDQSLSVAAEEHLEVLREAA\A ASEPDKGLPGP\EAFLQEPVLQFSAY RPAA
2208	7705	A	2395	1	333	GTRGERKAGLARGQVCGLSPFPKTN KESFPNSQLNPFWN\YCGASLSLV SFSCPATRLCGNALLPSLFFSMRGF GLAVRIRDNDNRLLSRMTSMCSISR VPEHVEFPNPK
2209	7706	C	2396	7	279	MXKGS\PRXNFLECEKKSGQNPWAG LLRPWWVGHP\SAKPLIPVFSSISFPL YNPHFPIXILCNKLKSHVCKKASKY TNNPISQQWTL\SF\K*
2210	7707	A	2397	35	416	SRAVEFVRSCAGYGERKAGLARGQ VCGLSPFPKTNKESFPNSQLNPFW\N YVWGLGPCGASLSLV\SFSCPATR LCGNALLPSLFFSMRGFGLAVRIRD NDSRLLSRMTSMCSISR\VEHVEFP

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						NPK
2211	7708	A	2398	3	344	
2212	7709	A	2399	1	1359	
2213	7710	A	2400	1	463	LAQAACGPAALQLCPAGHGAAMA ATFFGEVVKAPCRVAGTEDEEEEE GRRETPEDREVRLQLARKREVRLLR RQTKTSLEVSLLKYPCKFIIAIGN NAVAFLSSFVMNSGVWEEVGCACL WNEWCRITDTHLSSTEAFVCFYH LKSNSVFLCQCSCYVAEDQQYQW LEKVF/GSCPRKNMQITILTCRHCT DIKTSESTGSLPSPFLRALKTQNFK DSACCPILLEQPNIVHDLPAAVLSYC QVWKIPAILYLCYTDVIGLDFNTVE AFKPILSYRSLKGLV\KNIPQSTEIL KKLMTTNEIQSNIYT
2214	7711	A	2407	160	441	
2215	7712	A	2408	107	691	RTAILSRLMKIFLPVLLAALLGVERAS SL\MCFSCLNQKSNLY\CLKPTICSD Q\DNV\CVTVSAS\AGIG\NLVTFGH SL\SKTCFPCLPFPEGRSMLGVAS MGHSAFCQSFLVAIFSCGPMAGLRG KRSPLLGARACCLSLAGRALLRFG PLDRPEPCSPDPPAQEGKPSPFWIPQ CMGAPDSSRALICALGPRSG
2216	7713	A	2409	2	432	GRPPPDVEVMTSLKVDNLTHTSP DVYIPDRYTKESRCFAFVRHDKR DAEDAMDAMDGAVLD/GSELRLQ MARYGRTPDSHHSRRGPPPSYGC VGYGRRSRSPRLRRMP/RSRSTRSR SRSTRSRYSRSKSRSTRSRSTRSTS
2217	7714	B	2410	1522	2003	MAIIYGVFSASNLITPSVVAIVGPQL SMFASGLFYSMYIAVFIQPPWFSFY TASVFIGIAAAVLWTAQGNCLTINS DEHSIGRNSGIFWALLQSSLFFGNLY IYFAWQGKTQISESDRRTVFIALTVI SLVGTVLFFLIRKPDSENVLGEDESS DDQDMEVNESAQNLTAKAVDAFK KSFKLCVTKEMLLSITTAYTGLEL TFFSGVYGTICGATNKFGEAEKSLIG LSGIFIGIGEILGGSLLFLLSKNNRFG RNPVVLGILVHFIAFYLIPLNMPGD APIAPVKGTDSAYIKSSKEVAILCS FLLGLGDSFNTQLLSILGFLYSEDS APAFKIFKQVQSICAAVAFFYSNYLL LHWQLLMVIFGFFGTIFFFTVEWE AAAFVARGSDYRSIMLKSFLLDSGDI LAQLCRRQQPRAPLTIRTSPDTRLR VFEKYGRVGDVYIPDRYTKESRGF AFVRFHDKRDAEDAMDAMDGAVL DGRELRVQMARYGRPPDSHHSRRG PPPS*
2218	7715	A	2411	2	229	
2219	7716	A	2412	3	353	FPLPFFTLVIWPGIRKFKLVHADGSL CEIFLIGPFKNMAGWNISVPYWFDQ SLSKYVPETETMCTLMGKLNFFLF KPRCIGKQCKRRTWGKRTT*SIRRR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SPWNKQLGYLKRLFW
2220	7717	A	2413	18	282	DPLKSGPRNRS*TRWTPSPRS\ARRS KSKSLSVSRSRSRSR\SRRESLPP VSKRESKIQVAMGEKREGSPSSP\EE EEGAGVLLRK
2221	7718	A	2414	2	830	LRSPSVLFCGKAFFVSPRGRQLPER RGVAPPRAEEAGASSRSGSPPLRA MSYGRPPPDVEGMTSLKVDNLT\Y\ RTSPDTLEGAVFEK\YGRVGDVVHP RGIRYTKGSSRGFAFVRFHDKRDAE DAMDAMDGAVLDGGELRVQMAR YGRPPDSHHSRRGPPRRYGG\G\GY GRRSRSPRRRRSRSRSRSRSRSR SRYSRKSRSRTRSRSRSTKSR SAR RSKSKYSSVSRSRSR\SRCRCGYRSP PPVSKRESKSRSRKSSPKSS\EEEGA VSS
2222	7719	A	2415	1	320	RGRASKECSGLSAHLVIHCGEKPYK CNECTRTSGTN/SSLTQQRSHTAKEP YTRNECGKVFG/HIARHQIHHSTEKP YKCN/NTLKAFSKHSGLMAHLLIDR PEKLCHYS
2223	7720	A	2416	733	1005	NPQTPMKNCWPLEKKAEP RPFLGS SMPLGFCPHGPPCSCDFLETHFLDE \EVKLIKMGDHLTN\HRLGDPEA GLGEYLFERLTLKHD
2224	7721	A	2417	148	1057	
2225	7722	A	2418	87	241	EGGLGNDPMTTDCSMAA*LFK**SP SS*ALGSFCEAQIIQSSKGLFSRGSC
2226	7723	A	2419	1	924	
2227	7724	A	2420	1	1004	MPVGAGRRAKGD PATLGALAVFTV GAKRSKGHSPKHPAGRLPPLPLR QRSTPMIDTLRPVPFASEMAISKTV AWLNEQLELGNERLLLMDCRPQEL YESSHIESAINVAIPGIMLRRLQKGN LPVRALFTRGEDRDRFTRRCGTDTV VLYDESSSDWNENTGGESVLGLLL KKLKDEGCRAFYLEGGSKFQAEFS LHCETNLDGSCSSSSPPLPVLGLGGL RISSDSSSDIESDLDRDPNSATDSG SPLSNSQSPFPVEILPFLYLGC AKDS TNLDVLEEFRGSSPYMILFHYGENG TSYVPI\TSHFRQKLAQGFVPSTGTP GFIYSAK
2228	7725	A	2421	686	1812	TCPVARASLTRGEDRDRFTRRCGTD TVVLYDESSSDWNENTGGESLLGL LLKKLKDEGCRAFYLEGGSKFQA EFSLHCETNLDGSCSSSSPPLPVLGL GGLRISSDSSSDIESDLDRDPNSATD SDGSPLSNSQSPFPVEALALPSYLG AKDSTNLDVLEEFGIKYILNVTPNL PNLFENAGEFKYKQIPISDHWSQNL SQFFPEAISFIDEARGKNCGLVHCL AGISRSVTVTVAYLMQKLNLSMND AYDIVK\KKKSNISP\NFNMG\QLL GLSRRDAGDSAGPCGQGSRSRL YFYHPFPTRNVLPGWDFLQSTWKD

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						PTPFLAGMCLALQQFLAASAGAA FFVCGPRCQNDTKLSVLRQGYQVR ELG
2229	7726	A	2422	66	187	WGGGGSAAAAMEANWTAFLFQAH EASHHQQAQNSLLPLLSSAVEPP DQKPLLPITQKPOGAPETLKDAIGI KKEPKTSFVCTYCSKAFRDSYHLR RHESCHTGIKLVSRPKKTPTTVVPLI STIAGDSSRTSLVSTIAGILSTVTSS SGTNPSSASTTAMPVTQSVKKPASK ACKKNHACEMCGKAFRDVYHLNR HKLSHSDEKPFECPICNQRFRKDR MTYHVRSHGGITKPYTCSVCGKG FSRPDHLCHVKVHVSTERPFKCQT CTAAFATKDRLRTHMVRHEGKVSC NICGKLLSAAITSHLKTHGQSQSIN CNTCKQGSKTCMSEETSNQKQQQ QQQQQQQQQTHVTISWPGKQVET LR\WEEAVKARKKEAANLCQTST AATTPVTLTTPFSITSSVSSGTMSNP VTVAAAMSMRSPVNVSSAVNITSP MNIGHPTITSPSMTSPLTLTTPVN LPTPVTAPVNIAHPVTITSPMNLPTP MTLAAPLNIAMRPVESMPFLPQALP TSPWPWRPTGPRSCSRPMKLPITNSR QHRTACCPS
2230	7727	A	2423	3	777	RTSLVYDYPLRRRWLRRQRGGGGF CFGCGGRSPGPGFGLSPTVVTLAEL LVLLAALLATVSGYFVSIDAHAEEC FFERVTSGTKMGLIFEVAEGGFLD\A DVEITGPDNIGILPTRLYNLSGKYTF AAHMDGTYK\CFNS\RMSTMTPK\A VMFT\DIGEAPK\GQD\METEAHQN KL\EEMINELAV\MTAVKH\EQEY MEVRERIHRAIQRRTTQNSRVVLWSF FEALVACCHDIWGQIYYLEGDFFEV RRSCFKKPLPG
2231	7728	A	2426	89	136	
2232	7729	A	2427	1	916	MFYHLVPDGKKPGATLKATSAPKG KANGGRQAHAPPRWASAGDVTHS AISELRESATAAASASSESAGSGPR MKSVIYHALSQKEANDSDVQPSGA QRAEAFVRAFLKRSTPRMSQARE DQLQRKAVVL\EYFTRHKRKEKKK KAKGLSARQRRELRLFDIKPEQQRY SLFLPLHELWKQYIRDLCSG\LKPD\ TQPQMIQAKLL\ADLHGGFLFISVT K\SKWPLLMLGITGNPFYQETK\HIF QNLSPKGRPALKVIPPSLNCRVPLW KPDGFIPPTFTGSKFPSLGQVNR\SA KKFQSEGNRLTL
2233	7730	A	2428	2	484	PDSSGPHRLRENPPWCLSPADKTNV \KAAWG\KVGAAHVSRMCAEALER MFLSFPTTKTYFPHFDLSHGFCPL RATGKKVD\EALT\KRRGAPLDDMP NAL\SSALEATLHAHKL\RVGPGSTS KLLKPLACLVDPGPGPPSPAEFHPL RCNVFPGDKVSWVSC



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2234	7731	A	2432	197	332	
2235	7732	A	2433	1	1788	
2236	7733	A	2434	3	111	
2237	7734	A	2435	220	423	HEELKSGPYLLTFRDCFLHFWALV SKR/LALNFM*TSAPT*KALSKRNIC LVNKNRNIKIPYPKKKKK
2238	7735	A	2436	273	499	RSGVRDQPGQHGKITSLLKIQLAR RGGACL*SQLLRRLRQENRLNPGG GGCSEPRSCHCTPAWETEQDSISKIK
2239	7736	A	2437	1	1176	
2240	7737	A	2438	245	394	
2241	7738	A	2439	458	701	GPAPTRRGPAHGAHTR**PAGTAR AACGSA*SAGTASPAHKGKGHHPG SRASGTGPGPCQRRRRSDHSSAGK WPLREASL
2242	7739	A	2440	365	814	AALRSSENSSRHRSLVKMSDKKAK DPVNIKSGGQPKRKNWSKGKSSG TSFNNLVLFDKATYDKLCKEVPNY NLITPAVGSERL\KIRGSLGQGGKPFQ ELLS\KGFI PNWFSKHRASSYFTPGIT KGGDAPSLLGEDCMNRSNPPVHLE K
2243	7740	A	2441	41	565	APSPRRPWGHFTEED\KATIK\NLWG KGEMWKDAGGKNPWERLPWLSYP MGPQRFFDQLLANLSLCLPIMGNP PKVKGTWPRKVLTSLG\SAHKSTW DDLKGHLLPKPEVNLHCADKPAW DPENFKAPGEMLLVTRFGQSHFRQ KNFTPGGCRASWGRKMGDLELASA LVPSRYH
2244	7741	A	2442	3	284	
2245	7742	A	2443	1	3339	VEGMTQCSCVSSIEGKVRKLQGVV RVKVSLSNQEA VITYQPYLIQPEDL RDHVNDMGFEAAIKSKVAPLSLGP DIERLQSTNPKRPLSSANQNFNSET LGHQGS HVVTLQLRIDGMHCKSCV LNIEENIGQLLGVS IQVSLENKTAQ VKYDPSCTSPVALQRAIEALPPGNF KVSLPDGAEGSGTDHRSSSSHSPGS PPRNQVQGTCTTLIAIAGMTCASC VHSIEGMISQLEGVQQISVSLAEGTA TVLYNPSVISPEELRAAIEDMGFEAS VVSESCSTNPLGNHSAGNSMVQTT DGTPTSVQEVAPHTGRLPANHAPD FLAKSPQSTRGSGHRRKCFFTDSKG MTC\ASCVSNIERNLQKEAGVLSVL VALMAGKAEIKYDPEVIQPLEIAQFI QDLGFEEAVMEDYAGSDGNIELTIT GMTCASCVHNIESKLTRTNGITYAS VALATSKALVKFDPEIIGPRDIKIIES KTSEALAKLMSLQATEATVVTLGE DNLIIREEQVPMELVQRGDIVKVVP GGKFPVDGKVLEGNTMADES LITG EAMPVTKKPGSTVIARSINAHGSVLI KATHVGNDTTLAQIVKLVEEAQMS KNPNKHISQTEVIIRFAFQTSITVLCI ACPCSLGLATPTAVMVGTVAAQN

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						GILIKGGKPLEMAHKIKTVMFDKTG TITHGVPRVMRVLLLGDVATLPLRK VLAVVGTAASSEHPLGVAVTKYC KEELGTETLGYCTDFQAVPGCGIGC KVS NVEGILAHSERPLSAPASHLNE AGSLPAEKDAVPQTFSVLIGNREWL RRNGLTISSDVSDAMTDHEMKGQT AILVAIDGVLCGMIAIADAVKQAAA LAVHTLQSMGVDVVLITGDNKRKA RAIATQVGINKVFAEVLPSHKVAKV QELQNKGGKKVAMVGDGVNDSPA AQADMGVVAIGTGTDVAIEAADVVL IRNDLLDVVASIHLKRTVRRIRINL VLALIYNLVGPIAAGVFMPIGIVLQ PWMGSAAMAASSVS VVLSLQKLC YKKPDLERYEAQAHGHMKPLTASQ VSVHIGMDDRWRDSPRATPWDQVS YVSQVSLSLTSDKPSRHSAAADDD GDKWSLLLNGRDEEQYI
2246	7743	A	2445	14	503	NNDFIVIGTGTEFGIPGPTHAYEKT IYDDYNCL*QEELETNQNLQRQF YDKRKLEAMLQGMVTETTMKWEK ECERRVAAKQLEMQNKLWVKDEK LKQLKAIVTEPKTEKPERPSRERDR DKVTQRSVSPSPVPLLFQPV*NAPPI RLRHRRSRVSGDRWV
2247	7744	B	2446	226	347	XGKIIVASCFFPFSSRKRSSSTVAPA QPDGAESEWTDVETR*
2248	7745	A	2447	8	2985	WIQYSSTLTPNDWNKRKKKEKKA MLSARAKTPRKPTVKKGPKRTLKT QLG/Y YCRVRPLGFPDQECIEVINN TTVQLHTPEGYRLNRNGDYKETQY SFKQVFGTHTTQKELFDVVANPLV NDLIHGKNGLLFTYGVTSKGTHT MTGSPGEGGLPRCLDMIFNSIGSF QAKRYVFKSNDNRNSMDIQCEVDAL LERQKREAMPNPKTSSSKRQVDPEF ADMIVQEFCKAEEVDEDSVYGVF VSYIEIYNNYIYDLLEEVFPDPINPL HNLNCFVKIKNHNMYVAGCTEVEV KSTEEAFEVFWRGQKKRRIANTHL NRESSRSHSVFNKLVAAPLDADGD NVLQEKQITISQLSLVDLAGSERTN RTAEGNRLREAGNINQSLMTLRTC MDVLRENQMYGTNKMVPYRDSKL THLFKNYFDGEGKVRMIVCVNPKA EDYEENLQVMRFAEVTQEVEVARP VDKAICGLTPRRRYRNQPRGPIGN EPLVTDVVLQSFPPLPSCEILDINDE QTLPRLEALEKRHNLRQMMIDEFN KQSNAFKALLQEFDAVLSKENHM QGKLNEKEKMISGQKLEIERLEKKN KTLEYKIELEKTTTIYEEDKRNQQ ELETQNKQLQRQFSEKRRLEARLQ GMVTETTMKWEKECERRVAAKQL EMQNKLWVKDEKLKQLKAIVTEPK TEKPERPSRERDREKVTQRSVSPSP VPLLFQPDQONAPPIRLRHRRSRAG

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						DRWVDHKPASNMQTETVMQPHVP HAITVSVANEKALAKCEKYM LTHQ ELASDGEIETKLIKGDYKTRGGGQS VQFTDIETLKQESPNGSRKRSSSTV APAQPDGAES\EWDRCRINKVFCGL WEMR\AGSQLGTWISASRHNPSAKS HETDSPSTERTF SFVWMISRKPCQK QSSRSSCRTPALVENHEPQLHHTLT PEQSFYGSQKTTSIQ\QNVYSVCFA \SNINSRGRLRVSSLYEF\FIMFFLK YISCILIN
2249	7746	A	2448	20	349	SFCLEFPCRPGELLALQDSAQNSTF DKTALPLPCLAPCPPPLGPQS\THIQP CFPHTGPCAPFFTTDLLQGQRLSLSL HTPLHPVPAHWALPARRALARLTD RPNARLTP
2250	7747	A	2449	3	384	PFLSVVSSQVAGHGRIFQCTYLMND CQTKQPCWSGATWPHPWMQVKGT PALRAHPQTLSESRLPEGTRGSRPE DCPKPQPADPPSLGT\QCPPWQLSP TQQKMSPTFAAAKGASQGLMWAH AVLSRA
2251	7748	A	2450	1	1503	
2252	7749	A	2451	1	855	NPRRRLRGRCRASASSPRRVRRRGQ RPRHPAPRRPQAARPSAAPRRRFL SQRPAAAAAAQRAALMQAIKCAG GWKAEAVGKTCLLISY\TNA\FPGE YIPTVFDN\YSA\NVMVDGK\PV\NL GLWDT\SGQKDYDRVTPPYPPYA/Q ADVFL\FCFPVSPAS\FENVRAK WY PE\VR\HHCNP\TP\ILVGT\KLDLRD DKD/TRIEKLKEKLT\PI\TPQGLA\ MAKEIGAVKYL\ECSALTQRGLKTV FDEAIRA\VLCPPPVKERGRENCLPV VNVSAPSFLGPVPLEPL
2253	7750	A	2452	41	556	APSPRRPWGHFTEEDQGLLSTSLWG KV\NVEKCWKEKTPGKGSLVVYP\ WT\QRFFD\SFGNLSSAFAHHGQTP KVKAHGK\KVLTFLGRCQQSTLDD LKGHLLPKPEVNCTVDKPAMWDPE NFKAPGEMLLVTRFGQSHFRQKNS PPEGCRASWAERWVT\GVASALVP SRYH
2254	7751	A	2453	2	454	RSFFFFCEVGSWVGS MRVVMARL LSEGEQCIPTACAAFAQQPGGRPRR GLAGVGEGGPQCSWVN YRCTLEFL VSLLGTDLARGRGNSATGP\TAPAD SKQLSCKTFIAVLSLSKEAGFCNVV QGWVSTSWGSSSPVPQFFPKLLEF TGK
2255	7752	A	2454	94	218	
2256	7753	A	2455	266	547	
2257	7754	A	2456	2	494	RGPVMAESWSGQ/SFLQALPATVLG ALGSEFLREWEAQDMRVTLFKLLL LWLVL SLLGIQLAWGFYGNVTGL YHRPGLGGQNGSTPDGSTHFP S\WE MAA\NEPLKNPTENKGRQQRVSKGI

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						HWVCWLLHWVLLLPRPQGQPAGG SGLVAGSTQLPTGLGLILPS
2258	7755	C	2457	12	356	MGDSFMDEVAPRLASVDSRFFSFSQ GAHIKFXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX X*
2259	7756	A	2458	764	1135	LLQTTSRNFKNLNQCTKSPICKKK GSVFFFFFFFETESCPVAQAGVQWR DLRSLQAPPPG\SRHSPTSASRVART TGAHHYTRLIFVCLVETGFHHVSQ DGLDLQDQFLESFLFCLLVRLRT
2260	7757	A	2459	1414	1761	SAINFFFLFETESRSV\AQAGVQWH DLRSLQAPPPG\SRHSPAPASRVAGT TGTRHHARLIFFFFFFFFFLVETGF HRVSEDDLDFLTSGDLPTLTSQSAGI PGMSHCAWRIDGI
2261	7758	A	2460	63	542	TALPNQLHGGRHLCPSHAFGSQGA ARPKRPQPGPG\AASEPWVQLQSHH PLPPPTQSPPEGGEFLREQRPKPLSF KPLLHPRGPLCPAAPKLPPWPCPLR VPQFPHPPLPPSGRKRDRERGMEEGE GGWAAGERRGGKEETLGRGPFTQR ERPRNQEGGG
2262	7759	A	2461	2341	2443	GRVWWLTPVIPALWEAEVGRSLT ARSLRPAWPTL
2263	7760	A	2462	28	403	NTTTCVKGLQTQSYKTSPDGNTTK QTNKVKHTHTII*II*NAPPAVSTTAIR NKFSKNGEQRFIEPYTNRPNHSIKL *RTIQYASSKNLEIKDFSWKKLQ* FLENRNKHECFQLFPKVNVGAS
2264	7761	A	2463	727	1156	ETTLSEARRGRSAAASCRGSALRRG RFPESSRRGREAAPVCPRHVLL*GAQ SKQAAVAGKRSRGRHASRWPKSLF TPRRRRISLKRALHFWQQSADPSPS VSRAPGSTWVGPKAPTEVTSVAPSR MMWQNEKKKVGGGERQDWRK
2265	7762	A	2464	10	302	MERFEAGLSHISPWLC*CCSHCGD CCLLGSRSWGLVGGGSCGALGPWG RCVCAGGEFPDRASLPVDPALAKLE CSHKFPTPKDFHPRDRSPSRFLL
2266	7763	A	2465	303	531	VLRIKVSSENSLFLSDITYLASIPN KTQTHCPEPAQKPSCKAQ*FWPKC KPHPPCCHWALPPGCCWACHRW E
2267	7764	A	2466	6	100	
2268	7765	A	2467	2998	3570	QDRKQGSSAPATPSRA*AAAAARAP RRPAGRWRG*DAPQSPAEPAPRSPP WRRAAD
2269	7766	C	2468	125	404	MMARPPPWLESHCTRVVRADGQV RXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX ADAW*
2270	7767	A	2469	1348	1807	CPTVDPLLQKNCNDGSATALARVP LHACREGRWASPSGFFCCCCCFLR

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						WSLALLPRLKCKGPSTHCNLRPLG SKDSPVSAS*VAGITGARHHAQLIFF VFLVETGFHQVGQAGLELLTSGDPP ASASQSAGITGVSHRARPVSWFNSQ SMNP
2271	7768	A	2470	538	676	VKRNPEAGAVAHTCNPSTLGGRRG WIS*AHEFDTSMGNMT*PHLYK
2272	7769	A	2471	40	336	EYLYRHFKNKLFLYANILCSSGIWR HYVLILRTVSELLD***GCRWGLSRS FDYLSNTGWV*VLLDISSFAFVTGP LIHGTGGLSAFDLHCEALSFYRD
2273	7770	A	2472	2063	2406	SQKKKIOWYLRMFRQFDIYVCFLEF SVVLLMIGLLSHRLIPVKQYIKLHL ALLRTGAGAHACNSSTSGGQGG*II RGQEFETSLGSSNPSASASQSAGTT GVSHHAQPIFFF
2274	7771	A	2473	22	273	LTQKMDHNQVKFKSTTFYSILGKSV LSLSRPEYISGKSDTYSENIYPLSIKS EIEPIETRCLNRSNASLVQK*YGHKT GLWWLP
2275	7772	A	2475	1269	1511	INFFFF*IIDRFSLCHPGWTAVAQSR LTATLLPSRFRFLCLSLPSSWEYRP LPPYPANFCSKLLICLSTFYKDCG NSA
2276	7773	A	2476	1411	1827	LHTCCLRRRPSGRGRSQGGHCSQSG SSPPRRPRSPAPEGPGFHAP*LCIPDL GHGSRKRGCVPPCGPRTGWADLV ASAQAACGCQGGPPPSGSCSL*GRG PVGGSGHGSPCWPQLVELCGRCWSW PGVAGSTWQWRRHPH
2277	7774	A	2477	1345	1642	WQFTGAVIHLAYVVLVCLVAFS SVSLGLNFFHKNFSDFQRERCWLF SPFKGCC*RCFFTQSLYYCQVCEFT KTLIILLIQDVPEIFWSLFCFFHGP
2278	7775	A	2478	113	584	WQDYIYKEVRVTASEKNEYKGVV LTDPVSPANIVLVNFLEDGMSVVG IMGHAVQTVETMNEGDHRVREKL MHLFTSGDCKAYSPEDSVREKEQP* INGFRRTHIPITEQGDAPRTLCVAGV LTIDPPYGPENCSSSNEILSRVQDLI EGHLTASQ
2279	7776	A	2479	658	785	KTHGWVQWLTVPVIAL*KAETGGW LEPRSSRPATQRDLS
2280	7777	A	2480	2	598	PLGKGKFTGQSAQLTTGTGRGLILA KGSATLQKHRINHTLTHKNPFLEE FWESPSSLNLALIKGLNGFCLGTEK LFEQMTYGGKKVKCPIGYFALQS WEFHPPPPTLFLSLPLAILWPGGENR GPRVSTKTGIKTRWPAPFLGPLSNR LGNPQPNPAPAAVPSLGLSPW*RG RGLPWGWAKPRCALWTPVSLPST
2281	7778	A	2481	253	286	NDDDP*LPCLGQPPRSSCQPSLP*S LLWSKMTTTPAQRS
2282	7779	A	2482	407	587	QAGRGRARGVSEEARNKPVPPPTET PQPTLSPQ*MGPAQDPAPQQDYRG KKSLNAWCGRS
2283	7780	A	2486	246	519	FQFGIHNTNYQRQGAkvffknkgv

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						WGGPRSLPYSC*EGLPLGESYQFEP QSLRDA*DIP*GSVGKNPVGSHWW VSGVIGGFIITGDYSQH
2284	7781	A	2487	470	977	TPPPAGLRQRGYPGPNRLEARNW ARAKGGKTSAGRVFTQP*FPEQQLP PGRPWWPRPGCPHLPTRACKWSG GVLAPESPEPPSLPEGSHSWLGDG LLASRKLRAGGSVATFTSPQLCPLG PHEDREAREGEGRLAPAQPVSSPSA PAGHSLSHPSRTGKLALVPGH
2285	7782	A	2488	393	618	IREWVNIFWNIHTEEYTVIKKN*V CQTWWLTTVIPELWEADVGGSLP RSSKLR*AMILPLYTSLDHKARLSL
2286	7783	A	2489	308	626	IRGTSNMNRKNVEKAYYAEA*LSL
2287	7784	A	2490	1222	1374	AQQVKRLEGQRGWKLRGGRGRWL TPVIPAL*EAEAGGSLEARSSRPAA AKK
2288	7785	B	2491	60	378	NAVLEADFAKRGYKLPKVRKTGTT IAGVVYKDGIVLGADTRATEGMVV ADKNCSKIHFI SPNIYCCGAGTAAD TDMTTQLISSLAAMAVFEDKFRPD MEEEEAKNLX*
2289	7786	A	2492	1	437	DPRATEGMVVADKTCQKSTGRLEPE LVTAIRMLKQMLFRYQGYIGAALV LGGVDVTGP/HLYSIYPHGSTDIAAG IFNDLGSGSNIDLCVISKNKLDLFRP YTVPNKKGTRLGRYRCEKGTTAVL TEKITPLEIEVLEETVQTMDS
2290	7787	A	2493	2288	2668	FGRGHYCRRSVSQEEEEAKNLVSEAI AAGIFNDLGSGSNIDLCVISKNKLDF LRPYTVPNKKGTR*VKETKFFLGPL ASWPPLVSPWHLDGVLVLSTLSTS SVPKSTSHDLRLVTCFMTVGCCQ V
2291	7788	A	2494	3	861	FLGKMAAVSVYAPPVGGFSFDNCR RNAVLEADFAKRGYKL\PRPRKTGT TIAGVVYKDGIVLGADTRATEGMV VADKNCSKIHFI SPNIYCCGAGTAA DTAMT\TQLISS\NLKLHSLASTGR\LP RV\VTANRMLKQMLFRYQGYIGAA LVLGGVDVTGPHLYSIYPHGSTDK VPYVTHGFLAPLA\AMAVFEDKFR PD\MEEEEAKNLVSEDSPPQFPSPS WRIFNGPGLPEANIDLCVISK\NKL FSPNTQLPNKKGTRLGWRYRCEK GTTAVLTEKIPLLWST
2292	7789	A	2495	466	607	KKKERSCLWCPS*SLKNYGLSCR KKKKGAVKKIILVQAWWLMPVITV LWEAEVGGLEARGLRPTRATW
2293	7790	A	2496	449	694	ILRILGTPISFPVNKISFLPFKCLFPDS YIENLMNIYQPIKKNEIHVPLQ*PW MHLETIILSELIQEQTKKKHKFSLR GS
2294	7791	A	2497	52	298	YNIEEQQNKRTQSNRHRPTPPPEPP NPEW/TPKPTPTK/PSSPQEG/P TGGPAPHAGAAPPF\SPANPTLFPS LTGGKV

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2295	7792	A	2498	112	485	YNIEEQQEQTYSKTE*SAQTHPSPGT AESRMEPKPTPPTKRLPPTGGGGRG GTWGDPPGPPCWGGHPPVFPSPCPTP TLFPIFDPLGGQSLAQLGWSMVET LQRATTLSTFLKMGRKKETVAPPQI
2296	7793	A	2499	32	392	RPTFGIWFYQVFPPELLLELKAKYIG KHCFSIHSPLDTPGLPGCP/SPPGRA ALGIHPGNLPAPEQKPCWDP/SPSSTL VWRMLNSASTSPSPAPSYISPPFPGQ SYFPAHPPTSSLSLGGIY
2297	7794	A	2500	914	1417	PQCLLPNRGGSVQVRLWGATASLS GWGFLASFHPIHPFGKFSSLPDTPW GLCLGCPFPQAERPWA*YPGTLPAP ELETLLGSLPSSTLVWRMLNSASTS PSPAPSYISPPFPGQSYFPAHPPTSSL SLGGIYHQLLPL*PLPSTDPCCAPLL TSPPLTFLKSPRP
2298	7795	A	2501	1120	1159	ERAVCGC*CIIVM
2299	7796	A	2502	1145	1367	IFFSFLHIYIHNTHMYIYYTLCVC VCCVYGMVCVCACVYSFSSKPKQVC VWIEGNLNY*LQVVCLWYLDFFHS
2300	7797	A	2503	155	454	GGFSVWHTETPPRMRLMHQVQFNL EYLTTPSTQKGGPTPLCIYGVVFFK SDYLYSLSLFFFRFLYFSSLL*YLML VNFLFRMLFSLFMSFCYLFIIIL
2301	7798	A	2504	901	969	RWPGMVAHACNPSTLGG*VGDPA
2302	7799	A	2505	903	1339	DKTVQSIRSMGGWKMDASDSKFV DLWIAEGIGTSWRNPGYQAPRPFLH HGCWGDGLGKSPPLPKPVSHITDVG WLRMMVSTGLSHLW*VPSQGQSSQ GPHPPAPGVQPPQTPPPASLKGKSL HLQGACSEGGAPFSIELFAGRS
2303	7800	A	2506	433	548	PSEYTLGFKNPKIKLTFNGGNSMSG VHF*TGFIITFL
2304	7801	A	2507	637	906	RIKKLSDGSYFLPGVSQIA*GSNYF* SKLGPDPGGASRLQSHHLGRPKVGV FHHVGQDGLDLLTLVIHPPSAFPEV LGFTGREPPRPSLHL
2305	7802	A	2508	211	575	RENHDLESQCKRGAPVPAGVPSSAL PQGPVSLLPAGALCPFERSQQASP QVSPQGVDPKICSLQTTSLCSFCDR CTGMGSL/C/SSCPPCSSS/CHGRSHS SPC/CL*STRSSVVGDEVCNTL
2306	7803	A	2509	274	488	SGDKTMQLRGPCGGWGSCPAGLGT CTAGSP*LCHHKGHCSIHSTSCFLA TVSPCAIFNSTSKAGRGAQP
2307	7804	A	2510	83	442	NFTMVMYTDHILRNAHLMYTSGR RLSVPKIACHITDHSHTHCYMPYL RD*Y*TMFSQGFHYAPYLHLHT*EH PFECCLAGRTFTDALFEPTYPTLTL LTPSHWQDGPPLTGSQMPG
2308	7805	A	2511	2	270	ARLGLPKCFVCFVFKTASRSVSQA GVQRCDHNSLQP*PPGLKRSSLASR VAWTTGSHHHAQLIWLICFKQYFV SSGFYLLLVALWWGG
2309	7806	A	2512	234	409	KGFYAHEKNARTWWLTPIIPTLSEA *GGKMA*ARSLRPAWATIRDPIAK

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						SKKKKKKS
2310	7807	A	2513	78	460	NVCRKMPPSDRLAGAYILQCNPVE VVGPEREDAPQNRVQVRHGCVAW PLLAPPPRHLQGEGLTSARKRVLR LGVTSGL*RTDSHNPPGPPQREQTE PRARPPALEHRAQQ*PGPGLGGHRG AGCHQ
2311	7808	A	2514	67	279	SHRVSRDAAACGAAPAAARLAGGQR NGRAISGRPGLSS*GAGGGNVFKVC LLLNKNRTGGGRGHGYLYSLQR
2312	7809	A	2515	683	933	YTSELIGKIISGQEVVVGAWCEDLG *GPRKSRGREGKG*G*EGSGNAGRI VGFKQGRRGEDAHSWSQRGRQEFV FYLKSTRNW
2313	7810	A	2516	2	208	SKIALLVHLK*ENRHQLFFELIPTVF FLFIFETGSHSVTLQECSGVIMVHCT LTSWAQASSPLSLPTA
2314	7811	A	2517	426	601	PSFRIFTQYSSFLKNSLRLGAVAH VCNLSTMGG*GGRTA*AQEFETSLV NVVRPPSL
2315	7812	A	2518	55	489	HSALIQASVWFRYKYPCGYLGASLP TN*GKKGSQVGSSAHFATTFTIPNG DNA*GAKSGSGCPGGECHPG*GPIS SCPLSEGQTCALNPLSCGSPGPDWLI LGKLGPLGCSKPKGSHFAFPLVVPF HPCSKTKLFPREELFVVR
2316	7813	A	2519	52	286	MMPCLRQQRQREREREREREH MRTQRKQLK*WITRFKNSSKRQR TEKNSKKPPVPHRGAGHSNGKLC FRPAAS
2317	7814	A	2520	3	296	TNTRYTIGDPALQDMNSRAHSH TYGHTLLWEGICDLTRPPKLGSCRE KECPRPHSLDR*SSGFWDPAARGE LMQWEMPQPCSPQPLPKPCRSSI
2318	7815	B	2521	83	241	SEWQKKLTPEQFYVTREKGTEPPFS GIYLNKEAGMYHCVCCDSPLFSV KLI*
2319	7816	A	2522	19	629	YFVLISPLLTFTSTHGFDLCYLICNTV HKTPCVFRSLWDIQKEVFSIKGSRSP SPSKGNGFDSEGPVRTIPGGLTVE*L GMGSGRGEWDRILLPGTTHRGTSW HVNDVSISSCSIVYVFHSSEKKYCSG TGWPSFSEAHGTSGSDESHTGILRR LDTSLGSARTEVVCKQCEAHLGHV FHDGPGPNGQRFCSVALKFKPRK H
2320	7817	A	2523	1	707	MGAGAETGRGQRAAAPERRHGRL LWLLRGLTLGTAPRAVRGQAGGG GPGTGPGLGEAGSLATCELPLAK\SE WQKKLTPEQFYVTREKGTEPPFSG IYLNKEAGMYHCVCCDSPLFSSE KK\YCSG\TGWPSFSEAHGTSGSDE\ SHTG\ILRRLDTS\LGSA\RTTEVVCKA \QCESSILGHVFP\DGPGPNGQRF\CI NQCWLWKFKPKGNHWTIFQESAFP CHPFHVAPSIHNSLE
2321	7818	A	2524	303	743	TGAQWGRGLGHVCWSMGFVSWE



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						CSGNGLSQAGLVKLLIHLHSTVQK GLTPRWGGMNTQLPGGVGGP*FP KMPGATL*PFEGKSPAPQLFPCQPW AGAAHGGAGGPSSGSVPGPPQCPV KALPVL RAGWATQPPGSFLWPTPS D
2322	7819	A	2525	102	421	VQYGSNWNKPYWNRVGP*SHTTG ELKKRWPHPRSCCPHGAAGQGAER CGRERGPEDTSDLLNK*QW*RRFPS GPAECGAAVAGL*GAAGCRGRSRP LKSRDAGLKS
2323	7820	A	2526	225	448	TQEGRGIDFGPWWPQLLPSSPSPG L*SPATPPQAWVPLPSSSSSPALILS GPNRKPEPPPGIPPQFYLTSL
2324	7821	A	2527	43	390	GDVPTVTGECPPSYRAMSPSYR*MS PQL*GKSPQL*GDVHQL*GNVPPVT GLCPITGQCPLIVSPSYTVLSPHYK VVSPVTR*CPPVTG*CPPIAGQCPPL *CPQAISWSPPVTG
2325	7822	A	2528	525	635	HIQQLWWPMPVISALWEA*EGGL LDPRSLRPAWAT
2326	7823	A	2529	66	432	TRGSWHKHALAPT VHRAGLWGGK AGTQASPGAADNVPPPY*TSGFCG WKAGTDFPTSKKPCPFLPHNPPLP PCKWQKGLSLFVISHSLICKVGMQL PRGSQVRLLLTKIQIHRLSLGRAE
2327	7824	A	2530	5	95	
2328	7825	A	2531	1	123	
2329	7826	A	2532	118	363	
2330	7827	A	2533	23	250	YLIVVWICISIGLYTY*LIIRALYILR KLTLFKYIPISH*SLSFIVFCSLVYIY MYIYIYVYIYIYIYIYIY
2331	7828	A	2534	346	611	TSVEAQDATDRLWPDSCCPAHGAC TRTVWPKKPPYFPVKKMECSVAQ AGVQ*CVLSSLQPPSPRFK*SPASAS GVAGITDFQKLFCQ
2332	7829	A	2535	267	682	HFSSLRMQARPPSFRPYLVLHPKNC WIFILINDSWMVLFFEASLPTVPSLV QTTIFLLGILQQPLTDLPSSTSTPF*S LHLSAV*VVFRKFLSWPGMVAHTC NLNTWGG*GGRTA*AQEFDTSLGNI VRPCLQKKSR
2333	7830	A	2536	45	280	
2334	7831	A	2537	1560	1885	QLGVLLAGPFTSSPYGGVSPGLKRP WPAPRSYPLPAL*PLPAPYGVQMSG LPNPKLGKNPLGPSSQKPPCGGPV KTSIVAHNYSALSLSLLPQPGSA PQALSL
2335	7832	A	2538	60	341	VTLHSLVILFSAHICRIKLNITNLQM YSVVHPNFHLDVTIPKIVVALCFRK KYAFFCFMQQKYM*SEIHYIFILS VVLNVNEINSIIQMY
2336	7833	A	2539	442	686	TSYNNLLNNLKNITFRKELSSLSHL CNRGQGILKSLIAWLGAHAHAGNP STLGGRRRIA*AQEFKTS LGNLRP VSPKK
2337	7834	A	2540	459	603	GFLLEIDKAEGGAHACNPSAFGGQ

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						DGRTT*GQEFKTSLSNVTRPHLY
2338	7835	A	2541	1	188	PEQVLWQTKVTYSGKKKKKATKRP GAVAHTCSPSTLGG*GGWIT*GQEF KTS LANMVKPCLY
2339	7836	A	2542	582	825	GLSNMVHLWIEHHPAARSRDCHSG RLRREACLG YRKIS*HWPGMVAHA CNPGLGG*GRRIT*GQEFKTS LAN MVKLCLY
2340	7837	A	2543	775	1019	DRSSPKKPPDDLPEFTEPQWFTLKH KQCFSDISRLRVGPGMVAHA YGVA YLSTLGG*GRRIT*GQEFETSLANM VKLCLY
2341	7838	A	2544	303	429	AACVLPSPPSAHSSTHTTGSTHLG* GPPCSGPAPTWGSWKT
2342	7839	A	2545	853	867	NP*NLACFCVLLFPPSF*RGFRRLG AVANICNPNTLGGQDGWITSGREFE TSLGNMVKPCIY
2343	7840	A	2546	357	560	KGSLVGLSLEERIFVVA VQPSLFHK KCLWQGTVAHTSNPSTLGGQGRSV A*PQEFKTS LGNIVRACL
2344	7841	C	2547	486	728	MWVGWVEVFGVVLGWGPVVML QSDGSWKLVPVHLHELLPFHMSWYP PQDDPNIWSLKQLGLPGCPPLSLC DVSYMVSSA*
2345	7842	C	2548	240	332	MACFSFSAQLKDRLLRSPATHTPL LNAPL*
2346	7843	A	2549	2	603	SLPYLPQHPLEFGPLNLHRDQ RAG AQTLTQPM SLCCSKSLQLPNALT DK RPCWVLFPA GLSSLLRNDS AKLPFR NKS GFPAQGLCPGGSRLTTWHLSF HGLFLLHQ RSAQRSTS QIPSNHTLT *CPTVTTETV PCLK*PRLSVVSVCFC SGSP*RALQCTPPGKSPFLS QLSLT DPLPSTNLLFHPVGTPRAPGWA
2347	7844	A	2550	132	419	
2348	7845	A	2551	1083	1563	PENQSSLYFLPANLLKMPFCFFVFF* DGVSLCCPGSAVAQLQPPAS*VQSD SPAFSLTSRWDCRRVPPRANFCIFS SDRGFSMLVRLVSNSRPQVIHLSQP PKVLGLQVETGPQKREWVPRELT SGQWKQGEPDQGEDSGTEGRWLPL LPSAGHSGED
2349	7846	C	2552	173	501	MPSPSAPSIVPVLHGCWVHICQADV YHTLLKGFLFLRQSPTLSRLECS GTILTHSNLRLQGSSDPAALASQEA GLKLLVSSDPPTSASXXXSAXLXCQ TGVSSXXRP*
2350	7847	A	2553	174	364	YDAEFPRCSFGLIYPRLSVKEASRLS AVAHTCNPSTLGGQGRWIT*GQEFE ISLANMVKLHLY
2351	7848	A	2554	61	283	GGRIA*TQHSILDNRVRLHLKKKKK KKQYLKKVHLP GAVAH/TYNPSTL GGQGGWIT*GQEFETSLANMAKLC LY
2352	7849	A	2555	1140	1313	HVENSEGASGERKLTQRLGVVAL ACNPSTLGGQGRIT*GQEFETSLA NMAKPHLY

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2353	7850	A	2556	99	296	WVLIVHVISSKCLVLEICVYRLGAV AHACNPSTLGGQGRWIT*GQEFETS LTNMVKSSLYLKYN
2354	7851	A	2557	175	332	RNPIFSLRKWPLRPGGVAHACNPST LGGQGWIT*GQEFETSLANTVKP RLY
2355	7852	A	2558	667	772	ARCTNPSTLGGQGRWIT*GQEFENS LANMAKNRLY
2356	7853	A	2559	7155	7302	IMKLKMYIWPAGVAPACNPSTLGG RGGWIT*GQEFETSLANMVKLRLY
2357	7854	A	2560	227	410	FQVDPDTWLFIEVTLFIFMAIFYLW QVLLVFHFTAVR*CSLFQGSYGIFGI EGRIPYSEL
2358	7855	A	2561	275	685	LKPLFTPSPGPAVPRGLCWKEAPT PGSLLGEEETELNVY*GPPGSLRPA SHWAPPEGLRPTSPLFAATSTIGPL PVLVTLGPHLSPLFGQFINKGRDDT VLLPPQSPGCRESLACQGEETSRLCF VSHTSPSSL
2359	7856	A	2562	20	354	PLYSQSFPIIYPFITLLPE*SF*NNNYC SFVNIPSLTPSHQLYKVHSPHPHPVF HTWAHPAPALCSSWVAMLTVYQG AVLYQCLSTAVSVQGPLRLLGFSNR DTLPSKGLS
2360	7857	A	2563	374	585	GNLINC*LHTHTHTHTHTHTHTHTH NLTNYPDFLYLLVTFPGDIVIQESAF IFFTKSPKHCGLGAIRNA
2361	7858	A	2565	918	1096	HCHSNSEFDTETLGMVAHTCNPSTS GDCGKQII*TQEFGTSLGNMVKPHL YQKKKKKSR
2362	7859	A	2566	101	327	LVKNQQTQKLAKHGWACL*SQLL ERLREENHLNAGGGGCSELR*RPCT PAWATETVDSLPMCLVLQPFLSL R
2363	7860	A	2567	347	478	RDHCRLGTVAHAYNPSILGGQGRRI A*DQQLETSIGNTVRPCLY
2364	7861	A	2568	622	761	KSVEVFYLSIGQEELPHIQIFFHAT IFIIGRAQWLTPGIPAFWETEAQEFK CIHICMQVWWHTSV*SVRNKSLYE ELLQARDPGKFVILHYHYWLFHGK A
2365	7862	A	2569	70	316	ISHPSPSTRWEAVTWALG*LFPCPC HLQGGRAQLPLPYPLPIVVAPPLI SRLNPDGDLAKTILDVTLYISSTTV GGSWG
2366	7863	A	2571	145	331	IFHSKMPISEWKLV*TLWQFFKELKI ELPFDPAIPLGI*PKFQRLKNTNGIC HYFYM
2367	7864	A	2572	918	1135	GFISASLCNWILTHLKFFKEMGSR VAQAGVQWLLTGAVMAHCNLKLL GSSNPLASAH*VAGAICMYDHWHA
2368	7865	A	2573	590	936	QLAACGGSCLSQHFERPR*EDCLN PGVQDQPEQNRETPISKILKSWA WWHIPVVPGTWRADVGGLPEPSRP KATVSCDCATALQPGRRRARLCLK NKYIKYSVQKCVIFFLF
2369	7866	C	2574	34	670	MXVFLSSAGNMPVTCWCWEAPRC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NQKCTDPAARRPDPQTCASQDRLR CAPCTCHQPLXSRYTQHPGLVPLPH HDRQSVPPQGPRVVQTDAAAXMVE VSVXVVLEGWGXPTTRRMKLSLLG IKMLRRGGTVRGAPGAGSALRCGW RWRPPAWRPQMSTSRVGVQARS TSSSPXPXXSGXLWVHVLLXLAQL DSQQGFDLLLAGRRXSGSNLI*
2370	7867	B	2575	70	165	EQIEALLESLRQAQQNMDPKAAEE QEEKEE*
2371	7868	A	2576	1	390	FFFFFFGVLPVFLDFHVCFLVFCWK HAGYMLVLGSAAVQPEMHRPSRPP PRPI*RRQTQK*LWFEPDVSWLQGR WVENQHFINRVLTCLERV*NRIYYG TSSSSPLRSGSEGVGPAGFSRPLYPC LGPPN
2372	7869	A	2577	435	861	RASLITVCVPGHLQAADQKNLHPLR AHVVGPCLAGSSCARRPSRA/RGPP RPTPEHGSRLPQPS/CAAASV*TTR GP*GTLCLS*WGKGTSPGCC\GIERP KAGGKCTGHSGVCPVTRKSNHSLC ARSPTSCRPKFAPAAGPRGGALPG RVILCSKAISGTGPPRPTPEHGSRLP QPSWLRRLSEPRGGLEGRFVCRDG ARAQVLDVVCIERPKAGGKCTGHS GVCVTRKSEGLGGGRLGLCISGCT AALPSTNM
2373	7870	A	2578	38	398	PVLFLDFHVWLFVFCWKHAGYML VLGSAAVQPEMHRPSRPPNYIAK MCKLSILSLSFLKEGAGDKNSSEPN LG*VP*FSLHPCLSNQMTLGNAKQA ESMSLCGFFLPDCFFLTYSKRIYL
2374	7871	C	2579	42	443	MKPAHSAVCPGHLASCETKEFAPR CGPTWLGPCPGRVILCSEAXSGTGP PRPTPEHGSRLPQPSWXRRLSEPR GGLEGRFVCRDGARAQVLDVVCIE RPKAGGKCTGHSGVCPVTRKSEGL PAEDKKTNMKV*
2375	7872	A	2580	871	1253	PRLPPGLPGADRSPAGSQACA\GPA EHGPQGRGGGGRGGGGGPGPLPH PTCGTWTSEGA\SRRAPPPAAKGG AGPRCSPDSPSSPEHFDQKGLHS PCCWLFPLFPSPISDLSKRRLPK NCL
2376	7873	A	2581	222	754	YPP*HVAPHPAPLPWQVQGGPPDW PRYLWKVPPASLWPRGTEKSPCWA WLVGAGLGLPPPFSLPNLSDLGTSL FPLPQTLPLCPAQGDLLKPKLGPK KGGSVLSTSPSSFPRGLVGGEAPPN LSPSHTHLGSNVCWTKKQEHLLV PTFSQSSQNPPLPSPSPIGAVKALFAS TMG
2377	7874	A	2582	2	431	PEGAAPAAMAVTALAARTWLGWV GVRTMQA\RGFGSDQS\ENVDRGA G\SIREA\GGAFGKREQAEEERYFR/ ALQVML*DLFGVKD*N*TLSHRVL VEAQSREQLAALKKHHEEEI\VHHK \KEIERLQKRNLNRHK\QKDSKLLKH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2378	7875	A	2583	1	232	RETACCGRDARGAAPAAVMTAL AARTWLGWVGVRTMQARGFGSDQ SENVDRGAGSIREAGGAFGKREQA EEERYFR*GSDQSENVDRGAGSIRE AGGAFGKREQAEEERYFR
2379	7876	A	2584	3	399	LARNERLLAGGRDARGAAPASQWP VTAVGRRGTWLGVRV/WGVRTMQA RGFGSDQSENFPTGPRAPHP/RKAG GALGKREQAEEERYFRAQSREQLA ALKKHHEEEIVHHKKENERLAEEKK FERHKQKIKMLKH
2380	7877	A	2585	3	316	LLQILGTEPQKAVIVLVENFY*YVS KYSLVKNKMSKSSFREMLQKELNH MLSDTGNRKAADKLIQNLDANHDG RISFDEYWTLIGGITGPIAKLIHEQEQ QSSS
2381	7878	A	2586	3	469	
2382	7879	A	2587	434	815	TQVDWTQRARPGPWRHPHPFPDD DSLCTGCTSHLPPHGD*L*NPPSSNGA NPRLSPAPHPHPREAQTPPGAGHR TPLSRACLGLAFPAQPVRLRRDTKR DGRKEQRETVPTTFFPDARGTRLIL RHK
2383	7880	C	2588	204	354	MWLQMTRAVLSSNLDPPYVCRRA RGRSSPSGSLXXKGEESWGPRHCY SP*
2384	7881	A	2589	390	681	RERGRRAGRRRETAVRSREKERER EGLDRSSRKR*PELVKGSRSAH*PQ SGRWSHRPRPAIVPTSFOPCDVRAG QPNGPSDLPDHLPTRRRKACDRR
2385	7882	A	2590	598	769	YPQCPTPCQAARVWWDShLAIPAL LGGRGRWII*GQEFETSLANMAKPH FYQKKKKK
2386	7883	A	2591	359	775	KKTQPLHQGYPKINFRSPSPPIPVV PLLALPK*GHSPFVSPPLQKIPPKG SPHDPTRQPSIAEGRAGTQLSSPL WMAGTLTEALHHKNRQYPLGSHN QLNLGSTGRTFSKRGKDGIPFDAQG LQGHLLKGTFFFF
2387	7884	A	2592	585	780	TFSLPRLDFFFLKARKPRIKNTKNRP GVVAHACNPSTLRGQGRIT*VQEF ETSLANMVKHHL
2388	7885	A	2593	436	1645	GMSALVQSRVSHLHRVSLLTRLT RAQETSSPPNTVTTPNQTLSTAQNK RTIPGPAME*VTLTRLSKEPLLVEK AAPTPHPQ*GPAPRPLQASALPLYPE QHRRAPSSSEDPWRPLTPPSH*GVS TWTP
2389	7886	A	2594	1	373	TCSCPWLAPLTQKNCPPHCHILSL LRKTKQNDAPKKSPPRGLPAVSGM KQDTVTLGRMEKPPRSIPQRPQWD GEATRSIPRRPRVPPVEPNPGHWQ NSPPG/EDQSILSTSNPRGPTPFKSGS
2390	7887	A	2595	502	798	SPKVQRHSSQAALRQAGGALSLWG CLPSQRRPRTVSSREGPHPGKGV* GGVQRSGKPHPLPTCPQGLTCLTPT DPGSAWNPTPT*NEKGNSEIIRH

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2391	7888	A	2596	1	136	HPCVHEPMSFEWPWQYRFPFFFT*G SDPKKHGWASLSPGPWAQP
2392	7889	A	2597	429	1003	VAYVIGFKSNMPAKHMIKNTSVRV FICPPSMEGKHG*SQPR*NNSPLSPQ NNLSPTLCPLFLPQLKQESMC*SFFN FYQPALAFSLYSIIPSDVLPSSPFE TRVSWEQFAYLLESAYLLVQAIE *ASSFFLLKHSTSLWIPLHCLFYITFD ICWSLYMNIIFFRGSHCSLQYDPGFL TLSNAPSITI
2393	7890	A	2598	367	463	SGHGAHAYNPNTLGGRGRRIA*SQE FNTRLN
2394	7891	A	2599	436	833	CLTSALLGCVYVYFFSPHPALFFLR RTSAYNLLKQLFFRYWNSAKSDLS GHSKTLMLCPKSGGGKACAVEPSC SLDTYLCPEIICQALFFICLFVHLLL FYCYWRGHEL*YSYCP*FNVKLIM MNSIACY
2395	7892	A	2600	53	95	DSILLTQAGMQWCELGSLQP*TRP PIVCFCLFIYLLRQHLAPHPSWNAV V
2396	7893	A	2601	432	825	NFKDTAKGFLHFDHQKILDPCLP SRARFGTYPECPHVPSTEAQETGL SVPSFGFHFHFLTYFLLLEYFYFH*G TLYLHLDLHQK*HCQAMRNFLYKS RIQRHHIYHSLDAYANLGHDAKDPF FSLDF
2397	7894	A	2602	83	111	
2398	7895	A	2603	1	71	
2399	7896	A	2604	215	758	LPLQYHRKNIHANTVALADARAPR TASRNRLGVRASGLASSSPRLGLQ GSISSASRGRPAQHVPGRPATLSPP AGAGPSR*ERSRAGARGRWLLDH AGERPAVRELSRPDPQVSFGPRNIS EIGQVLSPETSSCELPGIGDLLWQL EVYDARKHSLVGPESLSHRELGSPA GRRP
2400	7897	A	2605	211	323	LDSLIQHSASTLAQHSASKPWKPD FHTQFFHTVWKLQWCRAVVPATQ EGDAGGSLEPRSLRL*CVAGTTALH HCDSFHTVWKNVCVWKLSGFHGFE AECCASVEAEC
2401	7898	A	2606	75	232	TQPGHKGETPFFPKTPKISPERWWG PIPASWGVKAGKLF*PRGERFPLIW F
2402	7899	A	2607	325	566	FNDKYFYYPGRQIQCHITLFLNLKI TSDDFFCFKKTG*VAHTCNPSTLGD *GGGIA*AQEFKTS LGT**DPIYKN
2403	7900	A	2608	1114	1367	AIARTLIIMINLTVNFSAINENCTTT *RYFDLL*YTTGMFRKIVRKLKVTH LKWNN*SKYTFKCIKFNFLSEPF NHVCKVF
2404	7901	A	2609	100	450	FLEENYKVKFSCFSPFEELKKKGRL N**NFIS*I*IGPKIFSQTNS*NSNFYQ YLCILSGLIQDK*NFKILS*FYK*V GNFDILYIHTCVVCVCVCVCVCVF VCLWSTLRMTDTV

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2405	7902	B	2610	50	382	XGEQLVRQDL DAGVSEHSGDWLD QDSVSDQFSVEFEVESL DSEDYSLS EEGQELSD EDEDEVYQVT VYQAGES DTDSFEEDPEISLADYWKCTSCNEM NPPLPSHCNRCWAHX*
2406	7903	A	2611	1665	1787	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
2407	7904	A	2612	1431	1553	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
2408	7905	A	2613	1	752	DL DAGVSEHSGDWLDQDSVSDQFS VEFESL DSEDYSPSEGGQELSDE DDEVYQVT VYQAGESDTDSFEEDP EISLADYWKCTSCNEMNPPLPSHCN RCWALRENWLPEDTGDKDGEISEK AKLENSTQAE EGFDPDCKKTIVND SRESCVEENDDKITQASQSQESDY SQPSTSSSIYSSQEDVKEFEREETQD KEESVSSLPLNAIEPCVICQ/GST*K WLHCPWQNRTSYGLLYMCKEAKE KE
2409	7906	A	2614	426	813	SSRRFVWRAKLLCERAQSGTVYEI* QCAHRHPRHRHPGCCRHRLGYAGT AGPLAGYRPFQRHRSQSLWRAASAI CVDISMRTSRSTVRPLWPPPSPA RFATWSHYRLRDHGDHTRPVDLPT SQFTILL
2410	7907	A	2615	1740	1862	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
2411	7908	A	2616	1174	1354	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPLRPAGLFKH SPGLYSQPILT
2412	7909	A	2617	2271	2393	FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP
2413	7910	A	2618	1029	1197	FFFFFFFFFGFLVETGFHRVSQDSL DLLTS*SSRLGLPKCWDYRHEPPRPA EEGI
2414	7911	A	2619	402	990	
2415	7912	A	2620	1326	1716	KAKKKKRLFFFCIFLCFLWGLPASL LEPGNVWKHLVWNSLHWSTARVL SSPHLTSCNSWQKHPEHPKGAPKN HLKAGCSGSCLSQHFGRLRQEDGL RQGV*GCSKP*LHHCTPAWDKHL KNSNNSNH
2416	7913	A	2621	148	420	LSLSLCRFLGRFCGSSFSIFVLHFH SFL*FMFSFSLETQKFHTSCVCVC VCVCVCVT*RILSFGIK*SSIQI*AQH LINFILSEKWR
2417	7914	A	2622	565	916	VPRARTQHSREKGRAGAWFGLHY QGSIICGSNSTW*NPPQRGPKLLVRL MS*GHCPPSSTQSGSTTTGKEEVKS SSGSDVALALYNDYFSLFCSSSVSKI KREPQLYKQTERETGHT
2418	7915	A	2623	1132	1245	KWHLGKIQNYSTGKCNRIYIYI*I YLF*CHLSIGNC
2419	7916	A	2624	209	326	
2420	7917	A	2625	808	1010	EETEGRARWLTPVNPNTLGGRGRW IT*GREFETSLTNKEKPPSLLKNAKK

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						KKKRKKEIKPGMVATCL
2421	7918	A	2626	1602	1940	PSGNTSETSKGLNIRSHTRLFEDIKG VNHRSSQLFQKKPKNRDRIFQERYV RSLLSK*VHPCDICKRPTSFLTTL*Q QKHHHF*QKALENIKEEQTDKLILS CKRVLPFVKK
2422	7919	A	2627	2565	2748	KSLKLGMSLKIKFIFLIKGH LGFPHF LKICPKTNSIFNTHVS*YIYVCVYIY VYTYTHIY
2423	7920	A	2628	1032	1292	MYIPLNNGTVGVDSQMHLVDQIDY RVLFSYDDWCRNV*FGWAFTSCLP LHGNIGGFFKMCVSYFFWEGELFSS VYFLESSYRKPNL
2424	7921	A	2629	1640	1815	NSKGESSAPLFLPDSHLEKRKSYGT HPLYISLLKNYEK*NNSNLKAVIFK ALLKNKQT
2425	7922	A	2630	1089	1226	IQIQNKLLKECPSWVW*HMPVISAT QEGEVGRSLQPRSLRSAWAT
2426	7923	A	2631	197	430	SSFLLVYFFIFYFILFFETESRSVSRLE YSGAISAHCCLRFLGSSDSSCLSYSE G*GGSIDRAQEVKAAASCRTAL
2427	7924	A	2632	343	596	GYSLLYIQKQPTPLKTKARIGCSYY VNCIFLWNFWKAHTSCFPLCSFVGD FMYICCLERNPEVGSAQ*DNGKQM PCYYRAASEG
2428	7925	A	2633	1143	1553	QCRRVPRGKRLELGVHSSTG*QAPL LPSASATSSGFLADRRVGTGLRTP RSRRSAGPYLARPASSAARGPPVGR RGPPWGWAASAAISARSSPPSAAGS GPDWRRPGKRHSRPTAAASAHTS PSQSPAIPAGGR
2429	7926	A	2634	158	585	ALTWVHLSSVSFFPDCLKLTPSRSP ANPSTQQPPHPPHPAPKP*WEAGRI AAS*LPSKAGSWKPLLVPKAKLW SHVGRMEGDLQCPLCLWLHPILW FFGGSCFPQTEHSPVQSPDGLIIAWN CPASDAGIKDCLPKYFC
2430	7927	A	2635	1348	1540	SCCWACE*QCNWYVYISVCACVYT YICISTHIYIYTIHVHLMGYVKIKQ LFNACDSMEHLQAH
2431	7928	A	2636	263	615	LVNSEGNIWVKLCHELQHGPLNSSP FLILLSHSEKINRASIMLKRYKLIN NYILSAFNPPPGKIHTHTHTHTHT HTHTESQKVKST*EIT*IFPQQYTNL CQREEHCYFLSHSE
2432	7929	A	2637	270	665	KLGVVAHVYPYCQPARTLAPRLALS EGSFRATCPG*ELSGLRCSPICCPPRS PPALPLCPLKTKLPKC*KTQTYPGS GF*PSHPCKSGPKPLMGCPPTGGG QVDEWIVIYNKIYGRNTGLRRLHRP LYQFK
2433	7930	A	2638	54	311	SQHFRPRQVHHLRSGVRDQPGQH GEMPSLLKIQLAGHGATHL*SQLL GRLRQENHLNLGGRGCSEPEIVPLH FSLGKQSEALS
2434	7931	A	2639	26	229	CRMTMSRLVTMGVAVFLVVCERC DAVCPSGQSPSPWPWASPPECCRDH



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						ICPHPVGPPGPPSLALPAW
2435	7932	A	2640	133	586	THVMLCAQVGSHHPALPWASPECCRDHICHPVGPPGPPSLALPAWDTHTHTHTHTHTHARTRATHAHILPSHAVFYFPFDVQSGSLAGSPYPRGGGGWFLGGAKKGRECPGG*MGGPPMTPSSFQKQLLLPPSQGPTPKPPEGGCLQ
2436	7933	A	2641	186	609	RVGHHPPSVRHPHQHGPWLRDPVQLHLWSSCVAFPFGAPAGLPPSDQDPGPPLAISPTHWPPCGQPCKTIAAHGNGHTRTGGR*RPRL*SRPAEWP SAKGRSGGLPGSFQEPADSYPGCGTWCSACKGRQPSYS
2437	7934	A	2642	989	1790	NYTPFLPCSASAEFCELWGRPLVVFYFYFQPPLAVEPNNVIVICCVWRVKVGPAGAFPRGLRRDVQRADFSSRSEGLLMGWVRDFDNHQSTCALDPFSGGIGSLLVPGGSDLQIGCFQKSFQALIEN*CLNRHNSLG*TPKRSIKILWAE*ISRAGLCNSSPEHPACGHPPR*GQWEAGPTAARTCFSPPTSNPPNSGPQAHEAQVSGDHSIHGGS*GSPSPPLAYNLSTRKAQPKCGKKCMVLPSTCKNCTYCKPFALWNCMP
2438	7935	A	2643	92	330	RQVCLPPSERNVASLRTPHPRRGAQKSQEGPPGRQSPSELKSRYWCVENSTWVSRAPQGTGWPGWALPFPHQG*GWLGP
2439	7936	A	2644	1137	1290	HGQINQMEVNLPMDRKV*THHTHTHTHTHTHTHSSTSCPYTLKRNVKKS
2440	7937	A	2645	96	357	
2441	7938	A	2646	2648	2953	DWGYLPFKTLTYPGMVCHCLPLKS FPLFFPPLFSK*WMGPKLYPPKPHLYQNISPQYLCQKTPQTKMPILKKGVFFPFRM*APQESGTNVFCMFLCPS TL
2442	7939	A	2647	201	377	QTVFVKLCVYTHIYN*VYMLIHI*APLSVY*YIAYI*AHILSYIVHLVIYITEKYDF
2443	7940	A	2648	1917	2056	QSHAKEWIFLLTCFIF*KLLRNIIYIYIYTHTHAYIYIYIYIFQ
2444	7941	A	2649	246	717	KRQSEEGVFSCCQGWNESLLLKSKVLEYP*FLHFPSFSFDLYLFNYVFIYLFYFCSIQSQTQSKAERAYIYIYLMCCRQNTVNFTTTTKQLFCHLNHLRRRNEKRWGCHFLVYAFEARSMFIYFFSLCINENDPEWRLAERSMYWSKHHKSC
2445	7942	A	2650	191	657	SGGERNSSAPSAMSPSGSATTSPGT*PRIIDSERTPAFHARASTVKPPAGINTREHPPLPCTPKPCTKTHFTAPPPQRCRHTHTSSPPRNLIQIFTRDTHPPPTHTRHHTHTQEPGWWSFDWVGCLRGFSFECHTFHFPQNKGTFFKMSYIATY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2446	7943	A	2651	1108	1282	PPLWAPAPAILFLQERKRGNDPNW DARRGN*TKNKNKNKNKNKKTETL LRRPVFGAAN
2447	7944	A	2652	2	479	FIIAHPD TVLGELSYFVTEKMISIHLE CSCNVWRVLYYGFNLYIYIRYIICN YIS*YILYIK*YT*VFF*TMGVYYKIN NNMQTVVPVYLN YIQVCCY*QIYL TFIYYGSHFLIELRNY*TRMHMLLYI DLLPVFTLPLPFMLSMMLNMGGIFN GPNF
2448	7945	A	2653	341	622	YQNRLFPNQCFTCLLVWLWDSAP PPRPWQPPQGF AHT*DRKEEGDPI GIWAPEGKSCTPKPPPSLPTSPGW KRALQKGD TGCPGPSTAST
2449	7946	A	2654	597	785	NNSPSQ*CHFGTDSIICILKQRLGAV AYACTLSTLGG*GGRIA*AQEF EAS LGNIVRPCLYI
2450	7947	A	2655	237	656	RGQGWVGDSQGRGGAKEGLLP SH GLPTPNPIHPTSPIPPENYVQRNTEK SWSWREGGRWKEIGRGRMRGKPS VLPPPGDRVMEGGPPTLLQHRS PH PGERHGF S*SKFPPPGSRPQKERR KGQRGMCVRVGQIN
2451	7948	A	2656	109	290	NKLLNIYMD**IICQILLKLYLVPIKL MDTVYMSIYLSLELCFVISPFLLTGI YLNLYIY
2452	7949	A	2657	122	359	
2453	7950	C	2658	133	315	MQWLYIATLIPFFWTQRKGTFS GK SQLILDFLQGALAILSPDPHPGILHR SLWAHLPA*
2454	7951	A	2659	1399	1644	CERGLPGPFSPMAHQG*TRAGDTG QPASSLPLGLTAGPYFPPSGCLGPFT LDGCGLSPPPLYLPVFFPGLLKSSR PLSCLN
2455	7952	A	2660	592	943	RTGCGQTLTVSHPDQARHWP GP GF ALILLYYPAQGFHLLPEAGPEGRG SLLTEEGSREANSRSSLISAAQLPPA APPQGLGV*MQESSRWGGKGRSKG SLPINLGLNSKLKKTTP
2456	7953	A	2661	181	401	
2457	7954	A	2662	1163	1457	HPRICWHHSDLHTITKTSHST*SESQ NPHSESPGRGCEPPGPRGSEPPSL *LSLPPPLPFAFCSSCPGLMAGFPPK QALSITGPFSPSVALWLGHC
2458	7955	C	2663	275	327	MPFRLSQDCHHSAGAQQ*
2459	7956	A	2664	70	191	DLLQKPQV*DPSRTECVSM*CFLSPP *AETTSILPCFPRI
2460	7957	A	2665	40	142	THIHILGFLI*G*GLAMLPSLVNSW AQVILLPQH PKVLQLQAGSTVNQPA HRC
2461	7958	A	2666	479	722	YCIIFLG GFFCCCSQHILNVFLCLAS FFE*MISQL*KILLGLGAVAYACNPS TLGV*GGRIT*GKKFKTSLGNIVRA HLC
2462	7959	A	2667	265	518	VKTVFLSGLDPLSLNENNMV LIMTS IVIFSHPLHFRFETLIGEWPFNLILG QV*WLTPLIPGLWEAKVGG SLEPRS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LRTAWET
2463	7960	A	2668	626	695	GPAARARPGKGIRPFRL**HHFGCS LWMGWKMGSQCRSPVESIPLGRAR WLTIVPVLREAEAGGSLEPRGSIPG WATRVPRPLYIEKKKKK
2464	7961	A	2669	66	610	TNNGSKSFCLKEHRGSCGCCSSKDF GVPQRLVLGLVLLEDLILGELQVLA FGALSGSISIFPSIPPHSAIIKKNSHLR KIPPVPPRQPFRRVWTSGPPAPRAS PSFCFSPPLAPRPPGLRTRPPPS*APA APQSRRTGGPARCPRGVPVRSQPE *TPCKKNFLMEKISYDFHSQRSSD
2465	7962	A	2670	1077	1598	YVCHTSLYTSKSAHSSPWKFSWDV NPTPLAIHVTTSTKTVSFHTEEV RVW SVHSTLKRFGFGAGGGE*GISEKGG HMAQTGTSRRPIAGRDPGPRPGL LAEYRRPGEEAEVAPEPEDPH*CH HQHTGGPQAPSAQVKVQSSPRRPH QLPVSVSPWIPGGCRGPITTVGTS
2466	7963	C	2671	40	180	MSFEAEIVLSPDRTTALHPGLQIETL SHIIIIILSTISFHQLLH*
2467	7964	A	2672	1818	2154	PTPVFVPSLFPSHKHLPQALCGLCG LMSMATKGLSPYTSPLNLWRDTH QRLDFSSSYIIFKTNRLGAVAHTCDP STLGG*AGKIV*G*EFETSPCKKRD VSKIIFKKEQK
2468	7965	A	2673	137	1610	EENIKSYKEYKCHNLYVIRKELLGG GAVAHACNPSTLGLQV*AIPQKIKK YLNFKL
2469	7966	A	2674	1	490	GNRSRARRLASSPGSAAAAAYRRPLP AGPSVYPQHERPCASTARRATGFRE IKVPSKSEVTRILDGKRIQYQLVDIS QDNALRDEMRLAEQPQGHPTPDL STGDQYCGDYELLSWRLWKQNN AGVS*KLGLKSSPVPEFPLAGTPITN TPPQPFNLANERTF
2470	7967	A	2677	2	215	
2471	7968	B	2678	63	203	SFRRPMASASTHPAALSAEQAKVV LAEVIQAFSAPENAVRMDEAPG*
2472	7969	A	2679	433	895	VFHLPSAEPRASDALMASASTPNRR PLSAEQAK\VVLAEVIQGVSPRRJA VAHGTKAR\DNAC\ND\MGKMLQF\ VLP\ VATPRSQQEVIK\AYGFQLPTG EGVP*SFAPIWSSSYEA\QD\PEIRQA LSGKLEGACFCRP*TLTPWGLLVG GSVAAS
2473	7970	A	2680	235	442	RPTFFYIPFKISKIKPSKIST*RPPSLL VG*KSKEKASTQKCLTKIPVPSANL KDFLPKHDTEKREL RH
2474	7971	A	2681	199	1061	RRSEPKGWNRAAFPPKVGCVCVW EKTGMGDQNPETALPSSLHVSISQ RSPRSTQASPPTRGHPVQPRRVYTP FKAGRPRRQKQVTHGQTAATLQVE *ATLPTNT*TSTTRAPCENQRGGKQ RSGWLRATKPHTAERRPSLNRPLTP TEPNCKTTELKSYSLQSKTWRNKS* VKTCRSKG**VMER*WSGKHSVKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						VSTFPSPRGSSSRLKPEARVARKY GPSPQLKPRR WRERKHGKPREMGR SEKSESLEWDRSLPVLRLMVDGFSPG KQNRNGQGRGAQSMASW
2475	7972	A	2682	415	575	ISGWGVGGSCSLSQHFGRTREQEDHL NLGVRDQPGQHSENKVSIIKKKRN VISI
2476	7973	A	2683	457	549	VSTGNKVVPQGQKVAICI**KVLLK MQIAFTFCPGTTLTPVDT*NVKTHL NECNILASLWWLKHDLVFQLLATW LHFNLSISSENASAPSYCPTEGVAT LSKPIFNYPHFIPFLHFSHMTLS*PY LAFFLPSPCNSKRNLDSHMVAIEAN RCLAN*NKNYDL*ADVSSSFQNILQ FIVNHKIKLPT
2477	7974	A	2684	291	364	RLKL*SPHLSRSYFEKSKEQLASRTP TGQS
2478	7975	A	2685	2	361	TETLARPPSPLVTNMKLLAETVLLL TICSLEGALVRRQAKEPCVESLSVQ YFQTVTDYGKDLMEKVKSPELQAE AKSYFEKSKEQLATPLIQEGLGTGT WFNFFELFSVGTGTTAWPPS
2479	7976	A	2686	425	678	LLGAISWELWGTQCPHVEGVPGPF GLSNPQAGAFREQPTGPVP*SSSF SKEQLTPLIKKAGTELVNFLSYFVEL GTQPATQ
2480	7977	A	2687	64	287	RQMAALLKANKDLISAGLKEFSVLL NQQVFNDPLVSEEDMATVVEHSMN *YMSYYSLQATGEPQDLRPPCCS L
2481	7978	A	2688	983	1386	QEVRYRKVETLRCLLFSSCLVPVCA ASPVSRPGCRFLRSSLHWPTGRV RQRGETFLVPEKTVLRGVASAPAQ KAAGRTPVGRPRDARLRADARS*S C*RAARPRRGASGAVGARGCGRPG FPFLRSGGIFV
2482	7979	A	2689	473	706	NLTLASKISLKYCKQYLWILFRKRL WPGVVAHVCNPRTLGGRGGQTT*T QEFETILGNMVKPISTKYQKKKKK RAAA
2483	7980	A	2690	1400	1600	VGGGSGRSSKFPPLP*CPPPSCCSLPI SSPPCLSTPGPSLLHVS KGTRRISRL LDKRISKRFTNH
2484	7981	A	2691	6133	7646	YMLFLFLSTKGWTVIQNRQDGSVD FGRKWDPYKQGFGNVATNTDGKN YCGLPGNEQACKIKSFYKWDFF*L KNIHCWKPVLS*EEFPDKNVEAK DKGRKAVFSFPKFYFW*EILFCFSFR EYWLGNDKISQLTRMGPTELLIEM EDWKGDVKAHYGGFTVQNEANK YQISVN\KYRGTAAGNALMDGASH LMG\ENRDHDPFHNGHGSFQPPYD\ RD\NDGWYVWHSLLLL*KSH*YHY SESLTIFLIATTSWALTVSHCPKLFM HHSKAFQL*GRHSYSHTDEI*RDY VICPMSHNYPEIKLEFEHSYFLNNEH LDKYL\LYL\KCV*KLSFSFPGFSDT

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						KGCKSYYSIK*QTQSLDGLPQRPS YLSFLL*GTGGLWCISVTLCIAPK GK TTVHTSVAVFYG*SAKRNLT TVVLF LITPNTFSFRLTSDPRKQCSKEDGGG WWYNRCHAANPNGRYYWGGQYT WDMAKHGTTDGVVWMNWKGSW YSMRKMSMKIRPFFPQQ
2485	7982	A	2692	711	865	VTMKTFSLRHKACGQVKNTLTI*Q PNSSIQPTSHYYPHCQPNTGMLIRK G
2486	7983	A	2693	26	351	ASLPDVTNMKLRAATVLLLTICSLE GALNRTQATDPCSENLC SQYFQTVT DYGKDLMEKDMSPELQAEAKSYFE NSKEQLTPLITKAVT*LGNFLSYFV* LGIQPASQ
2487	7984	C	2694	10	123	MSTDRHQGQRRWLGRPPHCYQHE AARSNCATPHHLQP*
2488	7985	A	2695	6	409	FCPALSSSTALFFLRGLWFRGKRLG STDLT LHKPFNLTPQFLHWYEMG ESHIDPKMLKPESGRSKSLFPSAAFL DLQSSFLPSFLVFPPLSGSCRSLSL PSGTNPLLQLVPLPPSILLPLSTVLF* RATKG
2489	7986	A	2696	736	927	SVAHSSCVSHTMHMTLLGRRATINC LFRNGRGQVQWLTSAVPALRKADV GG*LEPRSSRPAT
2490	7987	A	2697	2	251	FFLKPCLTQVATSGGCNFWPQAIFL SWPPNSISYRTQPTIFFQYNINILQAL A*FTLFACNPSSLGG*G*WIMWPRS RHCTPV
2491	7988	A	2698	1278	1515	SMVIRIMKVNHPMGLLTKRAKRS LNEMLNVDGKSGGYILGAVAHTCN PSALGGRGGWIT*GQEFKTSLSNME KPLLY
2492	7989	A	2699	139	260	
2493	7990	A	2700	268	388	
2494	7991	A	2701	233	400	HFLRAKVSVTQARVQWLDNGSLQP PTSMK*SSYLSLSKCWDYRHVPM APRHFNK
2495	7992	A	2702	602	758	IICLSVI*NPRTLTGVAHTCN PSTFG G*GTWNS*GQKFETSLTNMAKLCF Y
2496	7993	A	2703	379	1160	LVDMQLWPPVFHENKCCLGPPPT TH*RPAPAVPTPQAGPTQGLATAS SVSMLCSDKLFPSDDQPRV*PGDAE LSVLGVGRSSRKESPDQAPLPVIC ELSFARVGGAPGEPLQRPVVL*TP GTLWSKEIA*LQAVLGQY*HEGCAT IMPADP*GRGPENSGSVTAQQQPL PGRP*NRTHLFFVPHPGQAASQSQS SSSPP*QSERRA*IVSPNSGQRYFFPE TEARRQ*GEPRGEGGGDLFPQFPQV LLAALVHI
2497	7994	A	2704	178	412	LLHSSLGHVARLPTLQNMKT LARD GSVCFQSHLLGRLRQEDHGCSKP*L HHCTPAWVTEQDPILLKTEIGPVCS FKR

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2498	7995	A	2705	67	398	ISLT LGRHHGKIN VYFLYLKMQG*Y FCCTFVS VVNCSDCLSGHSRRKTEG DKVRKEKQEA*AWCKTCETTLKTF PILLFTKKQAGHITPLMLPFLILHTV VTPYFNLEAD
2499	7996	A	2706	264	612	KHFSYNFFSFSFFLEGGGRVLLCPSG WSLAQCSLQLLGSSNPPTLAS*VAG TTGVCQRAWLILKFFCRDRVSLCCP GWSGNS*LQMILSPRPPKILGFQASA TALGPLTPFCLIV
2500	7997	A	2707	179	472	
2501	7998	A	2708	498	849	GSLLSRAPIPYPLNWVSFFIPEVRTPP DIHTIGSEFPRFLKYLKPTREKILVPA LSPPVQPGPSVPFPLPLSQDSSGQAK APWPSSLMH*PGALPLRTTSTQKCD SPSEQTSDASG
2502	7999	A	2709	768	1073	GVETGFDLIAFEDLHAVPRDSGISLF LQATSAPPPPGTARPHQESPLASHK* QARQAPEPLGYA*ARQAQRMEATK ARPRPKSSGARVGREPTCSKPAPRR
2503	8000	A	2710	5451	5678	
2504	8001	A	2711	396	687	TFCPRCGCPSGLAMRLFLSLPVLVV VLSIVLEGPAPA*GAPEVSNPFDGLE ELGKTLEDYTREFINRITQSELPAM WDFWSETFRKVKEKLKTD
2505	8002	A	2712	1	93	LPKRWNSCHEPLVPLFSPLLVNAVL GVLGSK*GKKIKDNEIGEEIKLSLFA YEMILFVLL*NPYS*PKNFTVKLL YQSLRK*SDTRLKSTIYLYTSNKLK LRELYSE*PKRWNSCHEPLVPLFSP LVNAVLGVLGSK
2506	8003	A	2713	376	469	NQLPGERWLTPIVITLWEARA*GL FEPRSL
2507	8004	A	2714	715	1050	
2508	8005	A	2715	404	559	VNIFHFKTFYLGPGAVAHTCNPSTL GG*GGQIT*GQEFKTSANMMEPHL Y
2509	8006	A	2716	3	180	FFFIGVLTLLPRLECSGAITAHCSLD LLGPGVYTT*TLQVLGITGVCHHGQ LIYFYFL
2510	8007	A	2717	1825	1958	LWTISVFWKAGVPLPC*QSPRWTKS ECLSFTPMFLNKS NFKKRI
2511	8008	C	2718	23	349	MPGRGSTAQRGFSKRYSRSGARSL CSLFLFLAKSLSRAMTSFSNISAGL ASKKNAVQHSPLSALIEQAGSFGF YGFISLLPWRQRDFNHVLLGICWA VTSVEASE*
2512	8009	A	2719	41	298	ASKVICQQRWHAGFAWLLSLEASL PREGTAGEAVVLAHCLSPSVLKEKR QPAVRAVRKASRP*ILQRHSRQNE GHRQEWCGHTA
2513	8010	A	2720	277	651	KPSRARLLYESKKEGEMLENCQFFL CLFAKEHLQAH*QKSS*TSMDRLIN EPSNDWDIYYWGHRS*TSRPNWK MKSWALLERLCLKTKTKRQLRGP SFWSTSLEKPRWSCAPRPGHGGSV GW

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2514	8011	A	2721	76	185	VWQCLPLYPLPNTLRAVAFRFLAIG YAFPLSCLCALWIFQNLTSLVTDY *FGWSK*DPQ*FVICLCVCVCVCVC VCVISKLCSSSTDSSR
2515	8012	A	2722	1685	2124	
2516	8013	C	2723	299	577	MFCFDQSSLGSIVLESWITVKPLTLI SSTLMRRDDNFICCHAGRLFLLTVP YRWHTLSGVALFPGPCCGIFFCHSG FQCGRLLPYRVHAPQG*
2517	8014	A	2724	14	213	VDMGSHRVSQDGLELMTP*SARLS LPKCWDYRRDTPRLALLVLLNLPV PLGASHVGHCLLSYFCS
2518	8015	A	2725	1169	1404	SFLYFNGLMNFRRPGQAFEDSHEFKY KY*K*ARL*IAHTCNPSILENQQGQI P*AQVFETSLDHTPRPCIYPPKKKKK K
2519	8016	A	2726	44	417	CGCGLGEICLSHGVAQHNRGSNCQ KALFNAEPKCASSSSSGKGG/TILVP PAGGKGPNLI*WNPGGPPGARGFPGL TPPRGGKKGRAQPPENLVF*EKTG FPIVQRGGLKPPPGPPKGGE*RGGPP
2520	8017	A	2727	624	1023	CWLWSRGILPAPWSCAAQPWLQLP EGSF*C*TKMCSSSSSPKREFFPGPP AGRQGPQSNKREPPAPRVKGIPPPPP PKTGEKEDGPTTPINLGFPSRRVPP VTGGGYKPPPRPPKGGEKTGGTPTG HHRAL
2521	8018	A	2728	36	211	KTKNISQL*WHTPIVAATWEARAR GSPEPRSLRPAVSLQTAPTALQPSRL EMFVRRYP
2522	8019	A	2729	640	898	VLLTCLVCLVSSKTKPNITKQHTKI KFPQSSRARWLTPVIPKFWEA*AGG SPEVRSRLPAAGLEFLVSHLGRKC WDYRHKPPCLA
2523	8020	A	2730	707	1164	SCIFLNQVFNKNLYFLFFKIKNNLYF LCCMRILICAYNG*RFYLCGMK*GL *SWF*CFSLPSLFTAVKFIKFSVVF CSLSFTGYFFMYTFRIFCLLYPVVQ MISYILQMPFQFLFSFIKLPSCP NVQ FVSVCVCVCVCVNLIKFSARLPI
2524	8021	C	2731	270	371	MQNLQCFRAFELLTHNSASELPLSA PVTYTEDD*
2525	8022	A	2732	2553	2764	GIGPGWGIRPKRTRPRQVNSNVLKA QEWQAEYPGIFQRPYSYEQSFPP* TPPNPIKTSFPPRNCNSP
2526	8023	C	2733	25	288	MSKVQTWGRQKTSHTRLSLHTWK VAQRPGRGAPHLPDGVAARQRCSS LSTRVCCHHVSPQPNLGWAASVG DHSQACSHGPLQSPS*
2527	8024	A	2734	1043	1207	NMMTTHTLKKVGTGGRARWAHTC NASTLGG*GWWT*GQEFETSLAN MVKLHLY
2528	8025	A	2735	74	233	MVTFNCFLNH*TVTKGFTRLIV
2529	8026	A	2736	11	151	ICHDAVDRPR/CCRSAMTPWIDRDL PGRPTRPEPAVQRMISYDDKNRMG SDDVCIFLILE
2530	8027	A	2737	214	369	QKDSPD*SCDCVLKENEISNLRCPIQ

**MISSING AT THE TIME OF PUBLICATION**



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2554	8051	A	2767	108	279	
2555	8052	A	2768	3	314	LLALVKEGPVPLFLLMKEREGVSSV RSLDTHGILSSTPPVHLPKTG/TEAS GSSWGPADPQDAEKSCRPTSPTLGG GVPACVRCACVLLCCHGALSRLAA SLFFL
2556	8053	A	2769	1	465	
2557	8054	A	2770	192	400	
2558	8055	A	2771	1414	1597	SGVYKRCKGGGRFVFLECATSGLSL ISS\GLSWG/RLWGHGGCRLAGGWG GGGGGSGGGMALL
2559	8056	A	2772	673	988	
2560	8057	A	2773	749	1169	
2561	8058	A	2774	2	290	
2562	8059	A	2775	3	520	HERRVVAWAGRGFVCCARSSRSRV IFCSAPAGMAHKQI*YS\DKYFEEH YEYRFVMLPRELSKQVPKTHLMSE EEWRR\LVGQQK/SLGWVHY\MIHE PÆPHILLFRARPLPKSSTKMKFISGIV KSCFKFNVVYVYKVVFQWNTWRN GYKSFHPYLCMSCILHSNRARVKC NCK
2563	8060	A	2776	1134	1312	
2564	8061	C	2777	49	282	MFVFLSSAGNMPVTCWCWEAPRC NQKCTDPAARRPDPQTXXESQDRLR CAPCTXHQPLPLDTHNRTL VHNRL NIPQKL*
2565	8062	A	2778	1	306	
2566	8063	C	2779	54	212	MFVFLSSAGNMPVTCWCWEAPRC NQKCTDPAALIFLAPMPVQSDDSGK RQTG*
2567	8064	A	2780	34	308	
2568	8065	A	2781	35	407	
2569	8066	A	2782	41	360	
2570	8067	C	2783	105	302	MXNLKRLQISMKPAHSGVCFVTRX SEGLGGGRLGLCIXWLQRGASQHQ HVTGMFPAEDKKTNMKV*
2571	8068	A	2784	3007	3541	KRVDYWGKSSIICTTLLPHRSGLC KYYFFFLSLSKDSFWVIFFFCLSQR WKGERAKEKTNNKENEAFPSGYQ NAPGEEGTVRGAPGAGSALRCGWR WRPP/SRCGWRWRPPAWR/LRCPRP ARRWVCKPGPPPPPLPPRRPWGP CSAGPGAGLTPSRASICSWQARRQS GSHLITLERKRVRR
2572	8069	A	2785	272	801	
2573	8070	A	2786	659	842	
2574	8071	A	2787	156	203	
2575	8072	A	2788	441	785	
2576	8073	A	2789	2	28	
2577	8074	A	2790	5	1049	LRVAVLVAFKMSTKNFRVSDGDWI CPDKKCGNVNFARRTSCNRCGREK TTEAKMMKAGGTEIGKTLAEKSRG LFSANDWQCKTCSNVNWARRSEC NMCNTPKYAKLEERTGYGGGFNER ENVEYIEREESDGEYDEFGRKKKKY RGKAVGPASILKEVEDKESEGEED

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EDEDLSKYKLDEDEDEDDADLSKY NLDASEEEDSNKKKSNRRSRSKSR SHSRSSSRSSSPSSSRSRSRSSSS SSQSRSRSSSRERSRSGSKSRSSSR VTGALLPHEKDLIQVHHLLLRGTERE VVLDDLHLVIAKKDEQDHGHPKDA TGHHLDPILVPVQVQKRNNVLKFTS
2578	8075	A	2791	971	1106	
2579	8076	C	2792	291	444	MGCFFPNSWVRAGVLIPVPVICS RLTWGREAQRRGWVCRCSQNWVI FAP*
2580	8077	A	2793	1	672	
2581	8078	A	2794	1	691	MDFLLSWVHWSLALLLYLHHAKW SQAAPMAEGGGQNHHEVVKFMDV YQRSYCHPIETLVDFQEYPDEIEYIF KPSCVPLMRCGGCCNDEGLECVPT EESNITMQIMRIKPHQGGHIGEMSFL QHNKCECRPKKDRARQENGSAQAQ KRDNVRSRQLPTSSRP*SRRWRSW STSRPAPVTPRASPLRATSSRPSSRT SASRSREASRPWWATTSWARSR AAAARTCC
2582	8079	A	2795	312	394	
2583	8080	A	2796	490	2890	PVALTDRQTDTPSPSYHLLPGRRR TVDAAASRGQGPEPAPGGGVEGVG ARGVALKLFVQLLGCSTRFGGAVVR AGEAEPGAARSASSGREEPQPEEG EEEEKEEERGPQWRLGARKPGSW TGEAAVCADSAPAARAPQALARAS GRGGRVARRGAEEGPPHSPSRGGS ASRAGPGRASETMNLLSWVHWSL ALLLYLHHAKWSQAAPMAEGGGQ NHHEVVKFMDVYQRSYCHPIETLV DIFQEYPDEIEYIFKPSCVPLMRCGG CCNDEGLEC/VVPTESNIPMQIMRI KPHQGGHIGEMSFLQPNKCECRPK KDRARQEKSVRGKGKGQKRKRK KSRYKSWVPCGPCSERRKHLFVQ DPQTCKCCKNTDSRCKARQLELN ERTCRCDGSALAQKRDNVLFQAAT DEQPAVIKTLEKLVNIETGTGDAEGI AAAGNFLEAELKNLGFVTRSKSA GLVVGDNIVGKIKGRGGKNLLMS HMDTVYLKILAKAPFRVEGDKAY GPGIADDKGGNAVILHTLKLKEYG VRDYGTITVLFNTDEEKGSFGSRDLI QEEAKLADYVLSFEPTSAGDEKLSL GTSGIAYVQVQITGKASHAGAAPEL GVNALVEASDLVLRMTNIDDKAKN LRFQWTIAKAGQVSNIPASATLNA DVR YARNEDFDAAMKTLERAQQ KKLPEADV K VIVTRGRPAFNAGEG GKKLVDKAVAYYKEAGGTLGVEE RTGGGTDAAY AALSGKPVIESLGLP GFGYHSDKA EYVDISAIPRL YMAA RLIMDLGAGKEFH HHHHHAS
2584	8081	A	2797	326	1280	

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2585	8082	A	2798	356	518	
2586	8083	A	2799	27	225	
2587	8084	A	2800	470	754	
2588	8085	A	2801	707	907	
2589	8086	A	2802	2	502	VLSPEEDKATITSLWAKVNVE\NAG RKKPLGKAPLVVLPPWTPRGFLWN SFGKTL\ASALLAPSMGKTPQKSK ATLAKKGA*TSLGEDA\IKAPLDDSP RATFCPSLSEL\HCDKL\HVDPENFK A/LLGNVLVTVLA\IHFGKEFTPEV\Q ASWQKMVTGVA\SALA\SR\YH
2590	8087	A	2803	921	1146	
2591	8088	A	2804	1170	1482	
2592	8089	A	2805	1492	1853	
2593	8090	A	2806	909	1180	
2594	8091	A	2807	105	248	CTCSRVS\HNA\PRNSLVSMVFRMH PPPLDTFRQ/PQPSFNL*YP*PNYP
2595	8092	A	2808	662	843	
2596	8093	A	2809	263	408	
2597	8094	A	2810	701	950	
2598	8095	A	2812	1426	1525	
2599	8096	A	2813	1	1416	
2600	8097	A	2814	108	520	
2601	8098	A	2815	3	201	GRGLRSPDVTVTQRRRGRSPSAAER *PTRPGVLRALPAPA*GKHCPWPRP GARRRPPSSPAARPCP
2602	8099	A	2816	318	428	
2603	8100	A	2817	448	647	
2604	8101	A	2818	42	191	
2605	8102	A	2819	3	452	
2606	8103	A	2820	25	519	EFHRLRENPPMVAVSCPTKTNVKA\ AWG\KVG\AHAVRSMCAEALERMF LSFPTVT\TKTYFPHFDL\SHGFAQV*G ATGKKVADALTNAVAHVDDMPN\ ALSALS\DLHAHKL\RVDPVNF\KLLS H\CLLG*PWA\HLPRPSSTPGGCTPS LGTN\FLG\LLK\HRCLN\LPNNL
2607	8104	A	2821	270	453	
2608	8105	A	2822	115	427	
2609	8106	A	2823	1	1656	
2610	8107	A	2824	1	1188	
2611	8108	A	2825	1091	1764	SIAYQPKRVQDQTD\SQPILPELISNF SKVSGYKIN\AKKSQAF\LYTN\NRQT ESQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTKKWK NIPCSWVGRINIVKMAILPKVIYRFN AIPKLPMPFFTELEKTTLKFIWNQK RVRIAKSILSQKNKAGGVTLPDFKL YYKATVTKTAWYWYQNSMVLVPK QRYRSMEQNRALRNNAAYLQLSDL
2612	8109	A	2826	1	1449	
2613	8110	A	2827	2	1675	
2614	8111	A	2828	301	453	
2615	8112	A	2829	1	2139	
2616	8113	A	2830	83	1257	WQQTAVVDGGLKRLSLLNCRDGD CPSPQEPGPNSGRFQPAATDWLEFQ ARRRMKLKAIILSKLTQEQT\KHH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MFSLISGS*KMRIHGHK/VGEHHSPG PVEGVSMPTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENYKPLLNE IKEDTNKWKNIPCSWVGRINIVKMA ILPKGIYRFNAIPIKLPMTFFTELEKT TLKFIWNQKRARIAKSILSQKNKAG GITLPNFKLYYKATVTKTAWYWYQ NRDIDQWKRTEPSEIMPHIYNILFD KPEKDKQWGKDSL FNKWCWENW LAICRKLKLDPFLTPYTKINSRWIKD LNVRFKTIKLEENLGITMRDIGMG KDFMSKTPKAMATKAKIDKWDLIK LKCFC TAKE TTIRVNRQPTK
2617	8114	A	2831	1	1383	
2618	8115	A	2832	2	153	
2619	8116	A	2833	1	2436	
2620	8117	A	2834	1569	1835	
2621	8118	A	2835	933	2812	
2622	8119	A	2836	56	1692	KSKSKQHSKASRRQEITKIRAEKKEI EIQKTLQKINESRSWFFERINKIDRP LARLIKKKREKNLIDAIKTDKGDITT NPTEIQTTIREYYKHL YANKLENRE EMDKFLDTYTL PRLNEEEVESLNT ITGSEIVAIINSLPTKKSPGPDGFTAE LYQRYKEELVPFLKLFQSIEKEGIL PNSFYEASIIIPKGRDTTKKENFRP ISLMNIDAKILNKILAKGIQQHIKKLI HHDQVGFI PGMQGRFNIRKSINVIQ HINRTKDKNHMII SIDA EKA FDKIQQ PFMLKTLNKL GIDGTYFKIIRAIYDK PTASII LNQKLEAFRLKTGTRQGCP LSPLLFNIVFEILARAI RQEKEIGIQ LGKEEVKLS\LFADD MIVYVENPLP SQPQNLL*GWLSNFSK/MSSGYKIY KIDVQKS\QAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIHLTRDVKDLF KETYKPLLNEIK\EDTNKWKNIPCS WVGRINIVK\MAILPKVN\YRFNAIPI KLPM TVFTELEKNYFKVHMEPKKE PALPSQS
2623	8120	A	2837	2	433	
2624	8121	A	2838	371	452	
2625	8122	A	2839	307	497	
2626	8123	A	2840	95	314	
2627	8124	A	2842	2	311	
2628	8125	A	2843	1	602	
2629	8126	A	2845	571	690	CQQGFSFLQAYGPAQHAI S\MRKFK AKYPDYEVTWANDGY
2630	8127	A	2846	130	943	
2631	8128	A	2847	45	405	GIPGRRNMAVADLDLIPDV\IDSD GVFKYVLIPSPLGIPAPGIRPAESKEI VRGYKWA\GHHADIYDKSVGATCR KQGLRTVSILGGGRIS/HTKSPGQER FTVY\GYSMGLWSCPRTPIST
2632	8129	A	2848	1340	1504	
2633	8130	A	2849	3	200	GSCACAGSCKCKCKCTSCCKSEC GAISRN LGLWLR\CCSCCPLGCAKC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						AQGCICKGASEKCSCCA
2634	8131	B	2850	1	384	MWESVELPRDLLSGFAQNADSDMD NKVQVSDGDKELVGNWSKEKELPT VALHHALHVFHWLFSSRLGTPVSPR VAMEPKWSCEAGCCSCCPVGCACK AQVLRRLQRGIGEVQLLCLMWEQLF SQNCNT*
2635	8132	A	2851	1	2880	
2636	8133	A	2852	584	1253	
2637	8134	A	2853	1	2736	QSRARADQRITESRQVVELAVKEH KAEILALQQALKEQKLKAESLSDKL NDLEKKHAMLEMNARSLQQKLETE RELKQRLLEEQAQLQQQMDLQKN HIFRLTQGLQEALDRADLLKTERSD LEYQLENIQVLYSHEKVKMEGTISQ QTKLIDFLQAKMDQPAKKKKVPLQ YNELKLALEKEKARCAELEELQK TRIELRSAREEAAHRKATDHPHPST PATARQQIAMSAIVRSPEHQPSAMS LLAPPSSRRKESSTPEEFSRRLKERM HHNIPHRFNVGLNMRATKCAVCLD TVHFGRQASKCLECQVMCHPKCST CLPATCGLPAEYATHFTEAFCRDK MNSPGLQTKEPSSSLHLEGWMKVP RNNKRGQQGWDRKYIVLEGSKVLI YDNEAREAGQRPVEEFELCLPDGD VSIHGAVGASELANTAKADVPIYILK MESHPTTCWPGRITLYLLAPSFDPK QRWVTALESVVAGGRVSREKAEA DAKLLGNSLLKLEGDDRLDMNCTL PFSDQVVLVGTEEGLYALNVLKNS LTHVPGIGAVFYIYIKDLEKLLMIA GEERALCLVDVKKVKQSLAQSHLP AQPDISPNIFEAVKGCHLFGAGKIEN GLCICAAMPSKVILRYNENLSKYC IRKEIETSEPCSIHFTNYSILIGTNKF YEIDMKQYTL EEFLDKNDHSLAPA VFAASSNSFPVSIVQVNSAGQREEY LLCFHEFGVFVDSYGRRSRTDDLK WSRLPLAFAYREPYLFVTHFNSLEV IEIQARSSAGTPARAYLDIPNRYLG PAISSGAIYLASSYQDKLRVICCKGN LVKESGTEHHRGPSTSRSSPNKRG PTYNEHITKRVASSAPPEGPSHPRE PS\HPTATARGGPSCAGTS\PWPPPG AREVPRDAQHAERAVPREAV
2638	8135	A	2864	426	539	
2639	8136	A	2865	1	1134	
2640	8137	A	2866	766	1115	SARQIATFFNNGIKHLAIMGGDILH VAHIFVTPFNLEGAYTSINQRAEVG SLIVIFHRQQMFFIGNHPPLIV/YSMC MANGTPASNRHG WRYAPDR*RSVR RCDGDPLHPDVRRRSG
2641	8138	A	2867	61	390	
2642	8139	A	2868	627	1324	
2643	8140	A	2869	343	452	
2644	8141	A	2870	589	672	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2645	8142	A	2871	1	3000	
2646	8143	A	2872	2	191	
2647	8144	A	2873	251	505	GSSSRLGQRTD*ATASRRHF\KNKV PGEAKNCSPEDDEIPLYLKGGV\AD ALLYRATHMILTVG\GTSICPHYEL AVASFPKKAGS
2648	8145	A	2874	1780	1914	
2649	8146	A	2875	1154	1256	
2650	8147	A	2876	1	2629	
2651	8148	A	2877	334	468	YEEEEEDYD*EEEESEPPLDENDL EEDVVFQPPQIEGEAVYDA
2652	8149	A	2878	2	416	
2653	8150	A	2879	1	4116	
2654	8151	A	2880	3	3080	EEEELEASKSFGPGNEEEKEEKEYE EEEEEDYDEEEESSEAGNQRLQOV MHAADPLEIQADVHWTHIREREEE ERMAPASESSASGAPLDENDLEEDV DSEPAIEEGEAAENGHPGDTGAELD DNQHWYDSPSDADRELRLPCPAEG EAELELRVSEDEEKLPA SPKHQERG PSQATSPIRSPQESALLFIPVHSPSTE GPQLPPVPAATQEKSPERLFPPELL PKEKPKADAPSDLKAVHSPIRSQPV TLPEARTPVSPGSPQPRPPVAASTPP PSPLPICSQPQPSTEATVPSTQSPIRF QPAPAKTSTPLAPLPVQSQSDTKDR LGSPLAVDEALRRSDLVEEFWMKS AEIRRLSLGLTPVDRSKGPEPSFPTPA FRPVSLKSYSVEKSPQDEGLHLLKP LSIPKRLGLPKPEGEPLSLPTRSPSD RELRSAQEERRELSSSSGLGLHGSSS NMKTLGSQSFNTSDSAMLTPPSSPP PPPPPGEEPATLRRKLREAEPNASV VPPPLPATWMRPPREPAQPPREEVR KSFVESVEEIPFADDVEDTYDDKTE DSSLQEKFFTPPSCWPRPEKPRHPPL AKENGRLPALEGTLPQKRGPLPLVS AEAKELAEERMAREKSVKSQALR DAMARQLSRMQMELASGAPRPR KASSAPSQKERRPDSPTRTLGRS EEPTLKHEATSEEVLSPPSDSGGPDG SFTSSEGSSGKSKKRSSLFSPRNKK EKKSKEGRPPEKPSSNLLEAAAK PKSLWKS VFSGYKKDKKKKADDK\ SCPSTPFSGATVDSGKHRVLPV\VR AELQLRRQLSFSESDLSDDVLEK SSQKSRRPRPTYTEELNAKLTRRV QKAARRQAKQEELKRLHRAQIIQR QLQQVEERQRRLEERGVAVEKALR GEAGMGKKDDPKLMQEWFKLVQE KNAMVRYEELMIFARELELEDQRS RLQQELRERMAVEDHLKTEEELSEE KQILNEMLEVVEQRDSLVALLEEQR LREREEDKDLEAAMLSKGFSLNWS
2655	8152	A	2881	1	4132	
2656	8153	A	2885	1898	2056	
2657	8154	A	2886	1	233	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2658	8155	A	2887	1092	1339	
2659	8156	A	2888	363	512	EPLEGLLCLEGGKGVETILQAETPG EPLPP*KPHS*PGLCLRYRGHTL
2660	8157	A	2889	1	136	
2661	8158	C	2890	12	236	MTPGGLFLPYHSLPQPDFLASCPT HLSTPFLVADNELRLPKGQICPLHV FVLANRVVLKLCANSVWEHSGKIT *
2662	8159	A	2891	1548	1849	
2663	8160	A	2893	1	1441	
2664	8161	A	2894	954	1194	
2665	8162	A	2895	2039	2207	
2666	8163	A	2896	680	757	
2667	8164	A	2897	361	476	
2668	8165	A	2898	226	293	
2669	8166	A	2905	265	396	
2670	8167	A	2906	250	447	
2671	8168	A	2907	632	1038	
2672	8169	A	2908	3	363	VKDDPNDHEQGKRGHKPFLRELPR ATIFFLINL*VIAEVEVDSCIDQAES EMLLRSGAPDPGVPL*GCFVALVIT HTHSSRAAMAFVPTGKKASCYSQE PS*WQNSPNDTQDHSNDLSE
2673	8170	A	2909	57	448	
2674	8171	A	2910	62	371	
2675	8172	A	2911	398	789	VTGAPLMLPVLPGMPLAALVTG LSGLLWPCCAELVGTEFKLPALVHL PHCFFASLLESPVSPRLAMEPNCSC AAGVSCTCAGSCKCKECKCTCKK SECCSCCPVGC\SKCAQG\CVCKG ASEKCSCCD
2676	8173	A	2912	577	896	
2677	8174	A	2913	2	184	
2678	8175	A	2914	1	459	SSNTMNGWFWIDKCSLWLSQSLPY TRATQVTIKIPPATGV/SSGFVD*F WIDKCSLWLSQSLPYTRATQVTIKIP PNPATGVRRAALWIDSLRCAPLGLS TGGGKSRIKLGLGVPKFRGSDRNR VLIGAFYNPLAGYRALIGAFYNPLP PHLLQLLSVLLQPLLCCGKCKL KAPEGEETEFYVSPKAAV
2679	8176	A	2915	440	620	
2680	8177	A	2916	2	987	FGLRWPRGAVRRWQLWEEAAWK AEGAQARTNPHVSWAATVTRCSVP GKRNPAGWAAEPESGTVWSPPGA IRMFRFMRDVEPEDPMFLMDPFAI HRQHMSRMFSGGFWILAPFLSITD WQHCQGTRPASRRMQQAGSCSPL FG/MCLGIFGWFSWDMFWGLME*H DLGNMEHMTAGGNCQTFSSSTVIS YSNTGDGAPKVYQETSEMRSAPGG IRETRRTVRDSDGLEQMSIGHIRD RAHILQRSRNRHRTGDQEERQDYINL DESEAAAFDDEWRRETSRFRQRP LEFRRLSSGAGGRRRAEGPPRLAIQ GPEDSPSRQSRRYDW
2681	8178	A	2917	121	329	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2682	8179	A	2918	323	457	
2683	8180	A	2919	1	243	
2684	8181	A	2920	147	321	
2685	8182	A	2921	1	2310	
2686	8183	A	2922	319	773	
2687	8184	A	2923	85	369	
2688	8185	A	2924	1	681	
2689	8186	A	2925	1556	1953	HGVAAASLPSSAGRLSRARGPGSEE PAAAPAPRWRWQHPRGPGGPVSRR RRPPHGGTPGTVRRGGGGDPAAPG SGCPSPAVVPPRCPGAPLRRATLPP ACCGSLACSPLTL*PAPS/TPPL*ADD SCSVGLPT
2690	8187	A	2926	322	376	
2691	8188	A	2927	365	666	
2692	8189	A	2928	310	448	
2693	8190	A	2929	908	1189	
2694	8191	A	2930	761	913	
2695	8192	A	2931	1188	1373	EPHLKKKKKISRWWCIPVVPVTW KAEVGGSLPRRWRLQ*AEITPAHS SLGNGLTLLKKKK
2696	8193	A	2932	240	475	
2697	8194	A	2933	1212	1424	
2698	8195	A	2934	403	539	
2699	8196	A	2935	436	594	
2700	8197	A	2936	1	570	
2701	8198	A	2937	1086	1359	
2702	8199	A	2939	40	361	
2703	8200	A	2940	12	337	
2704	8201	A	2941	232	339	
2705	8202	A	2942	951	1069	
2706	8203	A	2943	286	621	
2707	8204	A	2944	299	513	HKCYFTLAHVHLIISFCAATLE*A*P SWGTCNSTPNFVNTTPTLAYYLGL WRSRLRPFSDSVSFSFCSGIL
2708	8205	A	2945	97	258	
2709	8206	A	2946	5	464	
2710	8207	A	2947	1	522	
2711	8208	A	2948	76	488	
2712	8209	A	2949	619	746	
2713	8210	A	2950	125	279	
2714	8211	A	2951	1300	1410	
2715	8212	A	2952	1867	1947	
2716	8213	A	2953	2	52	
2717	8214	A	2954	352	538	
2718	8215	A	2955	3	313	QEFGTRICPAACFPLESGTPGFSLAS KWTPNCSCSPVGS\CACAGS\CK\CN RVANRTVLTQTSCCSC\CPVGCAVA LPRGCICKGTS\DKCRSRCLDARDSC ALQM
2719	8216	A	2956	1172	1914	HFSAQPWASPCS/SLLLLGLEGQGIV GSLPEVLQAPVGSSILVQCHYRLQD VKAQKVWCRFLPEGCPPLVSSAVD RRAPAGRRFTLTDLGGGLLQVEMV TLQEEDAGEYGCMVDGARGPQLH RVSLNILPPGAVEDDVQAGRWRVA



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						SRDDVACGSEEEEEETHKIGSLAENA FSDPAGSANPLEPSQDEKSIPLIWGA VLLVGLLVAAVVLFAVMAKRKQV TIQLLQGNPTALAKSKEELSMPKS YQY
2720	8217	A	2957	3	632	
2721	8218	A	2958	3	728	
2722	8219	A	2959	194	451	
2723	8220	A	2960	2	484	NVLTSHQTQPNQRGKAATVTPALWR LTDVRLVTKYKIHFERNVGSFENSM KGNSIYF*GPGHDP LLNMNIVY*KS LTINNHMHKIT*ESL TEVLFSQGIFS VTNPHPEIFLVARIEKVLQGNITHCA EPYIKNSDPVKTAQKVHRTAKQVC SRLGQYRMPFA
2724	8221	B	2961	65	391	MAEVRKFTKRLSKPGTAAELRQSV SEAVRGSVVLEKAKVVEPLDYENVI AQRKTQIYSDPLRDLLMFPMEDISIS VIGRQRRTVQSTVPEDA EKRAQSLF VKECIKTY*
2725	8222	A	2962	1	2148	
2726	8223	A	2963	816	1014	
2727	8224	A	2964	2	358	
2728	8225	A	2965	84	176	
2729	8226	A	2966	137	426	QACIMREYKLVVLGSGGVGKSALT VQFVQGIFVEKYDPTIEDSYRKQV EVDAQQCMLEILGYLPGTEQFTSNE GFIHEKWTRICISLFHHSTVHI
2730	8227	A	2967	449	602	
2731	8228	A	2968	203	535	
2732	8229	A	2969	2	446	
2733	8230	A	2970	3	240	
2734	8231	A	2971	914	1291	
2735	8232	A	2972	188	266	
2736	8233	A	2973	191	306	
2737	8234	A	2978	1	440	
2738	8235	A	2979	3	670	TSRGRVGTQAGEPRDLRPPPCPSSPL RVAVV\CLEQPERGAWEAHNIPQP NGDSAVRSFG\TGTHVKLPGPAPD\ NPNVY\DFKTTYDQMYNDLLRKDK \ELFTQNGILHIA\RNKRIKP\GPERF QNCKDLFDLILT\CEERVYDRVGWK I*ISR\EQGDLSPVHVVNLDIQDNH EEATLG\ARFLICE\VCQCIQHT EYM HNEIDELLQEFEEKSGRTFLHTVCF Y
2739	8236	A	2987	367	492	
2740	8237	A	2988	49	332	
2741	8238	A	2989	582	923	
2742	8239	A	2990	523	668	
2743	8240	A	2991	942	1513	
2744	8241	A	2992	176	362	
2745	8242	A	2993	4937	5137	
2746	8243	A	2994	651	836	
2747	8244	A	2995	1686	1883	
2748	8245	A	2996	415	635	
2749	8246	A	2997	2	308	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2750	8247	A	2998	57	598	
2751	8248	A	2999	802	923	
2752	8249	A	3002	119	297	
2753	8250	A	3003	950	1314	
2754	8251	A	3004	1	579	
2755	8252	A	3005	27	483	RDAEDAIYGRNGYDYGQCRLRVEF PRTYGGRGGWPRGGRNGPPTRRSD FRVLVS/GWQ/DLKDHMREAGDVC YADVQKDGVMVEYLRKEDMEYA LRKLDDTKFRSHEGETSYIRVYPER STSYGYSRSGSRGRDSPYQSRGS PHYFSPFRPY
2756	8253	C	3006	34	171	MPKSFRVIAERSMHSWYVCFILICFIL HISITLHSLVMVFVTWREY*
2757	8254	A	3007	1688	1871	
2758	8255	A	3008	1	688	MSGWADERGGEGDGRIYVGNLPTD VREKDLEDLFYKYGRIREIELKNRH GLVPFAFVRFEDPRDAEDAIYGRNG YDYGQCRLRVEFPRTYGGRGGWPR GGRNGPPTRRSDFRVLVSGPSP\SG SWQDLKDHMREAGDVCYADVHK DGVMVEYLRKEDMEYALRKL *PPKFRSH\GETSLHRRFIPERSNQL MATSPVSGLSRGRDLSIPKARGSP HYFSSFPGP
2759	8256	A	3009	428	579	
2760	8257	A	3010	1924	2043	
2761	8258	A	3011	131	395	
2762	8259	A	3012	910	1173	
2763	8260	A	3013	1295	1489	
2764	8261	A	3014	1477	1604	
2765	8262	A	3015	443	805	
2766	8263	A	3016	1	2109	
2767	8264	A	3017	1297	1408	
2768	8265	A	3018	3	314	
2769	8266	A	3019	5	340	GSGTSAKAFRSIWGPLPPVHRHGSP RSSVQR/DGPGLTGEPVYIRNKV ANTGVPGAPGPSIGGVTAPATDYCH RIAPILARRRRRRRRRRRRRRRG GGGGVAGGGGGG
2770	8267	A	3020	1	1973	DGGARARGRAAARRRRRPRRRRRR RRRRRRRRRRRRRRRRRLGLERP QPTSRGRAPGASRAEEKMEELVVE VRGNGAFYKAFVKDVHEDSITVA FENNWQPDRIQPFHDVRFPPVGYN KDINESDEVEVYSRANEKEPCCW LAKVRMIKGEFYVIEYAACDATYN EIVTIERLRVSNPNKPATKDTFHKIK LDVPEDLRQMCAKEAAHKDFKKA VGAFSVTYDPENYQLVILSINEVTS KRAHMLIDMHFRSLRKLKSLIMRNE EASKQLESSRQLASRFHEQFIVREDL MGLAIGTHGANIQQARKVPGVTAI DLDEDTCTFHIYGEDQDAVKKARS FLEFAEDVIQVPRNLVVIGKNGKLI QEIVDKSGVVRVRIEAEKENVPQE EEIMPPNSLPSNNSRVGPNAPPEKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						HLDIKENSTHFSQPNSTKVQRCGMVP FVFVGTKDSIANATVLLDYHLNYL KEVDQLRLRLQIDEQLRQIGASSR PPNRTDKEKSYVTDDGQGMGRGS RPYRNRGHGRRGPGYTSGTNSEAS NASETESDHRDELSDWSLAPTEEER ESFLRRGDGRRRGGGGKG\QGGRG RGGGFKGNDHSDNRPRNPREA KGRITDGLQNTSSEGSRLTGKDR NQKKEKPDSDVGQQLVNGVP
2771	8268	A	3021	1	2116	
2772	8269	A	3022	656	883	
2773	8270	A	3023	303	589	
2774	8271	A	3024	2	478	MAGKQAVSASGKWLGMGIRKWYY NAAEFNKLGLMRDDTIYEDDEVKE AIRRLPENLYNDRMFRIKRALDLNL KHQILPKEQWTKYE/EGLCCSSSAL CFLLR*KDQPIECPSRSQEELL*SKLS PL*TAFET*AKENFYLEPYLKAEVIRE RKEREWAKK
2775	8272	A	3025	323	400	
2776	8273	A	3026	2	396	RPPTTTKFAAARQMAGKQAV*STQ AKGLNG/IFKKWYYNAARIQNKLG LMRDDTIYEDDEVKRS*EDFPEN LYNDRMFRH*EGHWTLNLKHQILP KEQWTNFEEKNFYLEPYLKE/VLF RERKEREWAKK
2777	8274	C	3027	144	341	MYHSLEKFSSCFKHIPDNFLKMTKI KQNIYRDHFLNLSFQGXQHKKNK TGQHFTSKCTEPFLQD*
2778	8275	A	3028	1070	1335	
2779	8276	A	3029	2	303	
2780	8277	A	3030	149	244	
2781	8278	A	3031	1642	1797	
2782	8279	A	3032	1115	1320	
2783	8280	A	3033	1240	1408	
2784	8281	A	3034	539	669	
2785	8282	A	3035	1155	1579	
2786	8283	A	3036	437	666	
2787	8284	A	3037	51	279	IKGRWEPPPLASFFLTSGHCSGDP GP*GWGEAVSPGRNTLSSSSWHW VPYSELRGRGVACRKEVYKIVQNT QH
2788	8285	A	3038	3	300	
2789	8286	A	3039	451	760	
2790	8287	A	3040	183	410	
2791	8288	A	3041	602	1145	
2792	8289	A	3042	2	496	
2793	8290	A	3043	710	896	
2794	8291	A	3044	143	601	
2795	8292	A	3046	120	280	
2796	8293	A	3047	2	424	
2797	8294	A	3048	3	452	
2798	8295	B	3049	240	420	XLKGHGQRKVAERADPKPLPQRGR TCPKRRCPLSDPARCTSFVRDPVN FQASLSHCLAW*
2799	8296	A	3050	310	401	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2800	8297	A	3051	544	700	
2801	8298	A	3052	1	568	
2802	8299	A	3053	686	787	
2803	8300	A	3054	8	182	
2804	8301	A	3055	227	547	
2805	8302	A	3056	1	523	ESLRKQLGQEPFFDMHMMVSKPE QWVKPMAVAGANQYTFHLEATEN PGALIKDIRENGMKVGLAIPGTSV EYLAPWANQIDMALVMTVEPGFGG QKFMEDMMPKVHWRRTQFSLDI* VDGGVGPDTVHKCAEAGANMIVS GSAIMRSEDPRSVINLLRNVCSSCS RNRSP
2806	8303	A	3057	919	1100	
2807	8304	A	3059	429	780	
2808	8305	A	3061	567	682	
2809	8306	A	3062	148	372	
2810	8307	A	3063	113	303	
2811	8308	A	3064	367	449	
2812	8309	A	3065	48	369	
2813	8310	A	3066	979	1254	
2814	8311	A	3067	173	776	
2815	8312	A	3068	1	111	
2816	8313	A	3069	33	494	
2817	8314	B	3070	100	154	MVHLTPVERVCRYCPVGQX*
2818	8315	A	3071	559	775	
2819	8316	A	3072	744	940	
2820	8317	A	3073	1	255	
2821	8318	A	3074	1	1206	
2822	8319	A	3075	905	1823	
2823	8320	A	3076	36	689	
2824	8321	C	3077	215	325	MSVYPLDHIQKRIARRSSLTSCMRG TIAWPTNSLT*
2825	8322	A	3078	1	831	
2826	8323	A	3079	97	236	
2827	8324	A	3080	409	602	
2828	8325	A	3081	818	1095	
2829	8326	A	3082	528	714	
2830	8327	A	3084	91	242	
2831	8328	A	3085	75	430	VSPGLPAARLFQVAYLDSHLKCPGC QHVPMTVTFISSKEKP*PRTVPRPP WMRLGHVILFSFLIPSNLSFSPVIFFL CGPFKVVICTELQNVSRSPQTTLAT VYCNKITSYICKKKK
2832	8329	A	3086	1000	1145	
2833	8330	A	3087	225	324	
2834	8331	A	3088	3	54	IIHYSLLIIV*CWVQF
2835	8332	A	3089	461	658	
2836	8333	A	3090	337	408	GIQDRASHCTQGPPPPPS*VPQASPA AGEGPCDPDPGRYPLRDSGQSVTLH AGSSATTIQEPRGA
2837	8334	C	3091	155	453	MLGALGAEELSLDSLPEGLLNFSKP GSEGGRLGLVPAAGEGPCDPDPGR YPLRDSGQSVTLHAGSSATTIQEPR GAGHALASXQECQWSRDRAAQAG E*

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
2838	8335	C	3092	121	393	MALPGRLPHRKLAGGTLEAPWPGIP SGAVRRHQPPPTTLXXWLGVKK PLRKRIEAKFLCAEGPEHIRQGSAA VPGGGGRSRNCEQCLI*
2839	8336	A	3093	270	573	
2840	8337	A	3094	15	297	
2841	8338	A	3095	970	1098	
2842	8339	A	3096	127	296	
2843	8340	A	3097	875	1075	
2844	8341	A	3098	171	404	
2845	8342	A	3099	186	392	
2846	8343	A	3100	2	202	
2847	8344	A	3101	2	242	ARGNMAAATLTSKLDLFRRTSTF ALTIIVGVMMFFIERAFDQGADAYFT DHIWNEGVVRPCAIPDLGTRLRGDSGV EKL
2848	8345	A	3102	79	1137	
2849	8346	A	3103	374	519	LDSRRK**C*LESRPHE*TS/DLSSGS LLI*GIWSILFYPMAP*KFQKEN
2850	8347	A	3104	1	1214	
2851	8348	A	3105	105	379	
2852	8349	A	3106	260	421	LLYGDCTWTSFHLQRLQLHCQVSQ PCREL*LVSSVLCFPFISEELHCVTG HF
2853	8350	A	3107	420	848	
2854	8351	A	3108	664	1059	
2855	8352	A	3109	73	269	
2856	8353	A	3110	307	566	
2857	8354	A	3112	316	410	
2858	8355	A	3113	200	403	
2859	8356	A	3114	258	377	
2860	8357	A	3115	1767	1893	
2861	8358	A	3116	1	389	
2862	8359	A	3117	3	569	RHGEERLQTRTLRAAELSARAPSHS LPAPRSAPTQKFSPTVEVERCIES LIAVFQKYAGKIDGYNNSLPRPE F/L*AFMNTLAAFTKNQEGPWVSL DRMMEETGTPNSDGSARISSGISLI WIGWALAMGLAWNFLPSRAVPFPR KAGPGGDPLGPGGFQTPPPFSFPGLS VLHLPQAHPSEAH
2863	8360	A	3118	362	712	
2864	8361	A	3119	2	152	
2865	8362	A	3120	134	760	
2866	8363	A	3121	670	891	
2867	8364	A	3122	44	63	SPSNRNTEEGTLNIIHNLGMYVFL HAVKGTPFETP*PG*KARAP*PPLGN NWDYGDRTSFTGSFFTISPILYFL ASFYTKYDPTHFILNHSFSS*VVLNS PKWPQLHGVRIFGN*KSKQQEH
2868	8365	A	3123	88	207	
2869	8366	A	3124	2	191	
2870	8367	A	3125	145	865	
2871	8368	A	3126	69	118	
2872	8369	A	3127	1148	1323	
2873	8370	A	3128	197	327	PLGKKFSCSKSLRLGPFQL*SLRF

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						RKTTY
2874	8371	A	3129	154	303	
2875	8372	A	3130	3	158	
2876	8373	B	3131	144	274	XICTLSEKERQIKKQTALVELVKHK PKATKEQLKAVMMISQLL*
2877	8374	A	3132	383	529	
2878	8375	A	3133	1981	2132	EKENEDQKLIHLFFFSLGVKPTPCL KNINFFNHFASFLCASINKKWKRI
2879	8376	B	3134	144	274	XICTLSEKERQIKKQTALVELVKHK PKATKEQLKAVMMISQLL*
2880	8377	A	3135	383	529	
2881	8378	A	3136	1979	2131	EKENEDQKLIHLFFFSLGVKPTPCL KNINFFNHFASFLCASINKKWKRI
2882	8379	A	3137	296	592	
2883	8380	A	3139	224	700	VLLPPTGKRYPKVYIGVFKGPRKM GSSEIPFQNPFSIFSKEGYFLCREDFP NGAQISLLEEPFQIHLKLTFMFKNTT NFIFTAELCDQCQGL*NLHLSSSP* KKRHLT/HNQTHPHIKTDFHC*FIHY LVV*KSQSTSQHLFKSTMGKDQRQI DNNIMN
2884	8381	A	3140	761	963	
2885	8382	A	3141	475	715	
2886	8383	A	3142	381	698	
2887	8384	A	3143	2	235	YASLEPPDRPQVGASCGPGTYV*GA VPPSPAGVGREGVAGKGTGGCTCDK PLSPCSLAGARRGSFRRPSWTSPRL LCW
2888	8385	A	3144	49	353	
2889	8386	A	3145	174	495	
2890	8387	A	3146	73	226	
2891	8388	A	3147	326	421	
2892	8389	A	3148	1306	1444	
2893	8390	A	3149	53	246	
2894	8391	A	3150	228	271	
2895	8392	A	3151	419	599	
2896	8393	A	3152	1	322	
2897	8394	A	3153	151	375	
2898	8395	A	3154	2017	2191	
2899	8396	A	3155	3	234	LWSASSAQDATWADSQELSMARLP HVRKCVVVVLLLQGLSLELLDFPP L/CLGPGCPCHLAHQHPCPRPLFQ LSGR
2900	8397	A	3156	43	408	
2901	8398	A	3157	3	374	
2902	8399	A	3158	1	823	MAVVAPRTLIIIIISGALALTQTWA GSHSMRYFSTSVSRPGSGEPRFIIV GYVDDTQFVRFSDAASQRMEPRA PWMEQEEPEYWDRQTEISKTNQI DLESLRIALRYYNQSED/VPPKTH MTHHPISDHEATLRCWALSFPYPAEI TLTWQRDGEDQTQDTELVEPTRPAG DGTFQKWASVVVPSGQEQRYTCHV QHEGLPKPLTLRWEPSQPTIPIVGIL AGLVLFGA VIAGA VVA VMWRRK SSDRKGGSYSAASSDSAQGS DVSL TACKV

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2903	8400	A	3159	1	1264	MAVMAPRTL L L L L L S G A L A L T Q T W A G S H S M R Y F F T S V S R P G R G E P R F I A V G Y V D D T Q F V R F D S D A A S Q R M E P R A P W I E Q E G P E Y W D Q E T R N V K A Q S Q T D R E N L R I A L P L T Y N Q S E A G S H T L Q M M Y G L G R G G S D G A L S F R G L P P V T A Y D G K D N I A L N E D L R S W T A A D M A A Q I T Q R K W E T / A A H E A E Q W R A Y L E G R C V E W L R R Y L E N G K E T L Q R T D P P \ K T H M T H P I S D H E A T L R C \ W A L S F Y P A E I T L T W Q R D G E D Q T Q \ D T K L V Q T R P A G D G T F \ H K G A S C V G P L G E E Q R Y T C \ H V Q H E \ G L P K \ P S T M R W * P S S Q P T H P P S W G I H C L A L V L L W K L * S L E A V V A A C E C G R R K S S D R K \ G G S Y T \ Q A A K P V T S A Q G S D V S L T A C K S V R Q L P C V G L R G K S C F L P F P L V D L E E P W T L F P A K G T L H V S V F M
2904	8401	A	3162	1	342	G S R T V P S P S P S S G L A S P G S P T H R S L G P T T P P M A S A T E D P V L E R Y F K G H K A A I T S L D L S P N G K Q L A T A S W D T F L M L W N F K P H A R A Y R Y D G H K D V V T S V Q F S P Y G Y L M A A G / S R D L S V R L W I P V ** E Y S * N G K Q L A T A S W D T F L M L W N F K P H A R A Y R Y D G H K D V V T S V Q F S P Y G Y L M A A G L E T Y P
2905	8402	A	3163	1	583	D M E S R S V T Q P G V Q W C Y L G * L Q P P P P R F * R F S C L S L P G S W D Y R C V P P H P A N F F I F S R D G V S H H V G Q A G L E L L V S S D P P A S A S Q S A G I T G L S H H A R P D / Y T F L L T V F E P F H G T H V R P P V T C G T L A S N W T P T A F I S L A E N T K V L K V A L K E V P F G F D I A I S K A S G T V Q I R A M S F M K T T F L S P S F V R E C T H D H V T L L Q S
2906	8403	A	3164	1	347	F F I L F F L R Q S H S V A * A G V Q W H N L D S L Q P L P P G F K Q F S / L S L P S S W D Y R R M P P R P A N F \ * F L V E T G F R H V G Q A G L E L L T S G D P P A S T S Q S A G I T G V S H G A Q S C P L L Y I E F P L S I L A A T
2907	8404	C	3165	13	399	M E K I P V L F R V A N L I S I I P A P N K S R L C G K T R I S R S A K S K A N T R V F L A C R F G L A G D N A I A N V H A P D A D L E A Q S D V E R T M D L K P C I W V P D T L G E A E Q T A P A D R L S M H T Q H F G R P R R A D H E V R R P R P S W L I W *
2908	8405	A	3166	168	414	N P L L L P N T F P A N G N T I L I K E K V L F L F F * D G S P V L S P R P D C G L Q W R N L G S L Q S P P P G F T P F S C L S L P S S W D Y R H P P L R P A N F F L Y F L V E T G F H R A S Q G V G L D L L T S R S / I P P R A S Q S A / R G L Q G V S H P R P A Y M S L R Y N K P A H V P L K I K V K K
2909	8406	A	3168	28	123	
2910	8407	A	3169	2	123	E N R L M A G G E / H M L A A I L L F T A L R C L C K V K H K P G L H A H * G T A P
2911	8408	A	3170	1	402	Q G F S P P A E S L R Y G \ S W E G K A L T F P Q P D T H K G S V L E D * * K R K A S L Q L R * E E G I C L \ C L S L G M E C L G V K P / V A Y I L F T E I G E S R L M A G G K / H M L A A I L L F T A L R C

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						LGKVKHKSGLRAHRGTAPFLKLIY DTEFAHMFSC
2912	8409	A	3171	1	399	SSSLQPPPPGFK*FSCIGLPTSRDYR CVPPRPANFVFSVETGFHHVQGAG LELLTSGDPSTSASQSAGMTGVTTV PRPVLLISEAHFWCKNSLFTGENVI EANQNLLALRFISAMDLQSLRIVRN QTFFF
2913	8410	A	3172	1	451	LYGEGWSFALVAQAGVQWCDLRL LQPLLPGFK\YSPASASRVAG/HYR WSL/DSVTQAGVQWHNLGSLQPPPP SFKRFSCSLPSS*DYRCTPPGLA*/F FIFLVEMGFSLLARLVNS*PSGDPS TLGLPKVLGLQGVSHHALVPHLLIL QKR
2914	8411	A	3173	2	346	
2915	8412	A	3174	1	2430	
2916	8413	A	3175	576	983	GRSFIVSFLLVNSGKVPTDK/ERLFD RMMNSNWG/RSAFKKVNSNLST*Q FKYKNKGICAAQCFSFLPK*PIPRL FFAGEHTIRNYPATVHGALLSGLRE AGRIADQFLGAMYTLPRQATPGVP AQQFPKACETDAF
2917	8414	A	3176	1	2930	RRAGSVKRGEARLFGPTERQSERPL RPSAARRPEMLSGKAAAAAAAAA AAATGTEAGPGTAGGSENGSEVAA QPAGLSGPAEVGPGAVGERTPRKK EPPRASPPGGLAEPPGSAGPQAGPT VVPGSATPMETGIAETPEGRRTSRR KRAKVEYREMDLANLSEDEYYYS EEERNAKAEKEKKLPPPPQAPPEE ENESEPEEPSGVEGAAFQSRLPHDR MTSQEAACFPDIISGPQQTKVFLFI RNRTLQLWLDNPKIQLTFEATLQQL EAPYNSDTVLVHRVHSYLERHGLIN FGIYKRIKPLPTKKTGKVIIGSGVSG LAAARQLQSFMDVTLLEARDRVG GRVATFRKGNVADLGAMVVTGL GGNPMVAVVSKQVNMELAKIKQKC PLYEANGQAVPKEKDEMVEQEFNR LLEATSYLSHQLDNFVNLNKPVS LG QALEVVIQLQEKHKDEQIEHWKKI VKTQEELKELLNKMVNLKEKIKEL HQQYKEASEVKPPRDITAEFLVSKS HRDLTALCKEYDELAETQGKLEEK LQLEANPPSDVYLSSRDRQILDWH FANLEFANATPLSTLSLKHWDQDD DFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVN TRSTSQTFIYKCDVLCCTLPLGVLK QPPAVQFVPLPEWKTSAVQRMG FGNLNKVVLCFDRVFWDPVNLFG HVGSTTASRGELFLFWNLKAPILL ALVAGEAAGIMENISDDVIVGRCLA ILKGIFRSASAVPQP/KETVVSRRWA DPWG\RGs*SYVAQGS\SG\NDYDL MAQPYHSWAPSIPGAPQPIPTLLC GENITIRNYPs/TPVHGALAEVGSRE



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						AGKEIARPSFWGAMY/TRLPRQVATP GCFLAQQVPQACETRCIPKGRGPM CPVSCPCKEGSSSNTRSPLEKSTPGI WAPDQLMELPDLTKGACLLNDLE HQGGTCPLVWNCVLRKD
2918	8415	A	3177	62	447	GDRAEESAEPRAWSHSDNSHRYTT LFICLTHTHVHNPVHS/HTHTHTHT HTHTHTHTVSYRHTETPPLLLKQTG LKFY*NSRDDTPRSRPGSSGLQRLSS SPPVPFQPGTVEASADFCGDDLLTT VRLQ
2919	8416	C	3178	90	233	MRIGYKVKDGTFLDLQMGGLPGXX XXSRPKRNHQLSKGEREINLGLK*
2920	8417	A	3179	462	929	SLFHTWKADGFFLTGNSSSRPGNNT ICKSKKCPILYLISNPHPQIMPLFFF CDGSFTLVGPGWEWQWCDLSSLQP PTPR/FN*FSCLSLPSSWDHRHPPSCP ANFLYF**RLGFHHVGQAGLELLAS SDPPASASHSVGITGVSHHTWPMPL LLLI
2921	8418	A	3180	160	272	FFL*DRALLCLPDWSAVV*SWLTAA LA\YRRKRSSYLSLPSSWDYRHLPP CPANFSYFL*RQSLTVLPRLVNSW TQVSLLTQPSVLGLQA
2922	8419	A	3181	6	270	RDRVLLCHTDWSIAVESQLTASSN SWVK*SSCLSLQRTRDYRHEPPYL ANF*IFCRD/RGLTMLPRLV*NSWPQ GILPPWPPKSLGLQV
2923	8420	A	3182	92	549	VWQGLHPQLHPHFASQNLQSLALS LKAGVQWHDLSLQPPRRFKPFS CLSLPSSWDYRRAPLCPANFFLYF** RQGFTMLARLVSNY*PRDPPASASQ SAAITGVSHCARPRLSSLQCFSSNS RLEHTDGIHFLSEAMSAIHESFPHI
2924	8421	A	3183	16	661	DRVSVTQAGVQWCNLGSLQPLPPR FR*FSCLSLSSWDYRRPPRPANFC IFSRD/MAFTTLARLVNS*PQ/CDPP TSASQSAEITGVSHRAWPVLSSPQPF FFFDMESHAIQAGVQWRHLGSLQ PPPPMFK*SSCLSLSSWDYRRPPR PANFFVFL*RDGVSPC*PGWSRSPD LVHPPWSPKSAGITGLSHCAQPYP QFSKHKDLRVSGKA
2925	8422	A	3184	288	489	CGLILELEKLLLVWIIQIQMSLNKA TI*SNDIFCPLST*NQVWCVFKGRSL HFEQKVVPSSNKVTG
2926	8423	A	3185	3	166	WLYSANVAHAPYRGSAWCLRDS RPPAQYWSAFQHYSL*PTQFPLEFT TKSLLS
2927	8424	A	3186	3	725	LALLGRVYDVLSARD/YYELGPQYS VSKMTQRRSHVYTTRLNT/ADIYDS DLVPLCPQLSAVPLHSRNSAPYPYN PLYSVP/LPG/VVTGRFYGEDGLPTP ALTQVEAAITRGLEANKLQLQEKQ TFPPCNAEWSSARGSRLWCSQKSPK DADDTSIYMFYQKVGDNDSIDSWKN AGR VFKDSKDFDANDPILKDQTQE

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						WSGSATFTSDGKIRLFYTDYSGKHY GKQSLTTAQNQGVKPEGTTETTMK
2928	8425	A	3187	1	1988	
2929	8426	A	3188	134	944	MLRCGGRGLLLGLAVAAAAMAA RLMGWWGPRAGFRLFIPELSRYR GRPR\DPGA*YLALLGRVYDD/DPP GRRHYEPGSHYSGFAGRDASRAV TGDCSEAGLVDDVSDLSAAEMTL HNWLSFYEKNYVCVGRVTGRFYGE DGLPTALTQVEACDSTRFGGQT NYKLQEKQTFPPCNAGGGAQPGAA RLWCSQKSGGVS RDW/ALAVPRKL YKPGAKEPRCVCVRTTGPPSGQMP DNPPHRNRGDL\DHPLAEYTGCPP LAITCSFPL
2930	8427	A	3189	1	312	AQPGVQ*RNLHSLQPPPPGSKRLSC LSLPSS*DHRRPPPCANF/SVFLVE MGFHHVGQAGLELPTSGDPPASAS QSAGITGASHRTRPES*FY*LRLGIII FR
2931	8428	A	3190	2	176	
2932	8429	A	3191	3	67	
2933	8430	B	3192	1	1587	MVKLSIVLTPQFLSHDQGQLTKELQ QHVKSVTCPCEYLKRVINTLADHH HRGTDGFGSPWLHVIIAFPTSYKVVI TLWIVYLWVSLKTFWSRNGHDG STDVQQRAWRSNRRRQEGRLSICM HTKKRVSSFRGNKIVLKDVITLRRH VETKVRKIRKRVTTKINHHDKIN GKRKTARKQLSQHSISHVLAFSDDP FCKKGSLLQAPPSADDNIKIPAEERL IPLPPSADDNLKTPSERQLTLPSPAP PSADDNIKTPAERLRGPLPPSADDN LKTTPSERQLTLPSPAPPSADDNIKT PAERLRGPLPPSADDNLKTPSERQL TLPSPAPPSADDNIKTPAERLRGPL PPSADDNLKTPSERQLTALPPSAPP ADDNIKTPAERLRGPLPPSADDNLK TPPLATQEA EAEKPRKPKRQRAAE MEPPPEPKRRRVGDVEPSRKPKRRR AADVEPSSPEPKRRRVGDVEPSRK KRRRAADVEPSSPEPKRRRVGDVEP SRKPKRRRAADVEPSLPEPKRRRLS *
2934	8431	A	3193	792	1024	SHRKMFRQAQELRRRAEDYHKCK/I SLNIQFLMCWLFQIPPSARKALCNW RMIISRHLPSVVLHVPLYQPRTRPRT LH
2935	8432	A	3194	1	1656	
2936	8433	A	3195	112	368	SHRKMFRQAQELRRRAEDYHKCK/I SLNIQFLMCWLFQIPPSARKPLCNW VSLLVFLAFEHSLPGQDMDTFFSLQ LCAQARTGRSD
2937	8434	A	3196	1	1353	
2938	8435	A	3197	1	452	
2939	8436	A	3198	1	510	
2940	8437	A	3199	2159	2958	

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2941	8438	A	3200	350	927	LFLVSPLKTISGSRNGVHDGSRDVQQ RA*SSNRRRQKKRVSSFRGNKIVLK DVITLRRHVETKVRKIRKRKVTTK INHHDKINGKRKTARKQKMFQRAQ ELRRRAEDYHKCKIPPSARKPLCNW VSLFVFLAFEHSLPGQDMDTFFSLQ LCAQALQREMAERKAA YRHHSPIP VGNRVVQKHLHPHPVGPLI
2942	8439	A	3201	1	277	FFFF*ERIWLCCPGWSALARTWLT AAPNSWAQTILPHSWG YRRLPPCP AFILFYLF/CRDK/SLAML PRLVLNS\ WAQVILPLQPPKVLGLQA
2943	8440	A	3202	1	340	SIHLPKAPPPNHSTGVVWQHRNFFL RWHLTQC/*PGWSAVAQSLLTATST SR\VKQSSHL SLLSSWDHRCAPPHL ANFLYF**RRDFTVLLRLVSNS*A*V ICPRWPPKVLGLQM
2944	8441	A	3203	2	354	ESLTGVQWHE\FASLKPL/PCLSLPR GWDYRRAPPRPAYF*FLVETGFHHI GRAGLKLLTSDPPVSASQSAGITG MSHRAWPLLKYFSALQTLNILQKN KNKNLIKTYFISLHVKIF
2945	8442	A	3204	166	373	EGALFCSQASELLSCGLLAVFTRFK LRGPHCCCAKKVYSLPRMGPHHTL H/TALNI*SCPCCLFIFLVC
2946	8443	A	3205	2	775	LHHLPGGGSVSHNKPALCGAVPAG RPDTGDNPAVPGRSNGSALTPVWV LIAQSPPIVKILKFGWFPILAMVIS SFGGLILSKTVSKQYKGM AIFTPVI CGVGGNLVAIQTSRISTYLMWSA\ LGVLP LLMKKFCPNRSTFCASQKL NSMSCSRLLLLLGGSGGHLIFFYIY LGGGVSQS*T/TPDL CGSNLLGRA* SRVTNPAVTGA EVELVRLTWHQGL DPDNHCIPYLTGLGDLLGTGPPGDS AFSLTGY
2947	8444	A	3206	2	348	IAFGRYELDTWYHSPWP EEARLG RL\HMCEF*IKYMNSLTILTMH MVN CAFD PPLGLPKELSLETRMETFFPAL PSFHSIHCPLCVQPELGKAFGCLSVG AWGCRTHLRFTGLH
2948	8445	A	3207	1	1503	
2949	8446	A	3208	1	635	
2950	8447	A	3209	1	665	MQAIKCAGGWKAEAVGKTCLLISY T\TNA\FPGEYIPTVFDN\YSA\NVMV DGK\PVN\WGLWDTSGQKDYDRVT PPYPYPA/QADVFLICFSLVSPASFE NVRK WYLNVRHHCPN\TP\IILVGT KLDLRDDKD/TRIEKLEK KLTPIIT YPQGLAHG*GRLGAVKYLG/CAPA AHTSEGLKTVFDEAIRA\VLCP PPVK ERGRENCLPVVNVSAPSFLGPVPLE PL
2951	8448	B	3210	1	693	MYGVSAFVVLSP TGRLP SVLQKEN QQQGV PNPPLHEQM QMDTGLCRL TPGLTLAQWTRGSDSLPGAGEAG RTSFLPMYNANSAASSATHTGAAS

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						RESCGERECVQFSQRTARDRWCIRG RAELEQDILDSAAVTIIQKWHIKGRP ALHPAGVLGHVEAPFSLVLQLERSR FLKNRWESAGARYPGREEGNEIRH RGCGDRGSQEA AVRCKGPPTPRAV ELPPRLPVLS*
2952	8449	A	3211	1	627	FFFGKSILLFKKINVTDFIEKDILKMF LKGLKRHLFWPGMVAPAC*SQHSG RPRRMDHLRSGVRDQPGQ\QGETPS LLKNIKKISRAWWQAPVIPATREG*/ E*GESPEPGEGKVCRRAEIAATCTP AWGVQSETLSSKKKKSFLNVPHH PRQASVSFHC FHKNQWGSPLWKKA RTFLLLGNGWLSCHLSTQGNLSA PHLAEAQTLSF
2953	8450	A	3212	114	411	EREF RFPQVELQGPDLG*LNLLLP RLKQFFGLTFQRIWNYKLAPPPVN LEFWAKTGFSHVNQVGFELLT*GDP P/AWASQRVKMTGPTHQAHLGNF F
2954	8451	A	3213	48	1400	HPMTPI*STPLLYPL/PVTSGLASLSS LTLQNSDS\LLQPLTSAM/PPSAIPTP QRTSTPGLALFPGLPSPVANSTSTPL TLPVQSPLATAASASTSVPVSCGSS ASLLRGPHPGTSDLHISSTPAATTLP VMIKTEPTSPTPSAFKGPSHSGNPSH GTLGLSGTLGRAYT\STSVPLSLAC LNPALSGLSSLSTPLNGSNPLSSISLP PHGSSPTIAPVFTALPSFTSLTNNFPL TGNPSLNPSVSLPGSLIATSSTAATS TSLPHPSSTA AVLGAFCFSTS\PAAP FPLNLSTAVPSLFSVTQGPLSSSNPS YPGFSVSNTPSVTPALPSFPGLQAPS TVAAVTPLPVGWQPQHPQLPVLPGF GSAFSHFNSRSWLHKPGFIWDFK AGRQFWFFRAFGPSRVSLGFLRLH NHPCKNYSIMRLHSQHCYSRSIQLR LWESYPAQPDGVS
2955	8452	A	3214	2	694	QLLNYAPGPGGPRYVDCDLF*NGY HL\WYHD\YGHLEF\RLQLATQFEN WYMKYQSPHIQTKYGAETVSGFPR DPPSDVPVRCPRKSLLEQ\YHLGLDS KPQKNTCLESPLWNF\ADFMTE\QSP \TKVLGNKKGIFTRAETTQSSAFL LRERYWKIAQ*NPGIPHSVARSQCL ENTACCSLSKTDTHLRVPSSPGGQR LPQQQNKCLLDCSRQTRTFSGLG FV VIYSSREH
2956	8453	A	3215	2434	2765	GIILFWAQLFPASFFFFFFF*DGVSLC CPGWSAVVRSQLTASSASRVQAILC LSLPSSWDYRHLPPCLANFFVFL/CR DGGFTMLARLVLS*AS*VHPPWPP QSAGDYQA
2957	8454	A	3216	2	481	LFLFLRHSFTLSPSLDVQWRDLGSL QPPPPRFK*FSCLTLPSSWYYRHVPL CLANF*FLVETGFCHVGQSGLELLT SGDLPASASQSVWITGMSHGARLH GHFLGSWENWTCQAPGSSKSDCS

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						PHMANAVSAGGPGTLLIPSAPSCPC NLAGGRCPLR
2958	8455	A	3217	126	364	RAWANLS*LKVLPPGLKGFSGTLT PSTGNNGLVPPPRVNFSGFSKNGVS PCGP/GWF*TTALRELGPLSLLEIGN PFFL
2959	8456	A	3218	132	342	SLSSLKNMYICLWNVFLFVFGYRAF LCHPGWSTVAQS*LT/IPGT/LWVKP SSLVLPKRWDRHEPLRPDLK
2960	8457	A	3219	2	264	QLTATPPPTGFKQFSCLSHPSSWD\Y RYVPPRPAKFCIFS/VRRGFTMLAR MVSIS*PCDLPTSASQSAGITGVSHR AWPVL*FVFLVETGFHHVQDGLN LLTLRSAHLSLPCWDYRRKPPGLA CFMILNSYL
2961	8458	B	3220	134	3038	PGMEDGSDDMDTSVEDIGGRSCVT RFVRTLLIMEHGKPHSKHLTEYF AFLYEFAMGEEESQFLSLQAIST MVHFYMGTKGPENPQVEVLSEEG EEEEEEEDILSLAEKYRPAALEKMI ALVALLVEQSRSERHLTSLQTDMA ALTGGKGFPFLFQHIRDGINIRQTCN LIFSLCRYNNRLAEHIVSMLFTSIK LTPEAANPFFKLLTMLMEFAGGPPG MPPFASYILQRIWEVIEYNPSQCLD WLA VQTPRNKLAHSWVLQNMEN WVERFLLAHNYPRVRTSAA YLLVS LIPSNFRQMFSTRSLHIPTRDLPLS PDTTVVLHQVYNVLLGLLSRKLY VDA AVHGTTKLVPYFSFMTYCLISK TEKLMFSTYFMDLWNLFQPKLSEP AIATNHNKQALLSFWYNVCADCPE NIRLIVQNPVVTKNIAFNILADHD DQDVVLFNRGMLPAYYGILRLCCE QSPAFTRLASHQNIQWAFKNLTPH ASQYPGA VEELFNLMLFIAQRPD MREELEDIKQFKKTTISCYLRCLD GRSCWTTLSAFRILLESDEDRLLV FNRGLILMTESFNTLHMMYHEATA CHVTGDLVELLSIFLSVLKSTRPYLQ RKDVKQALIQWQERIEFAHKLLTLL NSYSPELRNACIDVLKELVLLSPH DFLHTLVFPLQHNHCTYHHSNIPMS LGPYFPCRENIKLIGGKSNIRPPPEL NMCLLPTMVETSKGKDDVYDRML LDYFFSYHQFIHLLCRVAINCEKFT TLVKLSVLVAYEGSKSKCFLEANC GQFGSALFITNLISQYQNLQSDFSNR VEISKASASLNGDLRALAFAPVSTH SQTVPSSNSNSARAFKQMQLDSA TEKLTPRGKKPKERKTKDDEGGNS HLKGRAC*
2962	8459	A	3221	2170	3139	DLRALALLSVHTPKQLNPALPTL QELLSKCRCTCQQRNSLQEQEAKER KTKALALWTTITFRVGGGNTLG TGLRVVCSAEPKPKYK*KQN*LPTS PPNVILMTFREVSLLACVFTDDEGA TPIKRRRVSSDEEHTVDSCISDMKTE

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						TREVLTPSTSDNETRDSSIIDPGTE QDLSPENSSVKEYRMEVPSSFSED MSNIRSQAEEQSNNGRYDDCKEF KDLH\CSKDSTLA\EEEESEFPSTSISA VLSDLADLRSCDQALPSQDPEVAL SLSCGHSRGLFSHMQQHDILTLCR TIESTIHVVTRISGKGNQAAS
2963	8460	A	3222	3	344	PESHSAQAQGVQWPDLSLQSLP AFKQFSCSLPSSRDYRRASPRANF \*FLVETGFCHVSQAGLKLLASSDPP VSASQTARITGVSHHAQPRATFYRH KSVLVLPLKSPQ
2964	8461	A	3223	1411	1741	GYLQFSFSFFLFFFFFFFLLGESHSV T/RGLECSSVISTHCNLRPGSSDSR ASASRVARTRGMHHHTRQIFVFLV QMGFH\HVGQAGL/DSS*PSVVHPP\ RPPKVLGLQA
2965	8462	A	3224	361	462	RHLLSTETYCNSFF/RHSSSKNYTK LKRYE*VS
2966	8463	A	3225	3	89	
2967	8464	A	3226	1	336	VCQVCGFRSRLHTNVNRHLLLKNP KIFPHVCDDCGKGFSSMLEYCKHL NSHLSEGIYLCQYCEYSTGQIEDLKI HLDFKHSADLPHKCSDCMLRFGNE RELISHLPVHETT
2968	8465	A	3227	951	2075	RTANLNFCKILDKSQALNVNCPAET GL*LRANSRWP/PINCELCEFNSKYF SDLKQHMILKHKRTDSNVCRCVCKE SFSTNMILLIEHAKLHEEDP/N/YVCK YCEYKPVIFENISRHIADTHFRDPP\ HWCEQCDVQFSSSEL YLHFQEHSC DEQYLCQFCEHETNDPEELA*HVG K*GMHVN**ELSDKV/CNNGWNMG QYSLLSKITFDKCKNFFVCQVCGFR SRLHTNVNRHVAIEHTKIFPHVCDD CGKGFSSNNTWKRKRGGQKTFPLLI NLELSTSLTNYRGSPWASELSTSVE VSMAMLPAAEAETQGHDSGEREPF SQTPGLMQPFSIPVQITLQGSRRRQG RLPVLGDWRPFKLTCS SPALIIAQPI VGAQE
2969	8466	A	3228	2	415	LDPGSLAGFTSYIQFMYDEFVVEYE PTKADSYRKK/VAQDGEEVQIYIINT AGQEDYTAIKDNYFHCVFSITEMES FAATVDFKEQ/ILRVKKDENIPFLLV GNKSDLEDKRQVSIEEAKNRAD*W NVIYVETSPKT*AN
2970	8467	A	3229	607	1317	
2971	8468	A	3230	260	535	
2972	8469	A	3231	246	985	KLRHKMAANKPKGQNSLALHKVI MVGSGGVGKSALTQFMYDEFVED YEPTKADSYRKKVVLGDGEEVQIDIL DTAGQEDYAAIRDNYFRSGEGFLC VFSITEMESFAATADFREQILRVKED ENVPFLLVGNKSDLEDKRQVSVEE AKNRAEQWNVNYVETSAKTRANV D/KEWPFLKTRWWNTCKYISSHCPR

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						PAPVSRKTAHWAEVFFDLRMREIRARKMEDSKEKNGKKRKS LAKRIRERCCIL
2973	8470	A	3232	1	634	MAANKPKGQNSLALHKVIMVGS GVGKSALT\AQFMYDEFVED*E\PTK ADSSRKVVLDGEEV\QIGYPLDTA G\QED\YAAIRD\NYFRSGEGFLCVFS ITEMESFAATAE\FREQILRVKEDEN VPFLLVGNKSDLEDKRPGL*EEAK\ NRAEQWNVNYVETSAKTRANVVK VFFDLRMREIRARKME\EFYYLNGTK NTKRLAERIREGGCIL
2974	8471	A	3233	314	373	
2975	8472	A	3234	1	2129	PSVAGAATLWFHVTLPCARLCGR RSCTHSGIITEFHFFHL/PFRPIPLAC GNDDCRIHIFAQNDQFQKVLSCG HEDWIRGVWAAFGRLDLSASCSQ DCLIRIWKLYIKSTSLETQDDDNIRL KENTFTIENESVKIAFAVTLETVLG HENWVNAVHWQPVFYKDGVLQQP MRLLSASMDKTMILWAPDEESGV WLEQVRVGEVGGNTLGFYDCQFNE DGSMIIAHAFHGALHLWKQNTVNP REWTPEIVISGHFDGVQDLVWDPEG EFIITVGTDTQTRLFAPWKRKDQSQ VTWHEIARSQIHGYDLKWLAMINR FQFVSGADEKVLRFVFSAPRNFVGKF LCHYR\KSLNHVLCNQDSDLPEGAT \APALGLSNKAVF/LREDKAPQPPDE EELLTSTGFYQQVAFQPSILTEPPT EDHLLQNTLWPEVQKLYGHGYEIF CVTCNSSKTLASACKAAKKEHAAI ILWE\TTSWKQVQNLVFHSLTVTQ MGLLT**GSFLLGCFPEDSNLVIVEK AWIQS/TPEFEPVFSLFAFTNKITSVH SRIIWSCDWSPDSKYFFTGSRLDKKV VWGECDSTDDCIEHNIGPLPPSVL DRGWGCDQLSASACSHPSQRYVV AVGLECGKDLLIYLGKRLIKFQK*M T/ATHCVGNKSKPKVIHWAIQKIYC WEGICSGKT*TRREGRRC*VVYTFA SCG*DHTVKIHRVNKCAL
2976	8473	A	3235	451	778	GSGRWKSRVARAGMQISGAHLQL NCKPPPPGLKADPPWLSLPSWDP QMCPTPWLLFVCLVETGFTMLPQ AALQLLS*SDLSA*ASQNAGITGMS HHAGPDTVPLF
2977	8474	A	3236	1	186	FFFEMESRTVTQAGVQWHDLG\SL QPP\PPG\SSDSPVSASHVAITGAHH HTWLIFFFLFL*GVQWHDLGTLAT SSLLGSSDSPVSASHVAITGAHHH TWLIFFFLFL
2978	8475	A	3237	1	353	KIWLFFVFKTDVSLVHPRLECSGAI SAHCNLHLPGLSDSHTSAFRVAGTT GARHQAQLIFTFLVEMGFHHVGH GLKLPT*EIRPPRPPEVLGLHACAT VPGHKYVNEPIKMVLLK
2979	8476	A	3238	3	453	GQTGTWQGNTGQRPQLPPHPPPIH

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						LVSRRHGKLRHGFRLRPMPEPRGLES GKTGSARGVAACTSP*GRSGVQGGG PRDIAQQGGCRGSACGRRSHEALRP RVWCGEGPQWTWCAVCPNRSAP GAGLAD\RQHPGESRAWGETRLCE AGGAE
2980	8477	A	3239	232	472	LHSFIHSFIHLFIYLFDRVLLCCPDW STVERSQLTVTLKSRVVK*SSCLS/LP SSWGYRSVPPCPANYFYFL*RQRLT TLPS
2981	8478	A	3240	2	345	MVHVAVAGLNGTHSCPPASSSVLTF GHPWHEQLQQSVGPTSPHSPLL*PL SSLEVLGWGSEGVGGLQEIQKCSK ALPCKTPCGCFCIYLIFSPTQGDFIPH DPAPPLLLSASWV
2982	8479	A	3241	205	361	DAHSPAPAVSTPGQAWAAVLAMFP PGPWGEGSGRL\IPHPAPPLLLSAS WV
2983	8480	A	3242	137	959	IPFPVMLDPAGRQQQRWGRIMGY KVSLLGA*NLGRCKNIHKGSCREGL CLISLRAWEGRVLGEGFAQN*HTA HPEPGKSSHS*KIPFQRESGL*PATH PVPSKTPPLPGESSRARAWCLKGE DPCPRKPPAP*SLPPGPWGE/P*QGL QPRLGL*EQPGLGYEHLKFPF/PSA PAA*PPG\PAKAQAPRKSCAPT/TH ALLPPNPLPTQLGWKWISADQSQSN PFPRAYP/REPSLFPSNAPLSPSPHP TTFPEFPCSTPPPQIPHPQDFPRS
2984	8481	A	3243	23	438	SRHLGLPKCWDYRQEPLCLALSFFF RVRVS\VAQVVVQWHDGSLQPQ TPGPK\YPPATAS*VAGARLIFK*FL *RWDLTIMPKAGLKL PATGDPPACL LLSFSLIPTGGFTRFEPTRHSLLLEV GLSPMLVRHWLWA
2985	8482	A	3244	1	1061	ASRRALQLFGIPVRQLQKGACPLGL HQLSSPRYKFNFIADVLFKIAPAVV HIELFLRHPLFGRNVPLSSGSGFIMS EAGLIITNAHVSSNSAAPGRQQLK VQLQNGDSYEATIKDIDKSDIATIK IHPKKKLPVLLGHSDRTCRPGEVL WVAIRQIPSP*QNTVTTGIVSTAQR EGRELGLRDSMDY\QTDAINNYG NSGGPLVNL DGEVIGINTLKVTAGIS FAIPSDRITRFLTEFQDKQIKDWKKR FIGIRMRTITPSLVDELKASNS\DFPE VSSGIYVQEVVPNSPSQRRGGIQQGDI IVKVNGRPLVDSSELQEA VLTESPL LLEVRRGNDLLFSIAPEVVM
2986	8483	A	3245	1	268	QGSPSRDPSPLGGPNGGI FLAP/AGP NPP/RGTRGNPVFS*NSKICPGWGGP PVGPGS/RGELG*RAALAPGGPGGL DWAPGP*PGGQRGAPF
2987	8484	A	3246	20	353	KEVGRLTHSVNHSGGREKYVWHP GNAL*Y\GKLPVLPPIFIVNR*VQ*P *PERHMTVRGSGMNVWIMP/PGKPP RPAEVPVEVEGHLEWTAEDSSNHC QLQG*DQLQWGRWL



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2988	8485	A	3247	2	322	KLDNSSKWLENGTFDLSILQDLDNF C*KMGKWSEVPYVQAFFSIHSLPSL CSQCHL/CPDFPSFSP/YPLLLSPQT QSPLNPPFPLTPLTSLPRLLARLN QVPILP
2989	8486	A	3248	141	924	PFSSQTVKLSSGGATRNPVSSPKASG GQPSEGWEVALEGDSALMRQQ CPGLLKSRK/RAPGNPTASGS/APGA TKRSLGGRARRGLEFVVSRFFGGGR AQSSLGNAHPHSGTIPKAPHASQQG LGLRLGGLEPSTPPWVHPPARPRAS PDPSRVAGSPRSLPNPPAAGKGGRG SGEEARYFDLS*ILKSLPYGHERVY QEPQRGVKTSCSCSPF/HLPLLLFQS SPPPSTLVGAGLKIGFLRCPVGGILI GKGFFFNCLHST
2990	8487	A	3249	1	363	QVSLVINWDLPTNR*NYIHR*AYIW NTPLPLHTWPSLGLKLLIFLIFLEFQ VGRGGRLDRKGGAINKGTEYDERT LRDIETFYNTSIEEMPFNVADHMLM GCPATQPLSGLIIGASDQY
2991	8488	A	3250	1	87	LNETVLLWHSGWMSTVVQTQLLPA ASTWVKQSSHLSLLNSWDHSR\VP PHWANFLIFCR/DRSFAMLPKLVSN PWAQAVLPPLPIVL*LNETVLLWH SGWMSTVVQTQLLPAASTWA
2992	8489	A	3251	3	270	CFNSAWTEPGARSPPRPAHSQPSV TSSPHRTAPRPPPLQR\PS*SP*R PRPP/PHVRHNYPSGLKSHH*SAE*P GPLGPIPTVY
2993	8490	A	3252	3	452	
2994	8491	A	3253	1	477	TLLVPQDSERTHPWCLSPADKTNV KA\AWGKVGAGAHAGEYGAEALERM FLSFP\TTKTYFPHFD\LSHG\SAQG* RAHGK\KVA\DALTKAVAHV\DDMP KRRCP*SDLHGAQAFGWDPVQLQ SS*SHLPCLGEPWAAHLRPSFNPW RLQRLPWGQISWGFC
2995	8492	A	3254	3	295	LFLFFFFFF*MESHVTRLECSGTIW AH*NLHLPGSSDSPALASRVAGTTG MCHHIQLIFFVFLVEKGFHHVG*/D MSLSLDLVIHPPWPPKVLGLQA
2996	8493	A	3255	306	519	GTRVERHSRERPSCHLLCEPSQRY PLLFLVGL*CPPASPGKSPRTKENNF TADSKSQGQSEKSLWVTLA
2997	8494	A	3256	453	626	HGSCLLHHREQVPIPPGIPNLSDSIL* FPVLRIWMLCLYTSCMWFSQSFVI AVMYFV
2998	8495	A	3257	1537	1909	NVLTVEDHPIPIPSKNRPFHNLLPVN LAFFFFFLNRVSFCHLGWSAVARS HLTCNLLSPGFKQFSCSLSSWDY QACMHHTRLVFGVFSRDGGFTMLA RLVSNS*PQVILPPLPPKVLGLQA
2999	8496	A	3258	1	342	KTESHSVAQAGVQWCDLGSLLQPPP PRFKLFSCSLSSWDYRGALPRPT DLFA/QFLVEMGFCHVAQAGLELLS SGNLFASASQTARITGVNHHTWPVL

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						*F*VKKIPPSLPGLL
3000	8497	A	3259	1	338	FFLRWSL/NSVAQAGVQWRNLSSL QALPPGFRPFSCSLSPNS*DYRCPP RLANFFLYFLVETVFHRLY*RSRMV LIS*PGDPPTSASHSAVVRILLRRRQ CLRQGLCRASVF
3001	8498	B	3260	188	1504	MRTLLPPALLTCWLLAPVNSIHPEC RFHLEIQEEETKCAELLRSQTEKHK ACSGVWDNITCWRPANVGETVTVP CPKVFSNFYSKAGNISKNCTSDGWS ETFPDFVDACGYSDPEDESKITFYIL VKAIYTLGYSVSLMSLATGSIIICLF RKLHCTRNYIHLNLFSLRAISVL VKDDVLYSSSGTLHCPDQPSWVG CKLSLVFLQYCI MANFFWLLVEGL YLHTLLVAMLPPRRCFLAYLLIGW GLPTVCIGAWTAARLYLEDTCWD TNDHSPVWWVIRIPILISIVNFVLFIS IIRILLQKLTSPDVGGNDQSQYKRLA KSTLLLPLFGVHYMVFAVFPISISSK YQILFELCLGSFQGLVAVLYCFLN SEVQCELKRKWRSRCPTPSASRDYR VCGSSFSRNGSEGALQFHRGSRAQS FLQTETSVI*
3002	8499	A	3261	1	1047	MVSISWPRDLPASASQSAGITGLIGA LVLSVGIYAEVER/HEI*NP*KCLPGS SHHPHPGRRHVHGLLHWCAGVPP *QPPELLASRLSRGYGLVLSWLEP RYEKMISGMYLGEIVRNILIDFTKK GFLFRGQISETLKTGRGIFETKFLSQIE SDRLALLQVRAILQQGLNSTCDDS ILVKTVCVVSRRAAQLCGAGMAA VVDKIRENRGLDRLNVTVGVDGTL YKLHPHFSRIMHQTVELSPKCNVS FLLSEDGSGKGAALITAVGVRLRTE ASS
3003	8500	A	3262	178	568	IFFFFFFKMECSVAQAGVQWWDL SSLQPLPPGFMPFCLSLPSSWDYRR PPLL PANFLYF**RRGFTVLARMVSI S*PCDPPASASQSAGITGVSHCAQLE SKFYEGRDVHLFCSPLYFQKARKLP GIE
3004	8501	B	3263	776	5218	MLGDNSSMSVTAPKTFQWDMMW RRKGLILIALCRPKEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEDQLDT MLWDSSTNLTNTALSKEKTMFSSR AKIVKPNGEKPDEFESGISQALLELE MNLDLKAQLWELNITAAKEIEVGG GRKAIHIFVPVPLKSFQKTQVQLRR ILPKPTQKSC TNNKQKLPRSCTLTA VHDAILEDLVFPSEIVGKRIHVKLD GSHLIKIHLEAQNNVEHKVEPFS GVYKKLMGKDVNFEPFQMLPGT PGSLEMGLLTFRDVAIEFSPEEWQC LDTAQQNLYRNVMLNENRNLAFLG IALSKPDLITYLEQGKEPWNMKQHE MVDEPTGICPHFPQDFWPEQSMEDS

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						FQKVLLRKYEKCGHENLQLRKGCK SVDECKVHKEGYNKLNQCLTTAQS KVFQCGKYLKVFKFLNSNRHTIR HTGKKCFKCKKCVKSFCIRLHKTO HKCVYITEKSCCKCECEKTFHWSST LTNHKEIHTEKPYKCEECGKAFKQ LSTLTTHKIIICAKEKIYKCEECGKAF LWSSTLTRHKRIHTGEKPYKCEECG KAFSHSSTLAKHKRIHTGEKPYKCE ECGKAFSHSSALAKHKRIHTGEKPY KCKEKGKAFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTKHKIIH AGEKLYKCEECGKAFNRSSNLTIHK FIHTGEKPYKCEECGKAFNWSSSLT KHKRFHTREKPFKCKEKGKFIWSS TLTRHKRIHTGEKPYKCEECGKAFR QSSTLTKHKIIHTGEKPYKFEECGK AFRQSLTLNKHKIIHSREKPYKCKE CGKAFKQFSTLTTHKIIHAGKKLYK CEECGKAFNHSSSLSTHKIIHTGEKS YKCEECGKAFLWSSTLRRHKRIHTG EKPYKCEECGKAFSHSSALAKHKRI HTGEKPYKCKEKGKAFSNSSTLAN HKITHTEKPYKCKECDKTFKRLST LTKHKIIHAGEKLYKCEECGKAFNR SSNLTIHKFIHTGEKPYKCEECGKAF NWSSSLTKHKRIHTREKPFKCKEKG KAFIWSSTLTRHKRIHTGEKPYKCE ECGKAFSRSSSTLTKHKTIHTGEKPY KCKEKGKAFKHSSALAKHKIIHAGE KLYKCEECGKAFNQSSNLTHKIIH TKEKPSKSEEDKAFIWSSTLTEHK RIHTREKPYKCEECGKAQSPSHLT THKRMHTGEKPYKCEECGKAQSQS STLTTHKIIHTGEKPYKCEECGKAFR KSSTLTEHKIIHTGEKPYKCEECGK AFSQSSTLTRHTRMHTGEKPYKCEE CGKAFNRSSKLTHKIIHTGEKPYK CEECGKAQSSSTLNGHKRIHTREK YKCEECGKAQSQSSTLTRHKRLHTG EKPYKCGEKGKAFKESALTKHKII HTGEKPYKCEKCKAFNQSSILTNH KKIHTITPVIPLWEAEAGSGRQE METILANTVKPLLY*
3005	8502	A	3264	1	208	RDRVLF*HPHWSAVV*SKLTAASTS WVK*FSCLSFLSWCLAMLRLVLN SWPQVTLPPQPPKVLGLQV
3006	8503	A	3265	78	359	RHSSKNLGNVDSECE*T*FPDIIPFH* KKLTEGEYQKSVNH/MTNAVAHST LSSQLLLALQKTLCLFLMLLTKL PTIIHRTVDAHSLADDDVE
3007	8504	A	3266	48	330	VCGCVWMLRVLFYCYP\GW\SAVAQ S*LTAALISL\VNPSSSLSPSSWDHR RAPPRPANFFNL*RQELPMLLRVL/ NVWAQVILPPWPPKMLELQV
3008	8505	A	3267	200	1033	RSLAPRWHLGHKEKNVTTSVWG WSPGRNASNSAGVGAGLPFVSTW LAVSSKNIDITEHIDFATPIQQPAME

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PLCNGNLPTSMHTLG\HLHGVSNP QPCTYTGESQLTEVLQNLGQR/RNI HNSRLNRLAPRM/LQSFGKEPRPSW VL/CPAWQALYWRV*RPKERRPIEL PSAQLRHYGP\PMKDVPLISLANIL PQLPSSGNDVIVATHGQ*SLHHTL L*TPFHLGNVYVAMEEFKALVWY ESTLASLQPEFVPAKNRIQTIQCHLM LKKGRALLP
3009	8506	A	3268	2	2956	LADSSPSNLQIIKELLSMHQPDPA LTKEFDYLPVDSRSSSGFVGLRNG GATCYMNAVQQLYMQPGLPESLL SVDDDDTDNPDDSVFYQVQSLFGHL MESKLQYYVPENFWKIFKMWNKE LYVREQQDAYEFFTSLIDQMD EYL KKMGRDQIFKNTFQGIYSDQKICKD CPHRYEREEAFMALNLGVTSCQSLE ISLDQFVRGEVLEGSNAYYCEKCKE KRITVKRTCICKSLPSVLVIHLMRFGF DWESGRSIKYDEQIRFPWMLNMEP YTVSGMARQDSSSEVGENGSRVDQ GGGSPRKKVALTENYELVGIVIH SGQAHAGHYYSFIKDRRGCGKGK WYKFNDTVIEEFDLNDETLEYECFG GEYRPKVYDQTNPYTDVRRRYWN AYMLFYQVRSDQNSPVLPKKSRSVS VVRQEAEDLSLAPSSPEISPQSSPRP HRPNNDRLSILTKLVKKGEKKGLFV EKMPARIYQMVRDENLKFMKNRD VYSSDYFSFVLSLASLNATKLKHPY YPCMAKVSLQLAIQFLFQTYLRTKK KLRVDTEEVIATIEALLSKSFDAQ WLVEYFISSEGRELIKIFLLECNVRE VRVAVATILEKTLDALFYQDKLKS LHQLLEVLLALLDKDVPENCKNCA QYFFLFNTFVQKQGIRAGDLLRHS ALRHMISFLLGASRQNNQIRRWSSA QAIREFGNLHNTVALLVLHSDVSS QRNVAPG\IFKQRPPIAPSSPLLPL HEEVEALLFMSEGKPYLLEVFMFAL RELTGSL\ALIEMVVYCCFCNEHF SFTMLAFHLRNQLAETAPPEFKGI RFPTTFMEILVIEDPIQAERV\KFVFE TENGLLALMHHSNHVDSSRCYQCV KFLVTLAQKCPAAKEYFKENSHHW SWAVQRLHH\KMSDLYWTPLSNVS NETSTGKTF*RTISDHDTPYATALL NEKEHSGSRNGSKSRPANENGHRH LQQGSQSPDDWVSLRSDLDVDP
3010	8507	A	3269	68	301	NFRDLCDILCSETTRLNTINMSIL SNLTYRFSEIPF*IFRRLFVL*KL/ENS ILKYIWTCKGPRLVKTTFKNNSES
3011	8508	C	3270	224	518	MINKGQAGANIKSNXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXX*
3012	8509	A	3271	342	724	NTYPWAVL/VFFFFFLRWSTLVAR

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						LECRAGVQWCDLGSLQPLPPQ\FE* FSCLSLQLALPRPAKFFVILVEM\GF TMLAKMVSIS*PCDPPALASQSARIT ILDFMLAPACPLLIIPFTWTLFFRNTI
3013	8510	A	3272	3	367	
3014	8511	A	3273	58	553	VARSAPPDGAVCAGPGSRRTMAE QSDEA\K\Y\YTLERFQMHN\HKSST WLILHHKG\YDLTKFLEEHPGGEEV LREQA\GGD\AATENFEDVG\HSTDAR EMSKTFIIG\ELHPVDRPKLNKASGT FKGCV*GNLFTTI*FLVPSWWTNW \VIP\AISAVGRRLLGCIRL
3015	8512	A	3274	41	400	KRLGPRGGVGPSPNGGNQGL*GPKI FPWPSTLGTK/GEPLSSSSSSSPQK RGFPSSPEK\APGVPPPTPKGPSPPGG GVKKKGRA*KKKPLGLWEKGPNPA PGGPGTPTFGGPPGQYPG
3016	8513	A	3275	3	146	WGVITMMVTC\SV/A/CTLFWLIAIL AQCNP\LYRP*LKDETTWYLKHHWP
3017	8514	A	3276	161	472	
3018	8515	A	3277	3	273	AAAPGNGRASAPRLLLLFLVPLLW APAAVRAGPDEDLSHRNKEPPAP SSCSRSLWAVQGPEPARVEVSGPG WGERGCRAECAEYQAPGL
3019	8516	A	3278	124	672	FQRTKLLNGPGDVETGTSITVPQKK WLHVISPIFVQSLTLPFLAKWGDR QLLQIELAAREVSDI*EETV*NETYL LLCSRKTLDTLKWASIPSARLF YI**FSCSLKLAFSQFLPADPYGVA VGGTVGHCLCTGLAVIGGRMIAQKI SVRTVTIIGGIVFLAFAFSALFISPDS GF
3020	8517	A	3279	2	991	AAAAPGNGRASAPRLLLLFLVPLL WAPAAVRAGP\DEDLSHRNKEPPAP \PSSCSRSLWAVQGPEPARVEKIFTP A\APVHTNTEDPATQT\NLGIYPMQF VAIIQLL\IVSEIGVSRT\FFIAAIMA MRYNRPGPCWAGAMLCL/AGLMT CLFS/VLFGYATTVIPRGLYILMFQP VLFAIFGIRMLREGLK\MSPDGQEE LEEVQA\ELKKKDEEFQRTK\LLNG\ PGDVETGTSITVPQKKWLHFISPIF GQALTLTFLAEWGDRS*LTTIVLAA REDPYGVAVGGTVGHCLCTGLAVI GGRMIAQKISVRTVTIIGGIVFLAFA FSALFISP
3021	8518	A	3280	1	278	QHDLDQVDVAFTEEE*RLAGPAQR KLYRDVIVENLRNLLSVGHPPFKQD ISPIERNQDLWIMTTATRIPGNLGKN QTVISSYSKLFICFASS
3022	8519	A	3281	263	588	DSALPQKEELKMNMFKEAVTFKDV AVAFTEEELG\LLGPAQRKLYRDVM VEN\FRNLLSVGHPPFKQDVSPIER NEQLWIMTTS/TPRRQGNLDTLSVK ALLLYDLAQT
3023	8520	A	3282	1	1285	MEDSELPSARSVLPSKRIGVVQSQQ RPPLGERHYGPTTRDGALHSAYSPT

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						QARCVSHPTYEKYPHVWRGWPPFS PEKERQRLENLRRKEEAQLRRQK VEEDKRRRLLEEVKLKREERLRKVL QARERVEQMKEEKKKQIEQKFAQI DEKTEKAKEERLAEKAKKKAAAK KMEEVEARRKQEDARRLRWLQQ VRAQ/EGNRSREVK*HLKSHEPVCS GGDSRTHPQPLVHAWSQLP*RLA RVLRELQEREKALRLQKEQLQRELE EKKKKKEEQQLAERQLQEEQEKKA KEAAGASKALNVTVDVQSPACTSS PITPQGHKAPPQINPHNYGMDLNSD DSTDDEAHPRKPIPTWARGTPLSQA IIHQYYQPPNLELFGTILPLDLEDIF KKSKPRYHKRTSSAVWNSPPLQGA RVPSSLAISLKKH
3024	8521	A	3283	3	262	FHTEERSYECTECGKA\FKHSSTLLQ HRKVHTPERRQEDRAHGKVVC*H RVHQERSYSRKEVKESGRESAIRKK LNLAHPNTHPRE
3025	8522	A	3284	1	269	FFFFPQIGSHPI\RLCSDAITFCCSL NLPGRDPPASAS*VAETTGLHHHA GLIF*FFVE/MGL/HQAGLELLDKVIL PPLPPKELGSQM
3026	8523	A	3285	3	1191	KSCFNAFFNFEDMQEITQHFAVCH VDAPGQQEGAP/SPFPTGYQYPTMD ELAEMLPVLTSLSLKSIIGVGVGAG AYIL\SRFALNHPELVERPLCSLMVD PC/ALKGWIDWAASKLSGLTTNVV EIILAHHFGQEELQANLDLIQTYRM HIAQDINQDNLQFLNSYNGRDLE IERPILGQNDNKS\TLKCTLLVVG DNSPA\VEAVMADCGGLPHVVQPG KLTEAFKYFLQGMGYIPVCAAQSPE HRVSTASMTLARSRTHSTSSSLG SGESPF\SRSVTSNQSDGTQESCESPD VLDRHQ\TMEISLDDVLLSALLRNN GKSAQ\QKKISAKPKLEFLCPRPGTC DHGSRKFCYTVLVDPRERSKATAV ALGSFPAGGPAELSLRLGEPLTIVSE
3027	8524	A	3286	3	638	SSKLSGLTTNVVDI\LAHHFGQEELQ ANLDLIQTYRMHIAQDINQDNLQFL L\KSYNGRRDLEIERPILGQNDNKS TLKG\STLLVVGDNSPA\VEAVVECN SRLNPINTL\KLMADCGGLPPG*FS PGKLTEAFKYFLQGMGYIPLVLCYS TSGSMTSVARSR\THSTSSSLGSGES PF\SRSVTSNQSDGTQESCESPDVL DRQQTMEVSC
3028	8525	A	3287	1	407	FSIETESCSVAQAGGKWHDSGSLQP QPPRFK*FSCSLLSNWDYRAPP/* PG*LFFVFLVETGF/IHVGPGLKLL TSSDPPTSASQSAGITGLRDRAQPPP EDSNVQFENHWQRECTMLLFTLGP LKLFP\TELML
3029	8526	C	3288	157	468	MHHIHNASRTFQLIFSSFP\RGNAIVF MLKMGGFLELRGPRSGMDHHRGR GEANQ\FCPTSPAACGQNLPIKHGL

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						PRWSTKGETTADTDSVDLENPILYK YFQL*
3030	8527	A	3289	14	348	EFHSCRPGWSAMTQSRLLQPPPPG FK*FSCSLSSWDYRHTPPHPASF* LLVDTGFLHVGQAGLKLLTSGDSP TSASQSARITGVNHCARPSTFLRLQ RKAGRCSTSL
3031	8528	A	3290	1	2201	MTNLAMVERDSEAGTAASRFPGNH AAKGKAQAHYKVWRPAEVRCLKL GPEWVTLRYTIKHPYKLCGKRQH VFFFTSRSDVGFMLTLKPFGSVSV ESKMNNKAGSFFWNLRQFSTLVST SRTMRLCCLGLCKPKIVHSNWNILN NFHNRMQSTDIIRYLFQDAFIKSDV GFQTKGISTLTALRIERLLYAKRLFF DSKQSLVPVDKSDDELKKVNLNHE VSNEDVLTKETKPNRISSRKLSEEC NSLSDVLDAFSKAPTFPSSNYFTAM WTIAKRLSDDQKRFEKRLMFSPAF NQLCEHMMREAKIMQYKYLFLSLH AIVKLGIPQNTILVQTLRLVTQERIN ECDEICLSVLSTVLEAMEPCKNVHV LRTGFRILVDQQVWKIEDVFTLQVV MKCIGKDAPIALKRKLEMKALREL DRFSVLNSQHMFEVLAAMNHRSLI LLDECSKVLDNIHGCLRIMINILQ SCKDLQYHNLDLFKGLADYVAATF DIWKFRKVLFILFENLGFRPVGLM DLFMKRIVEDPESLNMKNLSILHTY SSLNHVYKCNKEQFVEVMASALT GYLHTISSNLLDAVYSFCLMNYFP LAPFNQLLQKDIISELLTSDDMKNA YKLHTLDTCLKLDDTVYLRDIALSL PQLPRELPSSHTNAKVAEVLSSLLG GEGHFSKDVHLPHNYHIDFEIRM/D TNR/NQVLP/SLDVGTTSAT/DIQR LTYISFAGLSELKS
3032	8529	A	3291	3	485	LHTLDTCLKLDDTVYLRDIALSLPQ LPRELPSSHTNAKGGQRS*AALLGG EGTPPSKDVHLAPHNYHIDFEIQN GTPNRNPSAYPLS/DVDTTSCLOIFK E*LCYVFPRSA YCLGSSHPRGFLAM KMRHLNAMGFHVILVNNWEDGQT RDGRCQSPFLKT
3033	8530	A	3292	1	530	LRKTFIPNRPLILLPPGNSLATHLFF ETVSRSVAQAGVQWHHLGLLQSPS PGFKRFSCSLSPSNWDYRHAPRLA NFYIFS*DGVSFHHVGQAGLKLLTS GDPLTLASQSAGITGVSHCTRPLIHK FGLSYRQRIENVSFLLPYTHASSLLQ LLLAPLVNTGQGQEQKPELVREVG
3034	8531	A	3293	115	463	VTKQLFNLSFIFHTSILIFFFLKME SCSVA/RLECSGTILAHCNLCPLGSS NSPASASRVSWDYKVCATMPG*FL YF**EQGFHHVGQAGLRTPGPQGD PARPWAPKVLGLQA
3035	8532	A	3294	503	1055	DIDFSPV*LVNVQMRRHALLMNLW DT/QDSHTSLRNAEYCSLMEEDMAP

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						SNKTTWLRPLTQQF*NLPQKKTLLA KK*KDFTHRVLF*TA*MCLPQSSSLW HL*NWKQSKCPSVGDWEH*FVQW GTPYQKEE*GTPIDKGQSTYNIMQI YICFFLKQYKDKNLKWLWRTGVS GGSETEIDSEVISGL
3036	8533	A	3295	3	304	FFLVETEFCCHAAQAGVQWCDLGLSL QPPPPGLQSSHLNLPKS*DYRCEPP MPG*FLETGFHPSCPRLVPKLLGSSS PPASAS\QSIGIS\GVSHCPEKPPF
3037	8534	A	3296	324	650	KKEHRVTCFSFWEMESRSVA*AEV Q*HDLDSLQPLPHGLKRVSCSLSPSS WDYRHLPPCLTNVCIFSRNGVSLY* PGWS\RTPDLVILPALAPQSAGITGG EPPCPATK
3038	8535	A	3297	2	564	FFFFPPQPPSPGFKQFSCSLTLPSSWD YRCPPPRPANF*FLIETGF/VHVQQA GLELLTSGDLPTPASQNAIGITGVRP GTQPASCF*MWQGLIGQNKMTISLL LQSILL
3039	8536	A	3298	352	392	
3040	8537	A	3299	20	200	FTLIQNCFHEIQIEQCGLDAVAHTY NPSTLGGQGG*IA*AQEFETSLGNM VKPHLSLKF
3041	8538	A	3300	971	9082	
3042	8539	A	3301	1	15447	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTPLYQSPVKELDKFKL DLGRNVPSNRHKSRLTVKTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYFSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYIAIHDETSYKGGKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QLDYKEAKCNKEKLQLFITPEADS LSRKTSVSQTSLEAKKWLRGIFD GQPERINTADYVGNYLYENNSNSTI AENDKNHLSEKQDTYLSNSSMSNS YSYHSDEVYNDSGYLSKNKLDSGIE PVLKNVEDQKNTSFSKVISNVKDA



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						NAYPQTVNEDICVEELVTSSSPCKN KNAAIKLSISNSNNFEVGPAPFRIAS GKIRLCSHETIKVKDIFTDSFSKVI KENNENKSKICQTKIMAGCYEALD DSEDILHNSLDNDECSMHSKVF DIQSEEILQHNQNMGLKSVKISPC DVSLETSDICKCSIGKLHKSVSANT CGIFSTASGKSVQVSDASLQNAQV FSEIEDSTKQVFSKVLFSKNEHSDQL TREENTAIRTPEHLISQKGFYNVNVN SSAFSGFSTASGKQVSILESSLHKVK GVLEEFDLIRTEHSLHYSPTSQRNV KILPRVDKRNPEHCNVSEMEKTCSE EFKLSNNLNVEGGSSENNHSIKVSP YLSQFQQDKQQLVLGTVSLVENI HVLGKEQASPKNVKMEIGKTETFS DVPVKTNIEVCSTYSKDSSENYFETE AVEIAKAFMEDDELTDKLP SHATH SLFTCPENEEMVLSNSRIGKRRGEPL ILVGESIKRNLLNEFDRIENQEKSL KASKSTPDGTIKDRRLFMHVSLEP ITCVPFRTTKERQEIQNPFTAPGQE FLSKSHLYEHLTLEKSSSNLAVSGH PFYQVSATRNEKMRHLITTGRPTKV FVPPFKTKSHFHRVEQCVRNINLEE NRQKQNIIDGHGSDDSKNKINDNEIH QFNKNNSNQAAA VTFTKCEEEPLD LITSLQNARDIQDMRIKKKQRQV PQPGSLYLAKTSTLPRISLKA AVGG QVPSACSHKQLYTYGVSKHCIKINS KNAESFQFHTEDYFGKESLWTGKGI QLADGGWLIPSDGKAGKEEFYRA LCDTPGVDPKLISRIWVYNHYRWII WKLAAMECAFPKEFANRCLSPERV LLQLKYRYDTEIDRSRRSAIKKIME RDDTAAKTLVLCVSDIISLSANISET SSNKTSSADTQKVAIIEITDGWYAV KAQLDPPLLA VLKNGRLTVGQKIIL HGAELVGSPDACTPLEAPESMLKI SANSTRPARWYTKLGFFPDPRPFPL PLSSLFSDGGNVGCVDVIIQRAYPIQ RMEKTSSGLYIFRNEREEKEAAKY VEAQQRLEALFTKIQEEFEEHEEN TTKPYLPSRALTRQQVRA LQDGAE LYEAVKNAADPAYLEGYFSEEQLR ALNNHRQMLNDKKQAQIQLEIRKA MESAEQKEQGLSRDVTTVWKLRIV SYSKKEKDSVLSIWRPSSDLYSLT EGKRYRIYHLATSKSKSKSERANMP AGRTV*K*SKKQKSFYKRRGLGCS MSPSTTFKSGIQ*Y*LSIPEKSF*S*K CQHSYFNSYFQGCSVKPSHDF*RQR IIQNVRQAQR*QL*I*C*INQKYSHG KESRCMCFK*KL*KR*AVAT*KIHE SSITFKKGTINQNTNLRVIQKNQEE TTSISKITVNPDSSELFSDNENNFVF QVANERNNLALGNTKELHETDLTC VNEPIFKNSTMVLYGDTGDKQATQ

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						VSIKKDLVYVLAEEKNSVKQHIK MTLGQDLKSDISLNIDKIPEKNNDY MNKWAGLLGPISNHSFGGSFRTAS NKEIKLSEHNIKSKMFFKDIEEQYP TSLACVEIVNTLALDNQKKLSKPQS INTVSAHLQSSVVVSDCKNSHITPQ MLFSKQDFNSNHNLTSPQKAEITEL STILEESGSQFEFTQFRKPSYILQKST FEVPENQMTILKTSEECRDADLHV IMNAPSIGQVDSSKQFEGTVEIKRKF AGLLKNDNCNKSASGYLTDENEVGF RGFYSAHGKLVNSTEALQKAVKL FSDIENISEETSAEVHPISLSSSKCHD SVVSMFKIENHNDKTVSEKNNKCQ LILQNNIEMTTGTFVEEITENYKRNT ENEDNKYTAASRNNSHNLEFDGSDSS KNDTVCIHKDETDLFTDQHNICLK LSGQFMKEGNTQIKEDLSDLTFLEV AKAQEACHGNTSNKEQLTATKTEQ NIKDFETSDTFFQTASGKNISVAKES FNKIVNFFDQKPEELHNFSLNSELHS DIRKNKMDILSYEETDIVKHKILKES VPVGTGNQLVTFQGQPERDEKIKEP TLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPKCKE MQNSLNNDKNLVSITVPPKLLSD NLCRQTENLKTSSIFLKVKVHENV EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNYLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDSGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNNFEVGPPAF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDECSTHSHKV FADIQSEEILQHNQNMMSGLEKVSIS PCDVSLSDICKCSIGKLHKSVS NTCGIFSTASGKSVQVSDASLQAR QVFSEIEDSTKQVFSKVLFSNEHS DQLTREENTAIPTPEHLISQKGSYN VVNSSAFSGFSTASGKQVSILESSLH KVKGVLEEDLIRTEHSLHYSPTS QNVSKILPRVDKRNPEHCNVSEME KTCSKEFKLSNNLNVEGGSSENNHS IKVSPYLSQFQDKQQLVLGTVKVS VENIHVLGKEQASPKNVKMEIGKTE TFSDVPVKTNIEVCSTYSKDSYNYF ETEAVEIAKAFMEDDELTDKSLPSH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEPSIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRTTKERQEIQNPNTA PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITGR

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						PTKVFVPPFKTKSHFHRVEQCVRNI NLEENRQKQNIDGHGSDDSKNKIN DNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEDYFGKESLW TGKGIQLADGGWLIPSNDBGKAGKE EFYRALCDTPGVDPKLIISRIWVYNH YRWIIWKLAAMECAFPKEFANRCL SPERVLLQLKYRYDTEIDRSRRSAIK KIMERDDTAAKTLVLCVSDIISLSA NISSETSSNKTSSADTQKVAIIELTDG WYAVKAQLDPPLLA VLKNGRLTV GQKIILHGAELVGSPDACTPLEAPES LMLKISANSTRPARWYTKLGFFPD RPFPLPLSSLFSDGGNVGCVDVIIQR AYPQWMEKTSSGLYIFRNEREEEEK EAAKYVEAQQRLEALFTKIQEEFE EHEENTTKPYLPSRALTRQQVRALQ DGAELYEAVKNAADPAYLEGYFSE EQLRALNNHRQMLNDKKQAQIQLE IRKAMESAEQKEQGLSRDVTTVWK LRIVSYSKKEKDSVILSIWRPSSDLY SLLTEGKRYRIYHLATSKSKSKSER ANIQLAATKKTQYQQLPVSEILFQI YQPREPLHFSKFLDPDFQPSCEVDL IGFVVSVVKKTGLAPFVYLSDECYN LLAIKFWIDLNEDIKPHMLIAASNL QWRPESKSGLLTLFAGDFSVFSASP KEGHFQETFNKMKNTVENIDILCNE AENKLMHILHANDPKWSTPTKDC TSGPYTAQIIPGTGNKLLMSPNCEIY YQSPLSLCMAKRKSVSTPVSAQMT SKSCKGEKEIDDQKNCKKRRALDF LSRLPLPPPVPICTFVSPAAQKAFQ PPRSCGTKYETPIKKKELNSPQMTPF KKFNEISLLESNSIADEELALINTQA LLSGSTGEKQFISVSESTRTAPTSSE DYLRLLKRRCTTSLIKEQESSQASTEE CEKNKQDTITTKKYI
3043	8540	A	3302	1	2163	
3044	8541	A	3303	1	5771	
3045	8542	A	3304	1	3395	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESHE KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLTVKTKMDQA DDVSCPLLNSCLSESPPVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYFSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDTDLDSNVAHQKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSFVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYIAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEET LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVS DIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDS LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNK WAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRK FAGLLKND CNKSASG YLT DENEVGRGFYSAHG TKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVS MFKIENHNDKT VSEKNNKCQLILQNNIEMTTGT FVE EIT/EM*HAFT*GFC*HSE*RNFTT*P KYVWIGESF*NITL*C*FGNFRYM* M*YREAS*VSLICKYLWDF*HSKW KICPGIRCFITKRKTSVF*NRR*YQA SLFQSIV*K*RTFRPAHKRRKYCYT YSRTFNIPKRLFI*CGKFICFLWI*YS KWKASFHFRKFLTQS*GSVRGI*FN QN*A*SSLFTYV*TKCIKNTSSC**E KPRALCKLRNGKNLQ*RI*IIK*LKC *RWFFRK*SLY*SFSISLSISTRQTTV GIRNQSLTC*EHSCFGKRTGFT*KRK NGNW*N*NFF*CSCENKYRSLFYLL QRFRKLL*NRSSRNC*SFYGR**TDR F*TAKSCHTFSFYMSRK*GNFVKF KNWKKRRAPYLSGRTL NQKKLIK *I*QDNRKSRKILKGFKKHSRWHNK RSKIVYASCFFRADYLC TL SHN*GT SRDTESKFYRTWSRISV*ISFV*TSDF GKIFKQFSSFRTSILSSFCYKK*KNET LDYYRQTNQSLCSTF*N*IAFSQS*T VC*EY*LGGKQTKAKH*WTWL****

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						K*D**Q*DSSV*QKQLQSSSSCNFHK V*RRTRFRNYKSSECQRYTGYAN*E ETKATRLSTARQSVSCKNIHSASNL SESSRRPSSLCVFS*TAVYVWRF*T LHKN*QKQCRVFSVSH*RLFW*GKF MDWKRNTVG*WWMAHTLQ*WKG WKRRIL*GSV*HSRCGSKAYF*NLG L*SL*MDHMETGSYGMCLS*GIC** MPKPRKGASSTKIQI*YGN**KQKIG YKKDNGKG*HCKNTCSLCF*HNFI ERKYI*NF*Q*N**CRYPKSGHY*TY RWVCC*GPVRSSPLSCLKEWQTD SWSEDYSSWSRTGGLS*CLYTS*SP RISYVKDFC*QYSACSLVYQTWILS* P*TFSSALIIAFQ*WRKCWLC*CNYS KSIPYTVGDGEDIWIIHISQ*KRGRKG SSKICGGPTKETRSLIH*NSGGI*RT* RKHNTTIFTITCTNKTASSCFARWC RAL*SSECSRPSLP*GLFQ*RAVKS LE*SQANVE**ETSSDPVGN*EGHGI C*TKGTRFIKGCHNRVEVAYCKLKF KRKRFSYTEYLASIIRFIFSVNRRKEI QNLSSCNFKI*K*I*KS*HTVSSDKK NSVSTTTGFR*NFISDLPATGAPSLQ QIFRSRLSAILF*GGPNRIRFCCEKN RTCPFRLFVRRMLQFTGNKVLDLP* *GHY*ASYVNCKQPPVATRIQIRPS YFICWRFFCVFC*SKRGPLSRDIQQN EKYC*EY*HTLQ*SRKQAYAYTAC K*SQVVHPN*RLYFRAVHCSNHSW YRKQASDVFS*L*DILSKSFITLYGQ KEVCFHTCLSPDDFKVL*RGERD*M PIGSKERPTFFEIFKTRCNKADLGPI LNWFEELSSEAPPYNSEPAEESCHK NNNYEPNLFKTPQRKPSYNQLASTP IIFKEQGLTLPLYQSPVKELDKFKLD LGRNVPSNRHKSRLTVKTKMDQAD DVSCPLLNSCLSESPVVLQCTHVTP QRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSSTVLIVRNEEASETVPHDATTAN VKSYSFNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTSNGSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDTDLDSNVAHQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						LSLTSSFGTILRKCSRNETCSNNTVIS QLDYKEAKCNKEKLQFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSEE LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRFASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKQPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF R
3046	8543	A	3305	1	5771	MPIGSKERPTFFEIFKTRCNKADLGP ISLWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTMDQA DDVSCPLLNSCLESPPVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVPPLACEWSQLTSL GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QLDYKEAKCNKEKLQFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSEE LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NKNSVKQHIKMTLGQDLKSDISLNI DKIEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSHNHL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRD/C/S/YLMIRKLIEAEDRL*KR *WKGMTQLQKHLFSVFLT*FH*AQI YLKLLAIKLVVQIPKKWPLLNLQM GGMLLRPS*ILPS*LS*RMAD*QLVR RLFFMEQNWWALLMPVHLLKPQN LLC*/RLLTVLGLLAGIPNLDSTLTL DLFLCPYHRFSVMEMLVVLML*LF KEHTLYSGWRRHHLDYTYFAMKE RKKRKQQNMWRPNKRD*KPYSLK FRRNLKNMKKTQQNHIYHHVH*QD SKFVLCKMVQSFMKQ*RMQQTQLT LRVISVKSS*EP*IITGKC*MIRNKL SSWKLGRPWNLLNKRNVYQGM QPWGSCVL*AIQKKKKIQLY*VFGV HHQIYILC*QKERDTEFIILQLQNLK VNLKELTYS*QRQKKLSINNYRFQM KFYFRFTSHGSPFTSANF*IQTFSHL VLRWT**DLSFLL*KKQDPLSSICQ TNVTIYWQ*SFG*TLMTLLSLIC*L LQATSSGDQNPNAFLLYLLEIFLCF LLVQKRATFKRHSTK*KILLRILTYF AMKQKTSLCIYCMQMIPSGPPQLKT VLQGRITLLKSFLVQETSF*CLLLIVR YIIKVLYHFVWPKGSLFPHLSQPR*L QSLVKGRKRLMTKRTAKREEPWIS* VDCLYLHLLVPFVHLFLRLHRRHFS HQGVVAPNTKHP*RKKN*ILLR*LH LKNSMKFLFWKVIQ*LTKNLH**IP KLFCLVQQEKNLYLSVNPLGLLPP VQKIISD*NDVVLHL*SKNRRVPRP VRKNVRKISRTQLQLKNIS
3047	8544	B	3306	16	10899	MPNVLEDEVYETVVDTSEEDSFSLC FSKCRTKNLQKVRTSKTRKKIFHEA NADECEKSKNQVKEKYSFVSEVEP NDTDPLDSNVANQKPFESGSDKISK EVVPSLACEWSQLTSLGLNGAQME KIPLLHISCDQNISEKDLLDTENKR KKDFTSENSLPRISLPKSEKPLNE ETVVNKRDEEQHLESHTDCILAVK QAISGTSPVASSFQGIKKSIFRIESP KETFNASFSGHMTDPNFKKETEASE SGLEIHTVCSQKEDSLCPNLIDNGS WPATTTQNSVALKNAGLISTLKKK TNKFIYAIHDETSYKGKKIPKDKS ELINCSAQFEANAFEAPLTFANADS GLLHSSVKRSCSQNDSEPTLSLTSS FGTILRKCSRNETCSNNTVISQDLQ KEAKCNKEKLQLFITPEADSLSCLQ EGQCENDPKSKKVSDIKEEVLA AAA CHPVQHSKVEYSDTFQSQSLLY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DHENASTLILTPTSKDVLSNLVMISR GKESYKMSDKLKGNNYESDVELTK NIPMEKNQDVCALNENYKNVELLP PEKYMVRVASPSRKVQFNQNTNLRV IQKNQEETTSISKITVNPDSSEELFSDN ENNFVFQVANERNNLALGNTKELH ETDLTCVNEPIFKNSTMVLGYDGTGD KQATQVSIKKDLVYVLAENKNSV KQHIKMTLGQDLKSDISLNIDKIPEK NNDYMNK WAGLLGPISNHSFGGSF RTASNKEIKLSEHNIKKSKMFKDIE EQYPTSLACVEIVNTLALDNQKKLS KPQSINTVSAHLQSSVVVSDCKNSH ITPQMLFSKQDFNSNHNLTSPSQKEQI TELSTILED SG SQFEFTQFRKPSYILQ KSTFEVPENQMTILKTSEECDAD LHVIMNAPSIGQVDSSKQFEGTVEI KRKFAGLLKNDCKNSASGYLTDEN EVGFRGFYSAHGKTLNVSTEALQK AVKLFSDIENISEETSAEVHPISLSSS KCHDSVVSFMFKIENHNDKTVSEKN NKCQLILQNNIEMTTGTVEEITENY KRNTENEDNKYTAASRN SHNLEFD GSDSSKNDTVCIHKDETDLFTDQH NICLKLSGQFMKEGNTQIKEDLSDL TFLEVAKAQEA CHGNTSNKEQLTA TKTEQNIKDFETS DTFQTASGKNIS VAKESFNKIVNFFDQKPEELHNFSL NSELHSDIRKNKMDILSYEETDIVK HKILKESVPVGTGNQLVTFQGQPER DEKIKEPTLLGFHTASGKKVKIAKE SLDKVKNLFDERARTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVANQKP FESGSDKISKEVVP SLACEWSQLTSL GLNGAQMEKIPLLHISCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETV VNKRDDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYS DTFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSSE LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLGY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKQPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKEQITELSTILEDSCGSQFEFTQF RKPSYILQKSTFEVPEQNMTILKTTT EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFRGFYSAHGTLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVSFMFIENHNDKT VSEKNNKCQLILQNNIEMTTGTTFVE EITENYKRNTENEDNKYTAASRNHSH NLEFDGSDSSKNDTVCIHKDETDL FTDQHNICKLKSQGFMKEGNTQIKE DLSDLTFLEVAKAQEAHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKESFNKIVNFFDQKPEEL HNFSLSNELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDERASHQWAK TLKYREACKDEACETIEITAAPK CKEMQNSLNNDKNLVSIE TVVPPKL LSDNLCRQTENLKTSKIFLKVKVH ENVEKETAKSPATCYTNQSPYSVIE NSALAFYTSCSRKTSVSQTSLEAK KWLREGIFDGQPERINTADYVGNV LYENNSNSTIAENDKNHLSEKQDQTY LSNSSMSNSYSYHSDEVYNDSGYLS KNKLDSGIEPVLKNVEDQKNTSFSK VISNVKDANAYPQTVNEDICVEELV TSSSPCKNKNAAIKLSISNSNNFEVG PPAFRIASGKIVCVSHETIKKVKDIF TDSFSKVIKENNENKSKICQTKIMA GCYEALDSEDILHNSLDNDECSTH SHKVFADIQSEEILQHNQNMGLEK VSKISPCDVSLSDICKCSIGKLHK SVSSANTCGIFSTASGKSVQVSDAS LQNAHQVFSEIEDSTKQVFSKVLFK SNEHSDQLTREENTAIRTPEHLISQK GFSYNVVNSSAFSGFSTASGKQVSI LESSLHKVKGVL EFDLIRTEHSLH YSPTSRQNVSKILPRVDKRNPEHCV NSEMECTCSKEFKLSNNLNVEGGSS ENNHSIKVSPYLSQFQQDKQQLVLG TKVSLVENIHVLGKEQASPKNVKM EIGKTETFSQVVPKTNIEVCSTYSKD SENYFETEAVEIAKAFMEDDELTD KLPSHATHSLFTCPENEEMVLSNSRI GKRRGEPLILVGEPSIKRNLLNEFDR IENQEKSLKASKSTPDGTIKDRRLF VHHVSLEPITCVFRTTKERQEIQNP NFTAPGQEFLSKSHLYEHLTLEKSSS NLAVSGHPFYQVSGNKGKMRKLI TTGRPTKVFPFVKTSKSHFHRVEQC VRNINLEGNRQKQNDGHGSDDSK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NKINDNEIHQFNKNNSNQAAAVTFT KCEEEPLDLITSLQNARDIQDMRIK KKQRQRVFPQPGSLYLAKTSTLPRI SLKAAVGGQVPSACSHKQLYTYGV SKHCIKINSKNAESFQFHTEDYFX*
3048	8545	A	3307	1	12500	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNRSRHKSLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHTDTAN VKSYFSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPHVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDTDPLDSNVANQKP FESGSDKISKEVVPPLACEWSQLTLS GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPPASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNG/K/TVMS**MPHRLVR*TAA SNLKVQLKLNGSLLAC*KMTVTKV LLVI*QMKMKWGLGAFILLMAQN* MFLCLKCKKL*NCLVILRILVRKLL QRYIQ*VYLQVNVMMILLFQCLR*KII MIKL*VKKIINAN*YKIIKL*LLALL LKKLLKITREILKMKITNILLPVEILI T*NLMAVIQVKMILFVFIKMKRTCY LLISTTYVLNYLASL*RRETLRLKKI CQI*LFWKLRKLKHHVMVILQIKNS *LLLKRSKI*KILRLLIHFFRLQVGKI LVSPKSHLIK*ISLIRNQKNCITFP*I LNYILT*ERTKWF*VMRKQT*LNT KY*KKVSQLVLEIN**PSRDNPVNM KRSKNLLCWVFIQLAGKKLKLQRN LWTK*KTFLMKKSKVLVKSPVLA NGQRP*STERPVKTLN*HVRPLRSQ LPQSVKCRILSIMIKTLFLLRLWCH LSS*VIIVVDKLKISKHQKVSF*KLK YMKM*KKKQKQVLQVLTOISPLIQS LKIQP*LFTQVVVEKLL*VRLHYLK QKNGLEKEYLMVNQKE*ILQIM*EII CMKIIQTVL*LKMTKII SPKNKILI*V TVACLTAIPTILMRYIMIQDISQKINL ILVLSQY*RMLKIKKTLVFPK*YPM* KMQMHTHKL*MKIFALRNL*LALH PAKIKMQPLNCPYLIVILR*GHLHL G*PVVKS FVFHMKQLKK*KTYLQT VSVK*LRKTTRINQKFAKRKLWQV VTRHWMIQRIFFITL*IMMNVARIHI RFLLTFRVKKFYNITKICLDWRKFL

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KYHLVMLVWKLQIYVNVV*GSFIS QSHLQILVGFLAQQVENLSRYQML HYKTQDKCFLK*KIVPSKSFPKYCL KVTNIQTSSQEKKILLYVLQNI*YPK KAFHIMW*IHLLSLDLVQQVESKFP F*KVPYTKLREC*RNL*SELSIVFTI HLRLDKMYQKYFLVIRETQSTV*T QKWKKPAVKNLNYQIT*MLKVVL QKIITLLKFLHISLNFNKTNNSWY*E PKSHLLRTFMFWEKNRLHLKT*KW KLVKLKFLMFL*KQI*KFVLLTPKI QKTTLKQKQ*KLLKLLWKMMN*QI LNCQVMPHILFLHVPKMRKWFCQI QELEKEEESPLS*WENPQSKETY*M NLTG**KIKKNP*RLQKALQMAQ*K IEDCLCIMFL*SRLPVYPFAQLRNVK RYRIQILPHLVKNFCLNLCMNI*LW KNLQAI*QFQDIHFIKFLQEMKK*D T*LLQADQPKSLFHLLKLNRIFTELN SVLGILTWKRKTDKSKTLMMDMALMI VKIRLMTMRFISLTKTTPIKQQL*LS QSVKKNL*I*LQVFRMPEIYRICELR RNKGNASFHSQAVCILPATTTQNSV ALKNAGLISTLKKKTNKFIYAIHDE TSYGKKIPKDQKSELINCSAQFEA NAFEAPLTFANADSGLLHSSVKRSC SQNDSEPTLSLTSSFGTILRKCSR ETCSNNTVISQDL DYKEAKCNKEKL QLFITPEADSLSCLQEGQCENDPKS KKVSDIKEEVLAACHPVQHSKVE YSDTDFQSQSLLYDHENASTLILT PTSKDVLNLVMISRGKESYKMSD KLKGNNYESDVELTKNIPMEKNQD VCALNENYKNVELLPPEKYMVRVAS PSRKVQFNQNTNLRVIQKNQEETTS ISKITVNPDSSEELFSDNENNFVFQVA NERNNLALGNTKELHETDLTCVNE PIFKNSTMVLYGDTGDKQATQVSIK KDLVYVLAENKNSVKQHIKMTLG QDLKSDISLNIDKIPEKNNDYMDKW AGLLGPI SNHSFGGSFRTASNKEIKL SEHNIKKSKMFFKDIEEQYPTSLAC VEIVNTLALDNQKKLSKPQSINTVS AHLQSSVVSDCKNSHITPQMLFSK QDFNSNHNLTPSQKAEITELSTILEE SGSQFEFTQFRKPSYILQKSTFEVPE NQMTILKTTSEECRADLHVIMNAP SIGQVDSSKQFEGTVEIKRKFAGLL KNDCKNSASGYLTDENEVGRGFY SAHGTKLNVSTEALQKAVKLFSDIE NISEETSAEVHPISLSSSKCHDSVVS MFKIENHNDKTVSEKNNKCQLILQ NNIEMTTGTFVEEITENYKRNTENE DNKYTAASRNSHNLEFDGSDSSKN DTVCIHKDETDLLFTDQHNICLKLS GQFMKEGNTQIKEDLSDLTFLEVAK AQEACHGNTSNKEQLTATKTEQNI KDFETSDTFFQTASGKNISVAKESF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NKIVNFFDQKPEELHNFSLNSELHS DIRKNKMDILSYEETDIVKHKILKES VPVGTGNQLVTFQGGPERDEKIKEP TLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPCKKE MQNSLNNDKNLVSIE TVVPPKLLSD NLCRQTENLKTSSIFLKVKVHENV EKETA KSPATCYTNQSPYSVIENSA LAFYTCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNYLYEN NSNSTIAENDKNHLEKQDTYLSNS SMSNSYSYHSDEVYND SGYLSKNK LDSGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNFEVGPAPF RIASGKIVCVSHETIKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDGKNIHSASN LSESSRRPSSLCVFS*TAVYVWRF* TLHKN*QKCRVFSVS/TLKILVRK VYGLEKEYSWLMVDGSYPMMER LEKKNFIGLCVTLQVWIQSLFLEFGF IITIDGSYGNWQLWNVPLRNLLID A*AQKGCCFFN*NTDMIRKLIEAEDR L*KR*WKGMTQLQKHLFSVFLT*FH *AQIYLKLLAIKLVVQIPKKWPLLN LQMGGMLLRPS*ILPS*LS*RMAD* QLVRRLLFFMEQNWALLMPVHLL KPQNLLC*RFLTLVLGLLAGIPNLDS FLTDLFLCPYHRFSVMEEMLVVL M*LFKEHTLYSGWRRHLDYTYFA MKERKKRKQNMWRPNKRD*KPY SLKFRRNLKNMKKTQQNHVHHVH *QDSKFVLCKMVQSFMKQ*RMQQT QLTLRVISVKSS*EP*IITGKC*MIRN KLRSSWKLGRPWNLLNKRNVYQ GMSQPWGSCVL*AIQKKKKIQLY*V FGVHHQIYILC*QKERDTEFIILQLQ NLKVNLEKELYS*QRQKKLSINNYR FQMKFYFRFTSHGSPFTSANF*IQTF SHLVLRWT**DLSFLL*KKQDLPLSS ICQTNVTIYWQ*SFG*TLMRLLSLI C*LLQATSSGDQNPNAFLLYLLEIF LCFLLVQKRATFKRHSTK*KILLRIL TYFAMKQKTSLCIYCMQMIPSGPPQ LKTVLQGRLLKSFLVQETSF*CLLL IVRYIHKVLYHFVWPKGSLFPHLSQP R*LQSLVKGRKRLMTKRTAKREEP WIS*VDCLYLHLLVPFVHLFLRLHR RHFHQGVVAPNTKHP*RKKN*ILL R*LHLKNSMKFLFWKVIQ*LTKNLH **IPKLFCLVQQEKNNLYLSVNPLGL LPPVQKIISD*NDVVLHL*SKNRRVP RPVRKNVRKISRTQLQLKNIS
3049	8546	A	3308	1	9344	
3050	8547	A	3309	1	18345	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESHE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSIFYSNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTSGNSFKVN SCKDHIGKSMNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVPPLACEWSQLTSL GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVS DIKEEV LAAACHPVQHSHKVEYS DTFQS QK SLLYDHENASTLILTPSKDVL SNLV MISRGKESYKMSDKLKGNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFS DNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFR TASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRK FAGLLKND CNKSASG YLT DENEVGFRGFYSAHG TKLNVS TEALQKAVKLFS DIENISEETSAEVH PISLSSSKCHDSVVS MFKIENHNDKT VSEKNNKCQLILQNNIEMTTGT FVE EITDACRKDSVKMIQKAKKFQI*KK RSWLQHV TQYNIQKWNTVILTFNP RKVFY MIMKMPALLF*LLPRMFC QT*S*FLEAKNHTKCQTSSKVTIMN LMLN*PKIFPWKRIMYVL*MKI IK TLSCCHLKNT*E*HHLQERYNSTKT QI*E*SKKIKKKLLQFQK*LSIQTLK NFSQTMRIJLSSK*LMKG IILL*EILR

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NFMKQT*LV*TNPFRTLPWFYMET QVINKQPKCQLKKIWMFLQRRTKI V*SSI*K*L*VKI*NRTSP*I*IKYQKK IMIT*TNGQDS*VQFQITVLEVASEQ LQIRKSSSLNITLRRACSSKILKNNI LLV*LVLKL*IPWH*IIRN*ASLSQL ILYLHIYRVV*LFLIVKIVI*PLRCYFP SRILIQTI*HLAKRQKLQNFLLY*KN QEVSLNLLSLENQATYCRRVHLKC LKTR*LS*RPLLRNAEMLIFMS**MP HRLVR*TAASNLKVQLKNGSLLA C*KMTVTKVLLVI*QMCMKWGLG AFILLMAQN*MFLKLCKKL*NCLV ILRLVRKLLQRYIQ*VYLQVNVML LFQCLR*KIIMIKL*VKKIINAN*YYK IILK*LLALLLKKLLKITREILKMKIT NILLPVEILIT*NLMAVIQVKMILFVF IKMKRTCYLLISTTYVLNYLASL*R RETLRLKKICQI*LFWKLRLKKHV MVILQIKNS*LLKRSKI*KILRLLIH FFRLQVGKILVSPKSHLIK*ISLIRN QKNCITFP*ILNYILT*ERTKWF*V MRKQT*LNTKY*KKVSQLVLEIN** PSRDNPVNMKRSKNLLCWVFIQLA GKKLKLQRNLWTK*KTFMLMKSKV LVKSPVLAINGQRP*STERPVKTLN* HVRPLRSQLPQSVKKCRILSIMIKTL FLLRLWCHLSS*VIIYVDKLKISKHQ KVSF*KLKYMKM*KKKQKQVLQ VTQISPLIQSLKIQP*LFTQVVVEKLL *VRLHYLKQKNGLEKEYLMVNQKE *ILQIM*EIICMKIIQTVL*LKMTKIIS PKNKILI*VTVACLTAPTILMRYIMI QDISQKINLILVLSQY*RMLKIKKTL VFPK*YPM*KMQMHTHKL*MKIFA LRNL*LALHPAKIKMQPLNCPYLIVI ILR*GHLHLG*PVVKSFVFHMKQLK K*KTYLQTVSVK*LRKTTRINQKFA KRKLWQVVTRHWMIQRIFFITL*IM MNVARIHIFLLTFRVKKFYNITKIC LDWRKFLKYHLVMLVWKLQIYVN VV*GSFISQSHLQILVGFLAQQVENL SRYQMLHYKTQDKCFLK*KIVPSKS FPKYCLKVTNIQTSSQEKILLYVL QNI*YPPKAFHIMW*IHLSDLKL QEKY*K*R*QIYCCQ*KFS*LRI*WQ *FK*K*YCLYS*R*NGLAII*SAQHM S*IIWPVYEGGKHS*RRFVRFNFFG SCSSRSMSW*YFK*RTVNCY*NGA KYKRF*DF*YIFSDCKWEKY*CRQR VI**NCKFL*SETRRIA*LFLKF*ITF* HKKEQNGHSL*GNRHS*TQNLKE SVPVGTGNQLVTFQGQPERDEKIKE PTLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPKCKE MQNSLNNDKNLVSIEVVPKLLSD NLCRQTENLKTSKSIFLKVKVHENV

SEQ ID NO: of nucleo- tide sequence	SEQ ID NO: of peptide sequence	Me- thod	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNYLYEN NSNSTIAENDKNHLSEKQD TYLSNS SMSNSYSYHSDEVYND SGYLSKNK LDSGIEPVLKNVEDQKNTSFSKVISN VKDANA YPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNNFEVGPAPF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDECSTHSHKV FADIQSEEILQHNQNMGLEKVKISKIS PCDVSLTSDICKCSIGKLHKS VSSA NTCGIFSTASGKSVQVSDASLQ NAR QVFSEIEDSTKQVFSKVLFKSNEHS DQLTREENTAIRTPEHLISQKGF SYN VVNSSAFSGFSTASGKQVSILESSLH KVKGVLEEFDLIRTEHSLHYSPTS R QNVSKILPRVDKRNPEHC VNSEME KTCSKEFKLSNNLNVEGGSSENNHS IKVSPYLSQFQQDKQQLVLG TKVSL VENIHVLGKEQASPKNVKMEIGKTE TFS DVPVKTNIEVCSTYSK DSENYF ETEAVEIAKAFMEDDELTD SKLP SH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEP SIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRTTKERQEIQNP NFTA PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITTGR PTKVVFVPPFKTKSHFHRVEQCVRNI NLEENRQKQNIDGHGSDDSKNKIN DNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPSGLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQHTEDYFGKESLW TGKGIQLADGGWLIPSNDGKAGKE EFYRALCDTPGVDPKLISRIVVYNH YRWIIWKLAAMECAFPKEFANRCL SPERVLLQLKYRSTASGKQVSILESS LHKVKG VLEEFDLIRTEHSLHYSPT SRQNVSKILPRVDKRNPEHC VNSEM EKTCSKEFKLSNNLNVEGGSSENNHS SIKVSPYLSQFQQDKQQLVLG TKVS LVENIHVLGKEQASPKNVKMEIGKT ETFSDVPVKTNIEVCSTYSK DSENY FETEAVEIAKAFMEDDELTD SKLP S HATHSLFTCPENEEMVLSNSRIGKR RGEPLILVGEP SIKRNLLNEFDRIEN QEKSLKASKSTPDGTIKDRRLFMHH VSLEPITCVPFRTTKERQEIQNP NFTA APGQEFLSKSHLYEHLTLEKSSSNL AVSGHPFYQVSATRNEKMRHLITT GRPTKVVFVPPFKTKSHFHRVEQCVR NINLEENRQKQNIDGHGSDDSKNKI NDNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QRQRVFPQPGSLYLAKTSTLPRISLK AAVGGQVPSACSHKQLYTYGVSKH CIKINSKNAESFQFHTEDYFGKESL WTGKGIQLADGGWLIPSNDGKAGK EEFYRALCDTPGVDPKLISRIWVYN HYRWIIWKLAAAMECAFPKEFANRC LSPERVLLQLKYRYDTEIDRSRRSAI KKIMERDDTAAKTLVLCVSDIISLS ANISETSSNKTSSADTQKVAJIELTD GWYAVKAQLDPPLLA VLKNGRLT VGQKIILHGAELVGSPDACTPLEAP ESLMLKISANSTRPARWYTKLGFFP DPRPFPLPLSSLFSDGGNVGCVDVII QRAYPIQWMEKTSSGLYIFRNEREE EKEAAKYVEAQQRLEALFTKIQEE FEEHEENTTKPYLPSRALTRQQVRA LQDGAELYEAVKNAADPAYLEGYF SEEQLRALNNHRQMLNDKKQAQIQ LEIRKAMESAEQKEQGLSRDVTTV WKLRIVSYSKKEKDSVILSIWRPSSD LYSLLTEGKRYRIYHLATSKSKSKS ERANIQLAATKKTQYQQLPVSEIL FQIYQPREPLHFSKFLDPDFQPSCE VDLIGFVVSVVKKTGLAPFVYLSDE CYNLLAIKFWIDLNEDIKPHMLIAA SNLQWRPESKSGLLTLFAGDFSVSF ASPKEGHFQETFNKMKNTVENIDIL CNEAENKLMHILHANDPKWSTPTK DCTSGPYTAQIIPGTGNKLLMSSPN CEIYYQSPLSLCMAKRKSVSTPVSA QMTSKSCKGEKEIDDQKNCKKRRRA LDFLSRLPLPPVSPICTFVSPAQK AFQPPRSCGTYETPIKKKELNSPQ MTPFKKFNEISLLESNSIADEELALI NTQALLSGSTGEKQFISVSESTRAP TSSEDYLRLLKRRCTTSLIKEQESSQA STEECEKNKQDTITTKKYI
3051	8548	A	3310	1	7988	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESHE KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLRTVTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVCGLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYFSNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMNPVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETFYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVS DIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDS EELFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIEKNNNDYMNK WAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQM TILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRK FAGLLKNDCKNSASG YLTDENEVGFRGFYSAHGTKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSV VSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDL LFTDQHNI CLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEACHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKELFNKIVNFFDQKPEEL HNFSLNSELHSDIRKNKMDILSYEE TDIVKHILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLDFEKEQGTSEITS FSHQWAKTLKYREACKDLELACET IEITAAPKCKEMQNSLNNDKNLVSI ETVVPPKLLSDNLCRQTENLKT SKSI FLKVKVHENV EKETA KSPATCYTN QSPYSVIENSALAFYTSCS*KSQNIK KYLFES*ST*KCRKRNSKKSCNLLH KSVPLFSH*KFSLSFLHKL*VRKTSVS QTSLL EAKKWLREGIFDGQPERINT ADYVGNLYENNSNSTIAENDKNH LSEKQDTYLSNSSMSNSYSYHSDEV YNDSGYLSKNKLD SGIEPV LKNVED QKNTSFSKVISNVKDANAYPQTVN EDICVEELVTSSSPCKNKNAAIKLSI SNSNNFEVGPPAFRIASGKIVCVSHE TIKKVKDIFDTSFSKVIKENNENKSK ICQTKIMAGCYEALDDSEDILHNSL DNDECSTHSHKVFADIQSEEILQHN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						QNMSSGLEKVSISKISPCDVSLETSDIC KCSIGKLHKS SVSSANTCGIFSTASGK SVQVSDASLQNA RQVFSEIEDSTKQ VFSKVLFSKNEHSDQLTRENTAIR TPEHLISQKGF SYNVVNSSAFSGFST ASGKQVSILESSLHKVKG VLEEFDLI RTEHSLHYSPTS RQNVSKILPRVDK RNPEHC VNSEMEK TCSKEFKLSNNL NVEGGSSENNHSIKVSPYLSQFQQD KQQLVLG TKVSLVENIHVLGKEQA SPKNVKMEIGKTETFS DVPVKTNIE VCSTYSKDS ENYFETEAVEIAKAFM EDDELTD SKLP SHA THSLFTCPENE EMVLSNSRIGKRRGEPLILVGESIK RNLLNEFDRIENQE KSLKASKSTPD GTIKDRRLFVHHVSLEPITCVPFRTT KERQEIQNP NFTA PGQEF LSKSHLY EHLTLEKSSSNLAVSGHPFYQVSGN KNGKMRKLIT TGRPTKVFPF KTK SHFHRVEQCVRNINLEGNRQKQNI GHGSDDSKNKINDNEIHQFNKNS NQAAAVTFTKCEEEPLDLITSLQNA RDIQDMRIKKQRQ RVFPQPSLYL AKTSTLPRISLKA AVGGQVPSACSH KQLYTYGVSKHC IKINSKNAESFQF HTEDYFGKESLW TGKGIQLADGGW LIPSNDGKAGKEEFYRALCDVKAT
3052	8549	A	3311	1	14305	MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEES KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLRTVTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTS GNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCR TKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNV AHQKP FESGSDKISKEVVPSLACEWSQLT GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSEN SLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIESPKE TFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATT TQNSVALKNAGLI STLKKKTNKFIYAIHDETFYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCS QNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYS DTFQSQK SLLYDHENASTLILTPTSKDVLSNLV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSEE LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTT EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTENEVGRGFYSAHGTLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTTFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDL FTDQHNICLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEACHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKESFNKIVNFFDQKPEEL HNFSLNSELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLDFEKEQGTSEITS FSHQWAKTLKYREACKDLELACET IEITAAPKCKEMQNSLNNDKNLVSI ETVVPKLLSDNLCRQTENLKTSSKI FLKVKVHENVEKETAKSPATCYTN QSPYSVIENSALAFYTSCSRKTSVSQ TSLLEAKKWLRGIFDGQPERINTA DYVGNLYENNSNSTIAENDKNHL SEKQDTYLSNSSMSNSYSYHSDEVY NDSGYLSKNKLDSGIEPVLKNVEDQ KNTSFSKVISNVKDANAYPQTVNE DICVEELVTSSSPCKNKNAAIKLSIS NSNNFEVGPPAFRIASGKIVCVSHET IKKVKDIFTDSFSKVIKENNENKSKI CQTKIMAGCYEALDDSEDILHNSLD NDECSTHSHKVFADIQSEEILQHNQ NMSGLEKVSISKISPCDVSLTSDICKC SIGKLHKSVSANTCGIFSTASGKSV QVSDASLQNAQVFSEIEDSTKQVF SKVLFKSNEHSDQLTRENTAIRTP HLISQKGFSYNVVNSSAFSGFSTAS GKQVSILESSLHKVKGVL EEFDLIRT EHSLHYSPTSRQNVSKILPRVDKRN PEHCVNSEMEKTCSEFKLSNNLN VEGGSSENNHSIKVSPYLSQFQQDK QQLVLGTKVSLVENIHVLGKEQASP KNVKMEIGKTETFSDDVPVKTNIEVC STYSKDSENYFETEAVEIAKAFMED

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						DELTDSKLPSHATHSLFTCPENEEM VLSNSRIGKRRGEPLILVGEPSIKRN LLNEFDRIENQEKS LKASKSTPDGT IKDRRLFMHHVSLEPITCVPFRTTKE RQEIQNPNTAPGQEFLSKSHLYEH LTLEKSSSNLA VSGHPFYQVSATRN EKMRHLITTGRPTKVFPFPFKTKSH FHRVEQCVRNINLEENRQKQNIQGH GSDDSKNKINDNEIHQFNKNNSNQ AAAVTFTKCEEEPLDLITSLQNARDI QDMRIKKKQRQRFPPQPSLYLAK TSTLPRISLKA AVGGQVPSACSHKQ LYTYGVSKHCIKINSKNAESFQFH/T *RLFW*GKFMDWKRNTVG*WWM AHTLQ*WKGWKRRIL*GSV*HSRC GSKAYF*NLGL*SL*MDHMETGSY GMCLS*GIC**MPKPRKGASSTKIQI *YGN**KQKITNILLPVEILIT*NLMA VIQVKMILFVFIKMKRTCYLLISTTY VLNYLASL*RRETLRLKKICQI*LFW KLRKLKHHVMVILQIKNS*LLKRS KI*KILRLLIHFFRLQVGKILVSPKSH LIKL*ISLRNQKNCITFP*ILNYILT*E RTKWTF*VMRKQT*LNTKY*KKVS QLVLEIN**PSRDNPVMKRSKNLL CWVFIQLAGKKLKLQRNLWTK*KT FLMKKS KVLVKSPVLAINGQRP*ST ERPVKTLN*HVRPLRSQLPQSVKCC RLSIMIKTLFLLRLWCHLSS*VIHV DKLKISKHQKVSF*KLKYMKM*KK KQKQVLQVLTQISPLIQLKIQP*LF TQVVVEKLL*VRLHYLKQKNGLEK EYLMVNQKE*ILQIM*EHCMIHQIT VL*LKMTKIISPKNKILI*VTVACLT APTILMRYIMIQDISQKINLILVLSQ Y*RMLKIKKTLVFPK*YPM*KMQM HTHKL*MKIFALRNL*LALHPAKIK MQPLNCPYLIVILR*GHLHLG*PVV KSFVFMKQLKK*KTYLQTVSVK* LRKTTRINQKFAKRKLWQVVTRHW MIQRIFFITL*IMMNVARIHIFLLTF RVKKFYNTKICLDWRKFLKYHLV MLVWKLQIYVNVV*GSFISQSHLQI LVGFLAQQVENLSRYQMLHYKTQD KCFLK*KIVPSKSFPKYCLKVTNIQT SSQEKKILLVYLQNI*YPKKAFHIM W*IHLLSLDLVQQVESKFPF*KVPY TKLREC*RNLI*FRTEHSLHYSPTF*T KMYQKYFLVLIRETQSTV*TPEMEK TCSKEFKLSNNLNVEGGSSNNHSI KVSPYLSQFQODKQQLVLGTKVSL VENIHVLGKEQASPKNVKMEIGKTE TFS DVPVKTNIEVCSTYSKDSENYF ETEAVEIAKAFMEDDEL TDSKLPSH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEPSIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRTTKERQEIQNPNTA

SEQ ID NO: of nucleo-tide sequence	SEQ ID NO: of peptide sequence	Me tho d	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITTGR PTKVFVPPFKTKSHFHRVEQCVRNI NLEENRQKQNIIDGHGSDDSKNKIN DNEIHQFNKNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEDYFGKESLW TGKGIQLADGGWLIPSDGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIIWCLAAMECAFPKEFANRCL SPERVLLQLKYRYDTEIDRSRRSAIK KIMERDDTAAKTLVLCVSDIISLSA NISSETSSNKTSSADTQKVAIELTDG WYAVKAQLDPPLLAVLKNGRLTV GQKIILHGAELVGSPDACTPLEAPES LMLKISANSTRPARWYTKLGFFPDP RPFPLPLSSLFSDGGNVGCVDVIIQR AYPQWMEKTSSGLYIFRNEREEEEK EAAKYVEAQQKRLEALFTKIQEEFE EHEENTTKPYLPSRALTRQQVRALQ DGAELYEAVKNAADPAYLEGYFSE EQLRALNNHRQMLNDKKQAQIQLE IRKAMESAEQKEQGLSRDVTTVWK LRIVSYSKKEKDSVLSIWRPSSDLY SLLTEGKRYRIYHLATSKSKSKSER ANIQLAATKKTQYQQLPVSEILFQI YQPREPLHFSKFLDPDFQPSCSEVDL IGFVVSVVKKTGLAPFVYLSDECYN LLAIKFWIDLNEDIKPHMLIAASNL QWRPESKSGLLTLFAGDFSVFSASP KEGHFQETFNKMKNVTENIDILCNE AENKLMHILHANDPKWSTPTKDCCT SGPYTAQIIPGTGNKLLMSSPNCEIY YQSPLSLCMAKRKSVSTPVSAQMT SKSCKGEKEIDDQKNCKRRALDF LSRLPLPPPVSPICTFVSPAAQKAFQ PPRSCGTKYETPIKKKELNSPQMTPF KKFNEISLLESNSIADEELALINTQA LLSGSTGEKQFISVSESTRTAPTSSE DYLRLLKRRCTTSLIKEQESSQASTEE CEKNKQDTITTKKYI
3053	8550	A	3312	11089	17637	NHCHRFHLEWMPWCGCRSPSGPRH VNQKPEELHNFSLNSELHSDIRKNK MDILSYEETDIVKHKILKESVPVGT GNQLVTFQGGQPERDEKIKEPTLLGF HTASGKKVKIAKESLDKVKNLDFE KEQGTSEITSFSHQWAKTLKYREAC KDLELACETIEITAAPKCKEMQNSL NNDKNLVSJETVVPKLLSDNLCRQ TENLKTSKSIFLKVKVHENVEKETA KSPATCYTNQSPYSVIENSALAFYTS CSRKTSVSQTSLLLEAKKWLREGIFD GQPERINTADYVGNYLYENNSNSTI AENDKNHLSEKQDITYLSNSSMSNS YSYHSDEVYNDSGYLSKNKLDGIE PVLKNVEDQKNTSFSKVISNVKDA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						NAYPQTVNEDICVEELVTSSSPCKN KNAAIKLSISNSNNFEVSDILFQIY QPREPLHFSKFLDPDFQPSCSEVDLI GFVVSVVKKTVRNEEASETVFPHD TTANVKSYSFNHDESLKKNDRFIAS VTDSENTNQREAASHGFGKTSGNSF KVNSCKDHIGKSMPNVLEDEVYET VVDTSEEDSFSLCFSKCRTKNLQKV RTSKTRKKIFHEANADECEKSKNQV KEKYSFVSEVEPNDDPLDSNVAH QKPFESGSDKISKEVVPSLACEWSQ LTLGLNGAQMEKIPLLHISSCDQNI SEKDLLDTENKRKKDFLTSENSLPRI \SSLPNPEEPLNEETV\NKRDEEQHL DSHTDCILQ*KQAISGTFPVASSFQG IKKSIFRIRESPKETFNASFSGHMTDP NFKKETEASESGLEIHTVCSQKEDS LCPNLIDNGSWPATTTQNSVALKN AGLISTLKKKTNKFIYAIHDETSYKG KKIPKDQKSELINCSAQFEANAFEA PLTFANADSGLLHSSVKRSCSQNDS EEPTLSLTSSFGTILRKCSRNETCSN NTVISQDL DYKEAKCNKEKLQLFIT PEADSLSCLQEGQCENDPKSKKVSD IKEEVLAACHPVQHSKVEYSDTDF QSQKSLLYDHENASTLILTPTSKDV LSNLVMISRGKESYKMSDKLKGNN YESDVELTKNIPMEKNQDVCALNE NYKNVELLPPEKYMVRVASPSRKVQ FNQNTNLRVIQKNQEETTSISKITVN PDSEELFSDNENNFVFQVANERNNL ALGNTKELHETDLTCVNEPIFKNST MVL YGDTGDKQATQVSIKKDLVY VLAENKNSVKQHIKMTLGQDLKS DISLNIDKIKEKNNDYMNKWA GLL GPISNHSFGGSFRASNKEIKLSEHN IKKSKMFFKDIEEQYPTSLACVEIVN TLALDNQKKLSKPQSINTVSAHLQS SVVVS DCKNSHITPQMLFSKQDFNS NHNLTSPQKAEITELSTILEESGSQF EFTQFRKPSYILQKSTFEVPENQMTI LKT TSEECRDADLHVIMNAPSIGQV DSSKQFEGTVEIKRKFAGLLKND CN KSASGYLTDENEVGFRGFYSAHGT KLVNSTEALQKAVKLFSDIENISEET SAEVHPISLSSSKCHDSVVS MFKIEN HNDKTVSEKNNKCQLILQNNIEMTT GTFVEEITENYKRNTENEDNKYTAA SRNSHNLEFDGSDSSKNDTVCIHKD ETDLLFTDQHNICLKLSGQFMKEGN TQIKEDLSDLTFLEVAKAQEACHGN TSNKEQLTATKTEQNIKDFETSDTFF QTASGKNISVAKESFNKIVNFFDQK PEELHNFSLSNELHSDIRKNKMDILS YEETDIVKHKILKESVPVGTGNQLV TFQGQPERDEKIKEPTLLGFHTASG KKVKIAKESLDKVKNL FDEKEQGT SEITSFSHQWAKTLKYREACKDLEL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
						ACETIEITAAPKCKEMQNSLNNDKN LVSIETVVPKLLSDNLCRQTENLK TSKSIFLKVKVHENVEKETAKSPAT CYTNQSPYSVIENSALAFYTSCSRK TSVSQTSLLLEAKKWLREGIFDGQPE RINTADYVGNYLYENNSNSTIAEND KNHLSEKQDITYLSNSSMSNSYSYHS DEVYNDSGYLSKNKLDGIEPVLKN VEDQKNTSFSKVISNVKDANAYPQ TVNEDICVEELVTSSSPCKNKNAAI KLSISNSNNFEVGPAPFRIASGKIVC VSHETIKKVKDIFTDSFSKVIKENNE NKSICQTKIMAGCYEALDDSEDIL HNSLDNDECSTHSHKVFADIQSEEL QHNQNMGLEKVKISPCDVSLETS DICKCSIGKLHKSVSANTCGIFSTA SGKSVQVSDASLQNAQVFSEIEDS TKQVFSKVLFSNEHSDQLTREENT AIRTPEHLISQKGSYNVNVSSAFSG FSTASGKQVSILESSLHKVKGVL EEF DLIRTEHSLHYSPTSRQNVSKILPRV DKRNPEHCVNSEMEKTCSKEFKLS NNLNVEGGSSENNHSIKVSPYLSQF QQDKQQLVLGTVSLVENIHVLGK EQASPKNVKMEIGKTETFSVPVKT NIEVCSTYSKDSSENYFETEAVEIAK AFMEDDELTDKLP SHATHSLFTCP ENEEMVLSNSRIGKRRGEPLILVGEP SIKRNLLNEFDRIENQEKS LKASKS TPDGTIKDRRLFMHHVSL EPTCVPF RTTKERQEIQNPNTAPGQEFLSKS HLYEHLTLEKSSSNLAVSGHPFYQV SATRNEKMRHLITTGRPTKVFPVPF KTKSHFHRVEQCVRNINLEENRQK QNIDGHGSDDSKNKINDNEIHQFNK NNSNQAAAVTFTKCEEEPLDLITSL QNARDIQDMRIKKKQRQRVFPQPG SLYLAKTSTLPRISLKA AVGGQVPS ACSHKQLYTYGVSKHC IKINSKNAE SFQFHTE DYFGKESLWTGKGIQLAD GGWLIPSNDGKAGKEEFYRALCDT PGVDPKLISRIWVYNHYRWIWKLA AMECAFPKEFANRCLSPERVLLQLK YRYDTEIDRSRRSAIKKIMERDDTA AKTLVLCVSDIISLANISETSSNKTS SADTQKVAI IELTDGWYAVKAQLD PLAS
3054	8551	A	3313	1	207	CNLC LPSDDSPASASQVAGKTGLC HHTGVV FVFLVEMGFHHAGQAGLE LLT*VICVPQPPKALGLQV
3055	8552	A	3314	279	625	SLYVCMHVC MYVFILRRSFALVAQ ARVQWCGLGSLQPPPGFKRFISCL SLPTS*DYRRAPPHPTNFFVFAEME FHRVSQDGLYLLTSGDLHPRLASQS AGITGVSHRTRPFL
3056	8553	A	3315	1	418	GSIPPPGVYCVPYPLKHAPALP* TRQRGSPQSPGALRAK*HVLLET PQ PPGPAPPGARTRTRPESE*SQPGRSP

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						VSRQSLTGADALEGPCLGLATKQPS WPHRCGTSGSSPGWLLARGFQETQ QDCIVPLNAQDIG
3057	8554	A	3316	1	354	GFIPPPGVVYCVPYPLKHAPAPALP* TRQRGSPQSPGALRAK*HVLLETPO PPGPAPPGARTRTRPESGAWRWVR AGSSPPPPSPHPTPPCFFQVHQGLRS GSANEASLEDPPQSRDRA
3058	8555	C	3317	299	365	MSCPECNLTGISSKTNKKLNQ*
3059	8556	A	3318	33	302	PSSWDYRHAPPRLTNF*FLVEMGF HYVG/QAGLELLSSGDPALASQSA RITGMSR\RAWPK*HNVLRKFTNLS LGHQNHGPRVQAKP
3060	8557	A	3319	3	409	SNFRSNFGYNIPLKHLADRVAMYV HAYTLYSAVRPFGC/SGYWGCAIGK ARQAAKTEIEKLQMKEMTCRDIVK EVAKIIYIVHDEVKDKAFELELSWV GELTNGRHEIVPKDIREEAKEYAKE SLKEEDESDDDNM
3061	8558	A	3320	1	255	
3062	8559	A	3321	1	395	FGYNIPLNHLPDRVAMYVHAYTLY SAVRPFGCSFMLGSYSVNDGAQLY MIDPSGVSYGYWGCAIGKARQAAK TEIEKLQMKEMTCRDIVKEVAKIIYI VHDEVKDKAFELELSWVGEESLKE EDESDDDNM
3063	8560	A	3322	515	560	
3064	8561	A	3323	3	661	KDGVVLGVRKISPS*TYEEGFQTKR LF*CLIGNVEMA\WAG\LLADARSLA DIAREEASNFRSNFG\YTIPLKHLAD RVAMYVHAYTLYSAVRPFGCSFML GSYSVNDGAQLYMIDPSGVSYGY WG\CAMRQAR\QLAKTELERLQLK KLPSGDIVKEVAKIIYIVHDEVKDK AFELELSWV\VDLTK\*RHEILPK\D\ LRDEAEKYAKESLKEEDESDDDNV
3065	8562	A	3324	3	634	
3066	8563	A	3325	2	487	HIFGKAKEYANSQVVTKDQYAVIC LGGDVPSASLHVSETMEKT*KK/H RMSHFVTCLTEGRRKIVKPVHYD RVKKITQRKKEIPVFLNRVPEALG KCTHADPEAAEGK/LSRAMHFILQS APDIRRELQKILEARPQTPAVDFGR RLLRFSITDRTQMGR
3067	8564	C	3326	373	727	MKPRLWEFSLHREGNTGTTGLDSL LWPPARTTKWAHLTKRNQAQPGY AGPASPTSHVLCPAQPAYLTHDVNS QVSLIKTSLQASSGSXXXXXXXXXX XXXXXXXXXXGAQAFFFLGGGFF*
3068	8565	A	3327	2	536	VHLVPRQNACAIRLTECPPLRK*FS CLSLPSS/WDSQ/HAPPH/PGS/FCIFR RDGGSPMLS\GWFQTPDLRRSTRLSI PKCWDYRREPPHPVKIFLKLSFFSY WVFPVCALNLSLSLFVYTFLSNSLS LLYSSHTGSKLQCYEMLHVETHIPK GEGVLSRVERRKVRLSSHTKPCQFS HESA



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3069	8566	A	3328	3	334	FLRQGL/NSVTQAGVQWGDGLGSLQ PPPPKLGSSHPSPSSCRHYRHTPP/ RSG*FFVFL*RWGFAMLPRLV\*TSG \PSDMPALASQGAGTTSM SHHTWR PYLNF GKFP RKKN
3070	8567	A	3329	1	148	PKLKGLCLSFHEGKKRLSYF/CIMA* P*YPLDFGEQWPLHGSHAYSTIL*L DLFCKKEE*DEIPYV*CFMLLWKS TTM*KKRLSYFLSWLNLNTHWISEN SGHCMVLM LTVRSCS
3071	8568	A	3330	3	267	FFFFLRDRFSLCGPGWSAV/VQS*LT VNS/TFLGPSNPPLSLWSSY/DVR/R MPANLS*FFRS*/SLAMLP RPVLKSW PQAIFLRHAPKVLGVEV
3072	8569	A	3331	3	269	FETESH SVTRLECSG/TILAH CNTCL PGSSNSHASASQVAGIAGEHHHAQI IFIFLVETGFHHVGGAGLELLT*VIC LPRPPIVLGLQA
3073	8570	A	3332	1	299	FSLIKISMMLLMKMEK*NLQFIW/KP RRLQIAKARLNASSSSSSSSSSSSSS SSSVVWYWHKKRHIDHWNRLNS NINRHICSQILTKVPGANTKDHP
3074	8571	A	3333	3	261	RQDLSLCHPGWSAVVQS*LIALTS* \VKQSTYLRHPTSWG*RCVPPCPAN FCFFCRDRIL/TISPRLVSWAQVIELP QPPKVLGLQV
3075	8572	A	3334	3	290	VDFFFFFFSRNSNVLSHRLECSGTISS HGNLCLLGSSDSPASASQVARITGV HHHTQLIFIFLIETGFRHVDQAGLDL LT*VILPPQPPKMLGLQA
3076	8573	A	3335	3	358	
3077	8574	A	3336	76	386	VLPPPSSPALHSPAPPSTCPYLPGA/P PPLLPPCAGRSPFAAAAPHCPAPCA PRH*GSR*LESPAPQGPQSRARMP AWPLPPAPPTDPTAPPAPRSHWPAA PPT
3078	8575	A	3337	66	381	VLPPPSSPALHSPAPPSTCPYLP GAL PPLE/GPPSRRPPRTFIGNPGGQGPG E VSPIVLRSPSQPH*PGNQGPCSSQP PGSPRSEHGC*HRCWALYQQEKP APS
3079	8576	A	3338	1	303	KDRFSFCGPG*SAVTQLNLTADP*T PALK*SFHRSLLSRWDYRRAPPYLA N*KKFL*SRGLAMLPRLVFHSWPQ VILSPLSRARATAPSFPLFSSKDEPI
3080	8577	A	3339	2	212	RFSCLSLPSSWDMHHSPG*FFIFLVE TGFAHVGQAGLELPASNDPPASTS QSVVITAMSHRRALVPIF
3081	8578	A	3340	2	273	RRSSTQPPRLQCSGTIPAH CNLHPPS PSDYPAPASRVAGTTGARYHHAQPI SAFSSAETGFHHAGQDGLKLLT*AI HPPRPPKVPGPQA
3082	8579	A	3341	135	494	IKHRGMGLDFAVLPLQVKWPPDPG FLECIHFLQLKGTIPDLKERAPVTSR VEPGHAGHC/TSYGQVCHL*GRC/V EKRKGIACDCAFSMYDGLFCSNSNS RADWSHCTVSGTYQHTENSIMS

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3083	8580	C	3342	71	217	MPQPNFFVLLVDRGFHHVDQAGLD LLTSSDSPALASQSARITGVSHHA*
3084	8581	A	3343	1	106	
3085	8582	A	3344	2	1926	MAAAAVDSAMEVVPALAEAAPE VAGLSCLVNLPGEVLEYILCCGSLT AADIGRVSSTCRRRLRELQSSGKVV KEQFRVRWPSLMKHYSPTDYVNW LEEYKVRQKAGLEARKIVASFSCR FSEHVPCNGFSDIENLEGPEIFFEDEL VCILNMEGRKALTWKYYAKKILYY LRQQKILNNLKAFLQPPDDYESYLE GAVYIDQYCNPLSDISLKDIAQIDS IVELVCKTLRGINSRHPSLAFKAGES SMIMEIELSQVLDAMNYVLYDQL KFKGNRMDYYNALNLYMHQVLIR RTGIPISMSLLYLTARQLGVPLEPV NFP SHFLLRWCQGAEGATL\DIFDYI YIDAFGK GKQLTVKECEYLIGQHV T AALYG\VVNVKKVLQRMVGNLLSL GKREGIDQSYQLLRDSL DLYLA\MY PDQVQLLLLQARVYF\HLGAILPEKS FCLVLKVL DILQHIQTL\DPGQHGA VG\YL\VQHTLEHIL\ERKKEEVGVE VKL\RSDEK\HRDV\CYSFGFIMKA* RGMG\Y*LC*FYGWDP TWHGSGHE LDSRNMNV\HSLPHGHHPFY NVL VEDGSCRYA\AQENLEYNAEP\QEI SH\PDVGRVYSQRFT\RTHYIP\NAEL \EIRYPEDLEFV\YETVQ\NIYKCKRK ENIE
3086	8583	A	3345	59	339	
3087	8584	A	3346	1	342	FCSCQPQAGVQRRDLSSLQPLPPAGF K*FSCSLSPSSWD\YRRPPP/RPGYFL YYLVEIGFCHICQAGLKLLRSGDPP AWASQSAGITGMSHHAQPHLLLLN CLLPFLGIPLHSPL
3088	8585	A	3347	1	294	ETESHVTRLECSGTILAHCNLHLP GSSNSPASASQIAGTIGARHHTWLIF VFFVEMGFHHVGQTLELPGLK*SAC LKPLKVLG*QAGVQRHNLGSLQPPP PRFKQFSCSLSPNSWDHRCTPPHLA NFCIFCRDGFPPCWPDSRTPWPQVI CLPQASQSAGITGVEPLQPQRSYP
3089	8586	A	3348	2	268	EAESHVA\RLCSDAISAHCNLR LP GLSNSPASASRVAGIIGACHHDWLI FVFLVETGFCHVGQAGL/DNS*PQVI HPPRPPKVLGLQA
3090	8587	A	3349	3	444	FFFEIWSGSVA\RLCCGGTIF\AHCNL RLLGSSHPTAS*VAGTKGTCHHV QLIAFFVDTGFHHVARLVLS* TQ AICPPRPPKVLGSYASITAPGPTFFFL TIILGVQVDKRFYGNLTRKDIQKLG NYVWEGLELLSPQKFMLKP
3091	8588	A	3350	1	318	FFFFFLRQSFALAQAGM/QWHD LGS LQPPPPGFK*FSYLSLPSSWDYRYVP PRPASFEFLVEMGFHHVGQAGFELL TSSDPPASASQSAGIIGVS*RTQPGT NDFL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/770,160	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
3092	8589	A	3351	16	848	VGSGLVSAQQTGCGPGNPSPPGSVS GAMELRVEPAARGQGS LGDPPAIVL LPGALELPIPGSFFASQSCSPWVML QLTFPHF*LLLAPLPVSPAPTGWDL VSQLOPVSSPRGRCPRSGPDLLPLH GQPFHSSSFSSSMQASGEVQPCPS RSSGS/VKGGQLTVEPESGPGALKC EALAWLRG*GLLGHS GFAGSVPEV TPGSPHVLNP\GRGLPCAGYCLHPA AL*GMVFGLPPLPGSSLV*PTIWLLT LKSPTS*GIP*HRKPWVFSVMHKVG WKV
3093	8590	A	3352	1	293	VLROGLSLSTQDRMQWHYDSSLQP *TPGLK*SSASQVAATTGTCHHTWL TFLFVF/DFWRWSL/NCIAQAGLE/PP GFK*/CPKHWDYRHEPGMPGWVFLI S
3094	8591	C	3353	127	345	MFDFELELFXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXLI AQGECLYVWKINSQHSVFKLKLL CF*
3095	8592	A	3354	2	215	AHCNLC L PGSSD SPASASRV TGITG VHHRTQLIFVFLEEMGFCHIGQAGL ELLT*VICLPRPPKVLVLR T
3096	8593	A	3355	164	311	QRSQGIWVWRFIRRF*II
3097	8594	A	3356	1	381	YINVIIHFVHINCWRECQKVQLT*K\ SF*QFLKNLNIHLSYDLAIPVLGICPR EMKAYVHIKTCK*MLIAAFIAQN WNQ/P/RCPSTGEWYKQTVIFYTMQ HYS AIK NNE*LIHKTTWKNLKEARA SGV
3098	8595	A	3357	2	764	RTLHLFAGGCGGTVGAIFTCPLEVI ETRLQSSRLALRTDYYPHVHLGTIS GAGMARPTSATPGLFHGLKSILEKE GPKSLFRGSRPNLVGVAPSRAVYFA CYSKAKEQFNGIFAPNSNIVHIFSAG SA/GVRGSKQMNTLQCARYVYQTE/ GIRGFYRGLTASYAGISETIICFAIYE SLKKYLKEAPLASSANGTEKNSTSF FGLMAAA/GSF*GLSSCIAY/PHEVIR TRLREETSTSF CQTARLVFREESYL PL
3099	8596	A	3358	155	875	DQHPVTPGLFQVLKAVYFACYSKA KEQFNGIFVPNSNIGHIFPAGSAAFIP NPLMD\PIWMVKTRMQLEQKVRGS KQMNTLQCARYVY/HDRKAFFGGFY RGLTASYAGISETIICFAIYESLKKY LKEGPLAFFGKWD*GKIPQVFLDL WPAAALSKGLA SC MAYSHTEVH* GRRL\REKGHPSTKSF CPERRALGVP GEEGYPCLFIEGLFAPSFIRQIP\NTA\ IVLGYLWRLIVYLLGRP
3100	8597	A	3359	1	281	FFFAPETESYSVAIRLECSGTILVHCT LCLPGSSD SPASASQVAGTTGACHH TWLILVILVEIGFHHVQGAGLG/IS*L QVIRPPWAPKVLGIIG
3101	8598	A	3360	135	218	TLQFTSLISYSFCQSWGSKVPLSLPP

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						P*/PANF/*FLVETGFLQVGQVGLKL LISSDPPTSASQSAGITDVSHCAGPE F
3102	8599	A	3361	198	390	
3103	8600	C	3362	5	316	MPAKLFLMVEFSGVACSSAKXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX YRLLFSPCHSF*
3104	8601	C	3363	186	323	MPWLEHTAHFPDKAWITRMALLRN GIVPYDSL PWITLGRWPNGGT*
3105	8602	A	3364	2	3096	TPRLQSNTRALYQYCPPIPIINYPQLE NELFCNIYYLKQLCDTLRFPDWPIK DPVKLLKDTLDAWKKEVEKKPPM MSIDDAYEVLNLPQQGQPHDESKIR KAYFRLAQYHPDKNPEGRDMFEK VNKAYEFLCTKSAKIVDGPDPENIIL ILKTQSILFNHKKEDLQPYKYAGYP MLIRTITMETSDDLFSKESPLLPAA TELAFTVNCSALNAEELRRENGLE VLQEAFSRCVAVLTRSSKPSDMSVQ VCGYISKCYSVAAQFECEKITEM PSIHKDLCRVLYFGKSIPRVAALGVE CVSSFAVDVFWLQTHLFQAGILWYL LGFLFNVDYTLSESGIQKSEETNQQ EVANSLAKLSVHALSRLGGYLAEE QATPENPTIRKSLAGMLTPYVARKL AVASVTEILKMLNSNTESPYLIWNN STRAEGLEFLESQQENMIKKGDCDK TYGSEFVYSDHAK*LIVR*IFVRVYN EVPTFQLEDPKAFAASLLDYIGSQA QYLHTFMAITHAAKVESEQHGDRL PRVEMAFEALRNVIKYNPGSESECI GHCRCIFSLLRVHGAGQVQQV/AL* EVVNIVTSNQDCVNNIAESMVLSSL LALLHSLPSSRSAWFWETLYALDIR VQKLIKEAMAKGALNHLLDMFCNS THPQVRAQTAELEFAKMTADKLIGP KVRITLMKFLPSVFM'DAMRDNPE AAVHIFEGTHENPELIWNDNSRDK VSTTVREMMLEHFKNQDNPAN WKLPEDFAVVFGEAEGELAVGGVF LRIFIAQPAWVLRKPREFLIALLEKL TELLEKNNPHGETLETLTMATVCLF SAQPQLADQVPPLGHLPKVIQAMN HRNNAIPKSAIRVIHALSENELCVRA MASLETIGPLMNGMKKRADTVGLA CEAINRMFQKEQSELVAQALKADL VPYLLKLEIGIGLENLADSPAAT*GS ELVKALQGO*LEVLQYGENRVNEIL C/RFLSVWECLSKIQEHLDFIS*/ESH TAGYLTGPGVAGYLTAGTSTSVMS NLPPVDHEAGDLGYQT
3106	8603	A	3365	1	358	NRLNATPIKIPTAFFAEMDKLNPFL KLNS*NLYRNARDST*PKQY**RKR TWINKNNAGGLILPYCILLQRNNNQ DIG*KNVLKIM**WHRDRH\DQ*NR NQSPEIN*YGKLFSTVL

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3107	8604	A	3366	2	40	LPRLKQFS\CLSLPSSWDYKR\RPC PANF/SVFLVETEFYHVGQAGLELFT SSDLPTLASQIAGITGVSHCAWPE*AS
3108	8605	A	3367	1	223	IIVKKWKQPKCPPTDEWINKMWDI QAIEYNLAI*/DKVVIHATTCMKLEN IMLSERSQLQRATYCNDIAIYIKNPE
3109	8606	A	3368	307	332	TTYHFFF*TESHSAQAQAGHWRDLS SLRPPPPGFKPFSCLSWDYRRTPPH PANFLAFLADTGLHHAGQAGLKLL TSNDPPTPASQSAGTTGVSHRAQPF FSELPITFFSL
3110	8607	A	3369	3	411	QTLPSATVSPEQAGAFPLALHSAQE SLGPAQTVPGSTGPPQPAPSGPGPPG EPG*ERLCASHKAFISHKQSH*SPO* PFQGRFADFPGYKQQTRPGHT/GQK GLRGPRQTLSLTSQPTACSENSQG SQPSPKRTLS
3111	8608	A	3370	3	166	EESCSVVQGGVQWCDLS*LQTLPP\ GSSNFCASASRVAGITGAHHHAQL KKKMLF
3112	8609	A	3371	4	312	FLR*SFTLIVQAGVQWRYLGSLOPP PPGFKRLSCLSLPSSWDYRHVPP/*P GYFFVFLVKMGCLHVGQAGPKLLT SGDPAASASQSAGITGPHRTWLRS FLI
3113	8610	A	3372	3	282	FFFETGSNSVAQAGVQWCNHSRLR PRPSG\SSDPNSSSQVAWTTGVHH TQLLFKFFCKDEVSLCFPDWSQTV* RVEHIRDEYETTQHCLYPSN
3114	8611	A	3373	1	164	ETEFRSVAQAGVQWRDLGSLQPPPS GFK*SSCV/SLPSTWDYRYMPPCPA TLLNT
3115	8612	A	3374	1	114	ARAEMLIVQYILPRLTHCAIFTILFIF SLLT*VMLLSS
3116	8613	A	3375	363	1246	DTEIQICYEPEYGGKKYCTKQSR YVSWTTHFSSSFIDQSLLSESMA*KS TAPHSSDF*DFLT*KT*NLFFLRSL ALSPQAGVQWRDLGSLQAPPGFTP FSCAPASSWDYRHLPPCANFFVF FLVETVSIFVFTVLGMVSI*PQ/CD PPTLASQSAGITRLSHRARLCFVF* KKRNAREGGRRLLTIKADFLIFFSF FEMESCSVSKAGVEWHGLSSL*ALP HRFTPFSCLSLLSSWDYRRPPQLA NF\CIFSRDEVSPC*PGWSGSPDLVIH LPWPPKVLGLHA
3117	8614	A	3376	3	324	DRISLCCPGWSAIVQSQLTAA\SPLG LKQSFYISLPSS*GHRLAPLHPANIF GFPL*KWGLPMLPMLVLNSWAQVI LPKCWGLQASATVPGLFINFYDYIM DQSSFN
3118	8615	A	3377	3	673	RWSHSVTAQAGVQWRDLSSRQPPVP GSRDSPASAS*VAGTTGTHHAQFF FFFFLRRS/LSSV/SQDGVQWHDH SLQVPVPGFKQFSCLSLPSSWDYRC AAPRPANFFVF**RRVFSTLARL VSI

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						S*PCDLPTLASQTAGITGVSHCTQLA KFCIFS*DGVCHVGQAGAVLILCLF LHSHKINMFSPHCTPASTVYSHLPQ RPTKRRLYIRWRWERTWPANAEL
3119	8616	A	3378	2	323	RRSFTLVAQAGVRWHILGSLQPLPP GFKRFSCLSLPSGWDYRLMPPCPAN F*FLVEMRFHHVGQAGPERLTSGD LPA*ASQSAGITGVTATPSQYKLCSL IIMKLN
3120	8617	A	3379	1	311	DFFF*ETASHSVTQAGVQWCDPSSL QPPPPVFKQSSCLSLPSSWDYRHVP PCSVDT/CISILLIPFLRSGE*SPLLLS WSSCDLGQGTAPLGFWFPMGKARP V
3121	8618	A	3380	3	404	PCLANFF/VFFVETGTHYAA*CGLRL LGSSALPV*TS*SAGIIGMSHCTC/LQ ITLLKTESHS\VAQAEVQWHDLGSL QPLTPRFKRFSCSLPSRWYRCAS PRLANFCTFKFLYFLVETGVSPCWP GWSGTPDLR
3122	8619	A	3381	739	1003	NLYLNY/CFF*IETGSHSVTQSGMQ WHNLASLQRLPLRLKQTSLSLSS WDCRHMPNLA/NF/CVLRDRKISPF CPGWSQTPGLKQIEF
3123	8620	A	3383	1	299	ETESGS\LPRLCSGTISAHCNLRLL GSSNSPVAS*VAGTGACSHAQLIF VFSVESGFRHVGQAG\LN*PQVIHP PRPRKVLGLLPVSHHTRPISFFL
3124	8621	A	3384	12	336	SPVQL*F*LFLVFC*LWSWSAVVYL GPLGTPSADAHT/AGLSKTPPHWAA RARLDDVFSRLTFSSHSLNMELVQD LTASAPMYSSTSRDPP/CLGLPKCW DYKREPPRAH
3125	8622	A	3385	2	318	FLSSHLFLTQSL/DSVAQAGVQWHN LGSLQAPPPGFTPFSCSLPSSWDYR RPPRPANFF/VFLVKTGFTVLARM VSL*PHDPPASASQSAGITGVSHW CPANN
3126	8623	A	3386	1	325	ASTAQAGVQWPAAQLQTPPPGFTF FSCSLPSSWDYRRPPSPANFLYF* *RRGFTMLARMVIS*PCDPPASSSQ SAGITGLSHRARPVIRILRRAGRNT IGGLD
3127	8624	A	3387	3	530	RQSL/DSVAQAGVQWRNLGSLQVL PPGFMPFSCSLPSSWDYRRPPRPA /NFFVFLVET/GFTRGSIS*PRDPPAS ASQSAGITGVSHRTRPKDCYS*RCS YCKVLRCLFRKLLTGEEAPMP/PF* RQS*CLTSVTLSSAWRSICYDRLVDI QFKILFMKTKLPLFFSQNELYFIIL
3128	8625	A	3388	3732	4979	NFVFLYLRELSSQAKSLTSHPLSNFF FKRQGLAMLPRLECS/GLFTGAVIA HYSLQLLGSSNPASANQVAGTTGA CYHAQSIF*S*NFFIFLSSVS*NLCLN QNAGFYLFFYF*Y*MCRYASSTFLT NELCGKKK*TLSIEIKSIFKHVLY WLFGLVFLNLLLLLPVLYNEHRKIL

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						E*GRKVVYQDILPGFGCKF*RMVFLIF VHIL*APRYPSQ*GKLIPCI*LLYL*W LSPSPSTVSLAFHDKFVNLHFYIDMS LFHQACSIKMIFLKDVNCA*LIGYI LFCFFFFFFFRLRCGV\SVAQAGVQ WRNLGSL\QAPPPRFMPFS\CLSLPS SWDYRRLPPRPANFFFFFLDF**RPL VFL/SFTVLARMGL\IS*PRDLPTSAS QSAGITG\VSHHVQLPYFVLNKFTV LGSNSGF
3129	8626	A	3389	1	585	AFFFLRQGLALV/THAGVQGDYS SLQPLPPGLKAILLPQPECWDYRC MSPCLAN/FFVFFVAMGFRMLPTL/ VLELLGSSDPPTLAS*SAGITGVSHC TWPLFI*VWSFGKV*ELS*HRFCISSF IHI*KFWKRWG\SLCSPGWS*TAGL KRSS*LGLPKYRDYRHEPPCPAFFTF LLECYDLHILLICSHFYLR
3130	8627	A	3390	3	459	QPGVQWHDLSMQPPPPRFKCFSC SLL/SS*DYRCPAPMPQPNFCIFI*RY GFT\MLASLVLDL*L*VIRPPWVSQS AG\ITGVSHHTWARDRADF*MGVW ASPIARVPRGQQVRSCQPL*GS/WDP ET*HNGHFHFWIKQSEPPIFKGRR*N P
3131	8628	A	3391	1	258	FFFKTDSCSVA\RLYESGAISAHCNL RLPGSSDSPALAPQITGTTGMC/RS* FFIFLVETGFHHIGQAGLKLLTLWIH CPPKMLGLQA
3132	8629	A	3392	3	316	VAQAGVQWWYLSSLQPPPPGFTSC LSPQCSWDYRHAPPCSANF*FLVET GFHHDGQAGLELLTSSDPALASQS AGITGVHPPAPNSSCLHTDKRVHT WHKPS
3133	8630	B	3393	49	279	SSSDSDDEEKKHEKLKKALNAEEA RLLHVKETMQIDERKRPYNSMYET REPTTEEMEAYRMKRQRPDDPMAS FLGQ*
3134	8631	A	3394	2	357	
3135	8632	A	3395	1	1765	MSATVVDAVNAAPLSGSKEMSL PKKMTREDWRKKKELEEQRKLGN APAEVDEEGKDINPHIPQYISSVPW YIDPSKRPTLKHQRPOPEKQKQFSS GEWYKRGVKENSIITKYRKGACEN CGAMTHKKKDCFERPRRVGAKFTG TNIAPDEHVQPQLMFDYDGKRDRW NGYNPEEHMKIVEEYAKVDLAKRT LKAQKLQEELASGKLVEQANSKPH QWGEEEPNSQTEKDHNSEDEDEK YADDIDMPGQNFDSKRRTVRLRI REDIAKYLRNLDPN SAYYDPKTRA MRENPYANAGKNPDEVSYAGDNF VRYTGDITISMAQTQLFAWEAYDKG SEVHLQADPTKLELLYKSFVKKE DFKEQQKESILEKYGGQEHLDP APPA ELLQAQTEDYVEYSRHGTVIKQ QER AVACSKYEEDVKIHNHTHIWGSY W KEGRRGNKCCHSFSKSYCTGEAG

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						KEIVNSEECIINEITGEESVKKPQTL MELHQEKLKEKKRRKMKKKKHR KSSSDSDDEEKKHEKLKKALNA*E ARLLHVKETMQ\DERKRPYNSMY *TSRPIEEEMEA YRMKRQRPDDPM ASFLGQ
3136	8633	C	3396	106	426	MFLKEPVXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXRLXXXXG*
3137	8634	A	3397	25	435	TKYWLLFFLILPFFWRRSRVT QAGGQWHDLSLQPPPGFKQFSC LSLPSSWDYRRAPLHLANFYIFSRD/ MDFTMLARLVNSRSQ/CDPLASAS QSAGISGKSQHTRPVLVLLKTYTNS H/SF*VKGLGWEFIL
3138	8635	A	3398	3	320	KTESHSVTOAGAQQDLSSVQSP PGFKRFSCLSLPSNWDYRRVPLHPA NFL*/FLVETGFHHAG*VGLELLTSG DPPTLASQNAIGTGVSHCARPIVFL YLITSR
3139	8636	B	3399	70	199	XMQVTGFGRGQNHNVQGSTPTDAS PRRRDVCTAQTQDSKLVNS*
3140	8637	A	3400	198	397	TKNRNTLSRFLLEAPRVFGPPSP/RP PKP/ASGP*PIACPAGTHIPCGPYPC CHVGGGWPAQPLAALG
3141	8638	C	3401	164	313	MTLHFQELKSLKFYLNXXXXXXX XGGRFKGSLGGPKFTRACNVKAFL L*
3142	8639	C	3402	165	361	MVKFCANNQGKTKLIFMFFHKESHI IIGRPRAQREKKEKEEGNPNECLLD VSLRTGFSGHLPGRV*
3143	8640	C	3403	146	389	MTPISLKGRCRQLGDGKRCSLEDLA LIEGCPHAGRPPrKSTLEPAFGSPR CQDPVSAMCMTRSPANLDSAERQ APGLGR*
3144	8641	C	3404	157	404	MLSLTSSPLNQGVVSFVHAILKY QGCKPHFIKLSRXXXXXXXXXXXX XXKXXXXXXXXXXXXXXXXXXXXXP PAPSFLWGE*
3145	8642	C	3405	73	252	MHTPLLA WPGMAWCYRQPLSTPRL ILNYVKPRKMIFRTFAYIRLYLCTYF AVFHRRKWP*
3146	8643	A	3406	2	617	IYIFLKALNFCREVVPISPPKVRVLF KDSQVTSFPVPAL*KGQGLGYKT APYKEKTNLQARVNLGPSRGPLK RPPSSSSPNPNALLFIQTRVKLVNG KRPEATCLGRKASYSVRFSAAWDP PAGCAQPPTVSPDTPKQVSRTKAR N*TKNRNTLSRFPS*KLPRVSGPTQV PNPPKPRSRGD*QRTFPPVPDGNPV LN
3147	8644	C	3407	129	281	MSSHARVNLGPSKDPLKRPXXXXX XTQRQLFKTFINRCLQVDFFEKIKL *
3148	8645	A	3408	1	303	QAGVHWRNLGSLQPPPPPTLRRFS



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						CLSLPSSWDYRHPPSHPANFFFFLL LVEARFHHVGQGGLELLTSSDPSTS ALQIAGITGVSHRAEPAPFFK*CFG
3149	8646	A	3409	3	1039	QQPFVNPALPPGYSTGLPYTGMGP SAFQYGPTMFVPPASAK*HGVNLST PTPPFQQ/PVGYGQHGYSTGYDDLT QGTAAGDYSKGGYAGSSQGTKQV CRFWGLGKGVS SVSSTTGLPDMTG SVYNKTQTFDKQGFHAGTPPPFSLP SVLGSTGPLASGAGPWLCTPTIPTH LASPPAAPLTAAAPPSAGCTEWLG SAQPAQLPAAQVSSLQTCRLQLSIL GQLNPGERGGAGAKAYPGQERTTR ARIWEPKCPFSKNSPTCVSHALCGE SASPDWATVCNVFMYVFVNVIEVW GGVGGWRQMLARSAPPHSKPPSPN CSKISTPNPHLPFRSFLHSLATAQWA H
3150	8647	A	3410	2	344	LRQSVSLLPRTQAGVQWPNLGSLO PPPPRFQRFSCLSLLSSWDYRHAPPC PTKF/VFLVET/GFTMLARLVIS*PH DLPALASQS/AGITGVSHCAQHGV YIRCFRELA\SYSIL*SLQ\WPHV*SL AYSIL
3151	8648	A	3411	52	174	
3152	8649	A	3412	2	692	RPP/QADPPRCWPR/PLGLGGCVPW GAGRLRRGHGPEPDSPFRRSPPRGP ASPQR*PPRPDPWPPRQASPRCRPT D*SRTAGRTTDPQEEAVGGQGSPSR GG*APSNSEPPPLYGSGPLDSAFSLG TAFRKTLRIDLTSQSRPPHRSLSLYS GKGLAPGELADALNFLIYPTDFDGL HCTIGDVATGPWRCNQIKRRKHCQ LGKSKLIYFFFPPTPSPAKNFFSRY RHHS
3153	8650	A	3413	3	367	MLNYPLDFHPSFFVGFFFFEMESRS\ VARLEVPGVVISCHLCLPGS\SDS PASASQVAGTTGVCH*AQLIFVFLV ETGFHHFDQDGLDLTS*SVHLCPS KCWDYVIHPPQPPKVLGLQA
3154	8651	A	3414	1	595	MGIHVGQASLELLTSGDLPASASQ GRGVRLYYIEGRSSQSASVTALFLS SLPTVTSAMAGTRPPSARSHQTLQA CRAQKTKTRMSSI*GTGAKHQASSP GKAPLSTSPYFWKPSLQTSPCSGSR SLWASLPSLAALFLCFWQDAT*RS STTRSSLPSWPSRSTRALRLSTS*PE CAPSA*ASSKAGERSTGDRL
3155	8652	A	3415	259	941	PVSWSLNSCRFFFF* DQSLPSVV/Q AGSGQ*RNLDLQPLASRFK*FSSS RL\SSWDYRHMATMARLIFLVE MGFTMLARLVNFLTSSDPPTSAPP KWLGLQGVKPNTRAVGFN**LGY SIILYHSNSPGTDLVFIYLFYLF RQEONSAAQARVQ*WHNLGSLQSP PPGVH*FLCLSLPSSWDYRCAPPHQ ANFFIFSRDGVSPCWPGWS*TPDLR
3156	8653	A	3416	165	289	ISGLSGLYHIDRLLIVCNCKQKPTYS

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						*NPGLSW*TDFKCLI
3157	8654	A	3417	3	796	PGPRAPPIRCSPLRSAAPRRPST*SAA AWPASAAAGFCPCFYASAPSTSSR WPAAAGCSLATAKTSSRVVEMLP RRAAAAGSYEGRAVRA/VMEYAW GAAAA/DHALSVASSILVILFHPLLL RPLCWTPECLSS*EVIGLLALAAV FQIISLGNLPREVHPDLHPSCQAPLS LTSITGAYGFGVGQPRIILTRLCLLL LAASPTTEDGPSGAMPSPGTSTHLP NLGMKCGRKSLPAEMGLPEGRKLF LPGGLWNPIFWPVFHHY
3158	8655	A	3418	2	603	GFFFFKIVLIQDLFPSTPLPSSVHSGD YGDSDQDPSGTRNTFRRCSPSPFPS CQLPRPEATHANTRNPPSPHLLSF PHQSSEP*EGVKSLFEEA*KWGEMA ITP*PTPLWR*LWRTPNSFPLSGQPF STP\RPSPVSPIQPKTKHVQQHPPAS T*KTGSVPTSLTPSTGVLGEWPPEDP AKGLMPEGKEEQKAFGP
3159	8656	B	3419	34	375	MLLGRLTSQLLRAVPWASLPRKGA QLELEEMLVPRKMSVSPLESWLTA RCFLPRLDGTAGTVAPPQSYQCPS SQIGEGAEQGDEGVADAPQIQCKN VLKIRRRKMNNHKKYRKL*
3160	8657	A	3420	2	361	YSTSPAGQVGRSPSQGGPAGAGG DAG/TPGRCPSAPWRAGSRPAASCP DWIPG/PAGHVAPPQSYQCPSQIGE GPGGTPETQADQVRERPEAHLAEG GAKGSPRRAGRPPRSTCGANESG
3161	8658	A	3421	1	417	RITAATGGKGGARLICPAGR/CLGV CQPSGASFSPAFSQMPSSPCSAPSPI WLGGHW*DCGGAT/CPCGPGIQSG QEAAGREP/GSPGG*RTSSWGPASPP APAGPPCEGERPPYLGRPAMCKG ARRPGCPALQRRAKAGGR
3162	8659	A	3422	31	756	GRRALRQAGPGSSREGPGARQRDS RGGEPGEGAGLPVLGPFASERDTA RVGGLGASGRELCWKQSPPCGLGW RREKGSEGRGGTRRPSGPPATTEG AAA*PE/PGTCVPAPLGPAGPPPTDH APGAPDFPAVEGRSLGRRPPALAQ S/P/GSAGQPGRLSPFTHA/QPAGPGRR GLSPSQGGPAGAGGDAGPQEDVRQ PPGELGSRPARFLPQTGLPGAGTC GLHRNPTQCPPSPDRGKGPQGG
3163	8660	A	3423	69	258	PRTNRCATNHTPANF*FFVETGFLH VAQAGLELLGSSSSPALAPKQLVTG ASHHTRPQ*NFLQ
3164	8661	A	3424	8	292	QSFLFLKTRYLLRHP/GWNTVAQ*Q LTVVTSRLN*SFHLSLPSS\WAI AVR MPPCPANFLFF/TRDRVSLC*PRLVS NTWVQMILLQPPEMLGLQA
3165	8662	A	3425	123	357	WGKRPGQGGRNPNWGPPLPGGK/PP KKGFLGPFPTGRFQSSPGL*KGPFL KGGP/QF*KPKPGSQNRVFKPKIWE TPLGN